

GenCore version 4.5
Copyright (C) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 07:05:25 ; Search time 5997.24 Seconds
(without alignments)
241.810 Million cell updates/sec

Title: US-09-451-527-88
Perfect score: 166
Sequence: 1 ctaagcttagccagcctac.....caacctcaaggagctcatt 166

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:
1: gb_estl: *
2: gb_est2: *
3: gb_est3: *
4: gb_est4: *
5: gb_est5: *
6: gb_est6: *
7: gb_est7: *
8: gb_est8: *
9: gb_est9: *
10: gb_est10: *
11: gb_est11: *
12: gb_est12: *
13: gb_est13: *
14: gb_est14: *
15: gb_est15: *
16: gb_est16: *
17: gb_est17: *
18: gb_est18: *
19: gb_est19: *
20: gb_est20: *
21: gb_est21: *
22: gb_est22: *
23: gb_est23: *
24: gb_est24: *
25: gb_est33: *
26: gb_est34: *
27: gb_est35: *
28: gb_est36: *
29: gb_est37: *
30: gb_est38: *
31: gb_est39: *
32: gb_est40: *
33: em_estba: *
34: em_estfun: *
35: em_esthum1: *
36: em_esthum2: *
37: em_esthum3: *
38: em_esthum4: *
39: em_esthum5: *
40: em_esthum6: *
41: em_esthum7: *
42: em_esthum8: *
43: em_esthum9: *
44: em_esthum10: *
45: em_esthum11: *
46: em_esthum12: *
47: em_esthum13: *
48: em_esthum14: *
49: em_esthum15: *
50: em_esthum16: *
51: em_esthum17: *
52: em_esthum18: *
53: em_esthum19: *
54: em_esthum20: *
55: em_esthum21: *
56: em_esthum22: *
57: em_esthum23: *
58: em_esthum24: *
59: em_esthum25: *
60: em_esthum26: *
61: em_esthum27: *
62: em_esthum28: *
63: em_estin1: *
64: em_estin2: *
65: em_estin3: *
66: em_estin4: *
67: em_estin5: *
68: em_estom1: *
69: em_estom2: *
70: em_estov1: *
71: em_estov2: *
72: em_estpl1: *
73: em_estpl2: *
74: em_estpl3: *
75: em_estpl4: *
76: em_estpl5: *
77: em_estpl6: *
78: em_estpl7: *
79: em_estpl8: *
80: em_estpl9: *
81: em_estpl10: *
82: em_estro1: *
83: em_estro2: *
84: em_estro3: *
85: em_estro4: *
86: em_estro5: *
87: em_estro6: *
88: em_estro7: *
89: em_estro8: *
90: em_estro9: *
91: em_estro10: *
92: em_estro11: *
93: em_estro12: *
94: em_estro13: *
95: em_estro14: *
96: em_estro15: *
97: em_estro16: *
98: em_estro17: *
99: em_estro18: *
100: em_estro19: *
101: em_estro20: *
102: gb_est25: *
103: gb_est26: *
104: gb_est27: *
105: gb_est28: *
106: gb_est29: *
107: gb_est30: *
108: gb_est31: *
109: gb_est32: *
110: gb_est41: *
111: gb_est42: *
112: gb_est43: *
113: gb_est44: *
114: gb_est45: *
115: gb_est46: *
116: gb_est47: *

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query %	Match	Length	DB	ID	Description
1	57.4	34.6	581	219	AZ305110		AZ305110 1M0005P05
2	37.6	22.7	1996	170	BF867977		BF867977 963095D02
3	37.2	22.4	918	170	BF868214		BF868214 963104H02
4	37	22.3	225	130	BB300252		BB300252 BB300252
5	37	22.3	830	231	CNS04M4J		AL296956 Tetraodon
6	36.8	22.2	719	143	BF033106		BF033106 601454522
7	36.6	22.0	782	227	B21994		B21994 F23G15-Sp6
8	35.6	21.4	1979	144	BF131613		BF131613 601820420
9	35.4	21.3	247	133	BB435254		BB435254 BB435254
10	35.4	21.3	860	231	CNS041Q7		AL270520 Tetraodon
11	35.2	21.2	639	171	BF967613		BF967613 602287495
12	35.2	21.2	1756	141	BE897251		BE897251 601437224
13	35	21.1	844	229	CNS0052P		AL056652 Drosophil
14	35	21.1	919	229	CNS006S5		AL065856 Drosophil
15	35	21.1	1018	168	BF718319		BF718319 EST92 mic
16	35	21.1	1101	229	CNS017RP		AL108415 Drosophil
17	35	21.1	1236	170	BF868213		BF868213 963104G06
18	35	21.1	1409	146	BF257317		BF257317 HVSMEF001


```
C 19 35 21.1 1690 171 BF975197
C 20 34.8 21.0 543 161 BE031946
C 21 34.8 21.0 777 143 BF034619
C 22 34.8 21.0 839 229 CNS004NB
C 23 34.8 21.0 902 146 BF317377
C 24 34.6 20.8 949 173 BG106666
C 25 34.6 20.8 1872 146 BF310467
C 26 34.4 20.7 1225 173 BG115260
C 27 34.2 20.6 335 148 BF421354
C 28 34.2 20.6 494 172 BG052316
C 29 34.2 20.6 608 214 AQ947792
C 30 34 20.5 213 169 BF840572
C 31 34 20.5 505 30 AV603278
C 32 34 20.5 911 217 AL197129
C 33 34 20.5 997 229 CNS005TE
C 34 34 20.5 1081 144 BF139436
C 35 34 20.5 1405 145 BF204710
C 36 34 20.5 1498 144 BF137829
C 37 34 20.5 1517 145 BF206910
C 38 33.8 20.4 279 132 BB399409
C 39 33.8 20.4 280 126 BB152910
C 40 33.8 20.4 300 131 BB346864
C 41 33.6 20.2 543 220 AZ387482
C 42 33.6 20.2 836 229 CNS017X2
C 43 33.6 20.2 1186 145 BF256669
C 44 33.6 20.2 1653 146 BF338185
C 45 33.4 20.1 491 102 AI819748
```

ALIGNMENTS

```
RESULT 1
AZ305110 581 bp DNA GSS 29-SEP-2000
LOCUS AZ305110
DEFINITION 1M0005P05R Mouse 10kb plasmid UUGCIM library Mus musculus genomic
clone UUGCIM0005P05 R, DNA sequence.
ACCESSION AZ305110
VERSION AZ305110.1 GI:10341800
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
```

```
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 581)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: P column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 581.
```

```
Location/Qualifiers
1. .581
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGCIM0005P05"
/clone_lib="Mouse 10kb plasmid UUGCIM library"
/sex="Male"
```

```
/lab_host="E. Coli strain XL10-Gold, Tl-resistant, P-"
/note="vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adapted DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of PWD42 (gi14732114|gb|AF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adapted mouse DNA was annealed to
adapted vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

BASE COUNT 169 a 139 c 153 g 120 t
ORIGIN

Query Match 34.6%; Score 57.4; DB 219; Length 581;
Best Local Similarity 76.9%; Pred. No. 6.5e-05;
Matches 70; Conservative 0; Mismatches 21; Indels 0; Gaps 0;

```
QY 46 tcttcattgctggcctccatggcgtctgttgatgtgctatgctctaccctg 105
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 491 TCTCTACATGGCTCTGGGCTCTGCTGGGTGACTGCTGCTGCTGCTGCTG 550
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 106 cctcgtgctgctgctcccgagccctgtg 136
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 551 CTTTGGTGTCTCGCGCCGCCAGGCCGCTG 581
```

```
RESULT 2
BF867977/c 1996 bp mRNA EST 19-JAN-2001
LOCUS BF867977
DEFINITION 963095D02.xl C. reinhardtii CC-1690, Stress condition I, normalized
, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
ACCESSION BF867977
VERSION BF867977.1 GI:12258121
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii
```

```
REFERENCE Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
AUTHORS Grossman,A., Davies,J., Federspiel,N., Harris,E., Hauser,C.,
Lefebvre,P., McDermott,J.P., Shrager,J., Silflow,C. and Stern,D.
TITLE Analyses of the Chlamydomonas reinhardtii Genome: A Model,
Unicellular System for Analyzing Gene Function and Regulation in
Vascular Plants; project phase 3
JOURNAL Unpublished (2000)
COMMENT Contact: Charles Hauser
DCMB Box 91000
Duke University
Durham, NC 27708-1000
Tel: 919 613 8159
Fax: 919 613 8177
Email: chauser@duke.edu
```

```
Location/Qualifiers
1. .1996
/organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, Stress condition I,
normalized, Lambda Zap II"
/note="Vector: pBluescript II SK-; Site1: EcoRI; Site2:
XhoI; This library, constructed by John Davies and Jeffrey
McDermott, combines cDNAs from CC-1690 cells grown to
```

Sciences Center
The Institute of Physical and Chemical Research (RIKEN), Gencom
3-1-1 Koyadai, Tsukuba, Ibaraki 305-0074, Japan
Tel.: +81-298-36-9013
Fax: +81-298-36-9098
Email: genome-res@rtc.riken.go.jp,
URL: <http://genome.rtc.riken.go.jp/>
Carninci, P., Nishiyama, Y., Westover, A., Itoh, M., Nagaoka, S., Saito,
N., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
Thermotranscription and thermotranscription of thermolabile enzymes
thermostabilization and thermotranscription for the synthesis of full length
cDNA. *Proc. Natl. Acad. Sci. U.S.A.* 95 (2), 520-524 (1998)
Itoh, M., Katsunari, T., Akiyama, Y., Shibata, K., Izawa, M., Kawai,
Tomaru, Y., Carninci, P., Shibata, Y., Ozawa, Y., Muramatsu, M., Okazaki,
Y. and Hayashizaki, Y.
Automated filtration-based high-throughput plasmid preparation
system. *Genome Res.* 9 (5), 463-470 (1999)
Carninci, P. and Hayashizaki, Y.
High-efficiency full-length cDNA cloning. *Methods Enzymol.* 300
19-44 (1999)

TITLE Characterization and repeat analysis of the compact genome of the freshwater pufferfish Tetraodon nigroviridis

High quality sequence stop: 489.

Query Match 21.4%; Score 35.6; DB 144; Length 1979;
Best Local Similarity 54.6%; Pred. No. 26;
Matches 71; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

/tissue_type="pancreas"
 /cell_type="Islet cells"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Site_1: SalI; Site_2: BamHI; cDNA library was
 prepared and sequenced in Mouse Genome Encyclopedia
 Project of Genome Exploration Research Group in Riken
 Genomic Sciences Center and Genome Science Laboratory in
 RIKEN, Division of Experimental Animal Research in Riken
 contributed to prepare mouse tissues. 1st strand cDNA was
 primed with a primer [5',
 GAGAGAGAGAGGATCGAAGAGCTCTTTTTTTTTTTTNN 3'], cDNA was
 prepared by using trehalose thermo-activated reverse
 transcriptase and subsequently enriched for full-length by the
 cap-trapper. Second strand cDNA was prepared with the
 primer adapter of sequence [5',
 GAGAGAGAGATCTCGATGATTAATAATTCGCCCGCCCCCCC 3']. cDNA
 was cleaved with XhoI and BamHI. Vector: a modified
 pBluescript KS(+) after bulk excision from Lambda FLC
 I.-Islet cells were provided by Hiroo Iwata, Institute for
 Frontier Medical Sciences, Kyoto University, Sakyo-ku,
 Kyoto, 606-8507 Japan, whose assistance we gratefully
 acknowledge."

prepared by using trehalase thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTCGAGTAAATTAATTCCTCCCCCCC 3'], cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FIC I.-tslet cells were provided by Hiroo Iwata, Institute for Frontier Medical Sciences, Kyoto University, Sakyo-ku, Kyoto, 606-8507 Japan, whose assistance we gratefully acknowledge."

cap-trapper. second strand cDNA was prepared with the primer adapter of sequence [5', GAGAGAGATCTTCGATGTAATAATTCCTCCCCCCCC 3']. cDNA was cleaved with XhoI and BamHI. Vector: a modified pBluescript KS(+) after bulk excision from Lambda FIC I.-tset cells were provided by Hiroo Iwata, Institute for Frontier Medical Sciences, Kyoto University, Sakyo-ku, Kyoto, 606-8507 Japan, whose assistance we gratefully acknowledge."

	a	96 c	43 q	62 t
acknowledge.				

1
 2
 3
 4
 5
 6
 7
 8
 9
 10
 11
 12
 13
 14
 15
 16
 17
 18
 19
 20
 21
 22
 23
 24
 25
 26
 27
 28
 29
 30
 31
 32
 33
 34
 35
 36
 37
 38
 39
 40
 41
 42
 43
 44
 45
 46
 47
 48
 49
 50
 51
 52
 53
 54
 55
 56
 57
 58
 59
 60
 61
 62
 63
 64
 65
 66
 67
 68
 69
 70
 71
 72
 73
 74
 75
 76
 77
 78
 79
 80
 81
 82
 83
 84
 85
 86
 87
 88
 89
 90
 91
 92
 93
 94
 95
 96
 97
 98
 99
 100
 101
 102
 103
 104
 105
 106
 107
 108
 109
 110
 111
 112
 113
 114
 115
 116
 117
 118
 119
 120
 121
 122
 123
 124
 125
 126
 127
 128
 129
 130
 131
 132
 133
 134
 135
 136
 137
 138
 139
 140
 141
 142
 143
 144
 145
 146
 147
 148
 149
 150
 151
 152
 153
 154
 155
 156
 157
 158
 159
 160
 161
 162
 163
 164
 165
 166
 167
 168
 169
 170
 171
 172
 173
 174
 175
 176
 177
 178
 179
 180
 181
 182
 183
 184
 185
 186
 187
 188
 189
 190
 191
 192
 193
 194
 195
 196
 197
 198
 199
 200
 201
 202
 203
 204
 205
 206
 207
 208
 209
 210
 211
 212
 213
 214
 215
 216
 217
 218
 219
 220
 221
 222
 223
 224
 225
 226
 227
 228
 229
 230
 231
 232
 233
 234
 235
 236
 237
 238
 239
 240
 241
 242
 243
 244
 245
 246
 247
 248
 249
 250
 251
 252
 253
 254
 255
 256
 257
 258
 259
 260
 261
 262
 263
 264
 265
 266
 267
 268
 269
 270
 271
 272
 273
 274
 275
 276
 277
 278
 279
 280
 281
 282
 283
 284
 285
 286
 287
 288
 289
 290
 291
 292
 293
 294
 295
 296
 297
 298
 299
 300
 301
 302
 303
 304
 305
 306
 307
 308
 309
 310
 311
 312
 313
 314
 315
 316
 317
 318
 319
 320
 321
 322
 323
 324
 325
 326
 327
 328
 329
 330
 331
 332
 333
 334
 335
 336
 337
 338
 339
 340
 341
 342
 343
 344
 345
 346
 347
 348
 349
 350
 351
 352
 353
 354
 355
 356
 357
 358
 359
 360
 361
 362
 363
 364
 365
 366
 367
 368
 369
 370
 371
 372
 373
 374
 375
 376
 377
 378
 379
 380
 381
 382
 383
 384
 385
 386
 387
 388
 389
 390
 391
 392
 393
 394
 395
 396
 397
 398
 399
 400
 401
 402
 403
 404
 405
 406
 407
 408
 409
 410
 411
 412
 413
 414
 415
 416
 417
 418
 419
 420
 421
 422
 423
 424
 425
 426
 427
 428
 429
 430
 431
 432
 433
 434
 435
 436
 437
 438
 439
 440
 441
 442
 443
 444
 445
 446
 447
 448
 449
 450
 451
 452
 453
 454
 455
 456
 457
 458
 459
 460
 461
 462
 463
 464
 465
 466
 467
 468
 469
 470
 471
 472
 473
 474
 475
 476
 477
 478
 479
 480
 481
 482
 483
 484
 485
 486
 487
 488
 489
 490
 491
 492
 493
 494
 495
 496
 497
 498
 499
 500
 501
 502
 503
 504
 505
 506
 507
 508
 509
 510
 511
 512
 513
 514
 515
 516
 517
 518
 519
 520
 521
 522
 523
 524
 525

21.38; Score 35.4; DB 133; Length 247;

ity 55.28; Pred. No. 23;

servative 0; Mismatches 56; Indels 0; Gaps 0;

[illegible][illegible]

CCCCCAC TGCCCTGACACTCTGGCCCCCTGTGGACCTAGCAGACCTGGGGAT 145

ctgcctcgggtggccttgccctcccgagccctgtgactccctcccaacc 152

AGAAGTGGGGTGTCATGCTGGGCCCCAGACCTTTGCCCCACCCCTAAGGC 205

.....

860 bp DNA 18-MAY-2000 GSS

in HIV-1 genome survey sequence PUC-ORI end of clone library C from Tetradon nigroviridis genomic cDNA

Primary & From recidivism in grovillars, yellowic survey

.1 GI:7992444

some survey sequence.

U. nigroviridis.

a; Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:

erygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;

Yygi; Ctenosquamata; Acanthomorpha; Eucanthomorpha;

nopterygii; Acanthopterygii; Percomorpha;

milliormes; Tetraodontidae; Tetraodon.
s 1 to 860)

Collins, H.; Jaillon, O.; Dasilva, C.; Fizames, C.; Fisher, C.;

L., Billault, A., Quetier, F., Saurin, W., Bernot, A. and

ach, J.

ization and repeat analysis of the compact genome of the
er bufferfish *Tetraodon lineatus*

her patternish relation ingrowners
hed

s 1 to 860)

collus, H., Jaillon, O., Dasilva, C., Bouneau, L., Fisher, C.,

.. Fizames, C., Wincker, P., Brottier, P., Quetier, F.,
and Wojciechowski, T.

... and Weissbach, J. ... the number estimate provided by genome wide analysis using

the number estimates provided by genome wide analysers using an *nlqroviridis* DNA sequence.

S81230.NIH-2 3', mRNA sequence.
ACCESSION BF718319
VERSION BF718319.1 GI:12017418
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1018)
AUTHORS Darling,T.N., Koh,B.B and Yancey,K.B.
TITLE Delineation of Genes Expressed in Human Epidermis by Large-Scale
Sequencing of a cDNA library from Laser Capture Microdissected Skin
J. Invest. Dermatol. 112 (4), 673 (1999)
JOURNAL
COMMENT Contact: Yancey, K.B.
Dermatology Branch
National Cancer Institute
Building 10, Room 12N238, 10 Center Drive MSC 1908, Bethesda, MD
20892-1908, USA
Tel: 301 402 1863
Fax: 301 496 5370
Seq primer: M13R
High quality sequence stop: 132.
FEATURES
 source
 1..1018
 Location/Qualifiers
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /clone="S81230.NIH-2"
 /clone_lib="microdissected normal human epidermis"
 /sex="Male"
 /tissue_type="epidermis"
 /dev_stage="adult"
 /note="Organ: skin; Vector: pAMpl; Epidermis from 20
 cryostat skin sections (8 um thick) was selectively
 isolated using laser capture microdissection. Total RNA
 was extracted, reverse transcribed, and directionally
 cloned using uracyl DNA glycosylase (Krizman protocol 2,
 see [http://www.ncbi.nlm.nih.gov/](http://www.ncbi.nlm.nih.gov/CGAP/info/libconst.cgi#protocol2)
 CGAP/info/libconst.cgi#protocol2)."
BASE COUNT 27 a 332 c 41 g 504 t 114 others
ORIGIN

Query Match 21.1% Score 35; DB 168; Length 1018;
Best Local Similarity 54.2%; Pred. No. 34;
Matches 71; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 24 ctgctgctcttccctcctcctcctgctggtcctggctccatggcgctcgtggttga 83
|| || |||| |||| |||| || |||| |||| |||| |||| |||| |||| ||||
Db 425 CTCCT 484

QY 84 ctgtggtcattgctcctcctcctcctcctcctcctcctcctcctcctcctcct 143
|| || || |||| || || || || || || || || || || || || || || || ||
Db 485 CTTTCT 544

QY 144 ccccaaccctc 154
||||| |||
Db 545 CCCCTTCTTTC 555

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:16:04 ; Search time 9342.78 Seconds
(without alignments)
429.360 Million cell updates/sec

Title: US-09-451-527-89
Perfect score: 272
Sequence: 1 tggccttgcctcccgagcc.....cagtgaaagcagccgagaca 272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues 2566470
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

1:	gb_ba1:*
2:	gb_ba2:*
3:	gb_ba3:*
4:	gb_in1:*
5:	gb_in2:*
6:	gb_in3:*
7:	gb_om:*
8:	gb_ov:*
9:	gb_pat1:*
10:	gb_pat2:*
11:	gb_ph:*
12:	gb_pll:*
13:	gb_pl2:*
14:	gb_pl3:*
15:	gb_pl4:*
16:	em_ba1:*
17:	em_ba2:*
18:	em_fun:*
19:	em_htgo_hum:*
20:	em_htgo_inv:*
21:	em_htgo_rod:*
22:	em_htg_hum1:*
23:	em_htg_hum2:*
24:	em_htg_hum3:*
25:	em_htg_hum4:*
26:	em_htg_hum5:*
27:	em_htg_hum6:*
28:	em_htg_hum7:*
29:	em_htg_hum8:*
30:	em_htg_inv1:*
31:	em_htg_inv2:*
32:	em_htg_other:*
33:	em_htg_rod:*
34:	em_hum1:*
35:	em_hum2:*
36:	em_hum3:*
37:	em_hum4:*
38:	em_hum5:*
39:	em_hum6:*
40:	em_hum7:*
41:	em_in:*
42:	em_om:*
43:	em_or:*

44:	em_ov:*
45:	em_pat:*
46:	em_ph:*
47:	em_pl:*
48:	em_ro:*
49:	em_sts:*
50:	em_sy:*
51:	em_un:*
52:	em_v1:*
53:	gb_sts1:*
54:	gb_sts2:*
55:	gb_sts3:*
56:	gb_sy:*
57:	gb_un:*
58:	gb_v11:*
59:	gb_v12:*
60:	gb_vt1:*
61:	gb_vt2:*
62:	gb_vt3:*
63:	gb_vt4:*
64:	gb_vt5:*
65:	gb_vt6:*
66:	gb_vt7:*
67:	gb_vt8:*
68:	gb_vt9:*
69:	gb_vt10:*
70:	gb_vt11:*
71:	gb_vt12:*
72:	gb_vt13:*
73:	gb_vt14:*
74:	gb_vt15:*
75:	gb_vt16:*
76:	gb_vt17:*
77:	gb_vt18:*
78:	gb_vt19:*
79:	gb_vt20:*
80:	gb_vt21:*
81:	gb_vt22:*
82:	gb_vt23:*
83:	gb_vt24:*
84:	gb_vt25:*
85:	gb_vr1:*
86:	gb_vr2:*
87:	gb_vr3:*
88:	gb_vr4:*
89:	gb_vr5:*
90:	gb_vr6:*
91:	gb_vr7:*
92:	gb_vr8:*
93:	gb_vr9:*
94:	gb_vr1:*
95:	gb_vr2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB	ID	Description
1	272	100.0	1302	7	AF244915	AF244915 Canis fam
2	176.4	64.9	1270	93	HOMILI3A	L06801 Homo sapien
3	176.4	64.9	1282	92	HSNC30	X69079 H.sapiens i
4	176.4	64.9	1290	10	I34548	I34548 Sequence 1
5	174.8	64.3	417	88	AF043334	AF043334 Homo sapi
6	174.8	64.3	1297	9	A29948	A29948 Coding sequ
7	174.8	64.3	1297	10	I58488	I58488 Sequence 15
8	174.2	64.0	343	7	AF072807	AF072807 Bos tauru
9	165.8	61.0	384	9	A29950	A29950 Nucleic aci
10	165.8	61.0	384	10	I58489	I58489 Sequence 17
11	165.2	60.7	336	9	A29931	A29931 Sequence co

12 165.2 60.7 336 10 158494 Sequence 24
13 164 60.3 425 9 AR027065 Sequence 4
14 164 60.3 425 10 186198
15 164 60.3 4410 9 AS2326
16 164 60.3 4410 9 AR027062
17 164 60.3 4410 10 186195
18 163.6 60.1 336 9 A29930
19 163.6 60.1 336 10 158481
20 128 47.1 447 10 158495
21 128 47.1 1207 94 MUSS7CPE
22 128 47.1 1212 10 134549
23 117.2 43.1 443 94 RATIL13A
24 106.2 39.0 213343 78 AF276990
c 25 71 26.1 3714 93 HUM11DC99Z
c 26 71 26.1 4600 93 HUM11L13B
27 71 26.1 4740 93 HSUI0307
28 71 26.1 5670 93 HSU31120
c 29 71 26.1 50282 85 AC004039
c 30 71 26.1 78469 75 AC074127
c 31 70.6 26.0 3395 93 HUM11DC98Z
32 70 25.7 3520 7 BTA132441
33 69.6 25.6 78469 75 AC074127
34 51.6 19.0 4376 94 MUSIL13A
c 35 49.4 18.2 142732 88 AC084392
c 36 49.4 18.2 159500 94 AC005742
c 37 49.4 18.2 237823 66 AC020886
c 38 40.8 15.0 38390 3 SC2H12
c 39 38.8 14.3 34750 2 AP002998
40 37 13.6 39739 3 SGD16A
41 37 13.6 51440 12 AB025632
42 36.8 13.5 185300 2 AP000063
c 43 36.4 13.4 1091 94 AB015206
c 44 36.4 13.4 1122 94 MMU18723
45 36.4 13.4 2437 3 SAAJ3310

ALIGNMENTS

RESULT 1
AF244915 1302 bp mRNA MAM 16-OCT-2000
LOCUS AF244915 Canis familiaris interleukin-13 mRNA, complete cds.
DEFINITION AF244915
ACCESSION AF244915
VERSION AF244915.1 GI:7528273
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1302)
AUTHORS Yang, S., Borroughs, K.L. and McBernott, M.J.
TITLE Canine interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein
J. Interferon Cytokine Res. 20 (9), 779-785 (2000)
JOURNAL 20485146
MEDLINE 11032397
PUBMED
REFERENCE 2 (bases 1 to 1302)
AUTHORS Yang, S.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation,
1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES
Location/Qualifiers
1..1302
/organism="Canis familiaris"
/db_xref="taxon:9615"
1..51
52..447
/codon_start=1
/product="interleukin-13"
/protein_id="AAF63204.1"
/db_xref="GI:7528274"
/translation="MALWLTVVIALTCGLGLASPVTPPTLKLIELVNTQNOA"

SLCNGSMVSVNLTAGMYCAALLESILNVSPCSATQRTQRMKALCSQKPAAGQISSER
SRPTKIEVLQVLVKNLLTYRGVYRHGNFR*
448...1302
BASE COUNT 337 a 318 c 340 g 307 t
ORIGIN
Query Match 100.0%; Score 272; DB 7; Length 1302;
Best Local Similarity 100.0%; Pred. No. 1.4e-57; Indels 0; Gaps 0;
Matches 272; Conservative 0; Mismatches 0;
QY 1 tggccttgctcccgagccctgtgactccctcccaacccctcaagagctcattgagga 60
|||||
Db 96 TGGCCTTGCTCCCGAGCCCTGTGACTCCCTCCCAACCCCTCAAGAGGCTCATTGAGGA 155
|||||
QY 61 gctggtaacatcacccagaatcaggcagccctctgcaacggcgagcatgggtgtgagcgt 120
|||||
Db 156 GCTGGTCAACATCACCCAGAAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGAGCGGT 215
|||||
QY 121 caacctgacggcgagcgtactgctgagcagctctgagatctctgataatgtctccgactg 180
|||||
Db 216 CAACCTGACCGCGGCATGACTCGCGAGCTCTAGAATCTCTGATCAATGTCTCCGACTG 275
|||||
QY 181 cagcgccatcaaggagccagagatgctgaaagcactgtctcctcaaaagccgcggc 240
|||||
Db 276 CAGCGCCATCAAGGACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGGC 335
|||||
QY 241 agggcagatttcagtgaaagcagcagccagaca 272
|||||
Db 336 AGGCGAGATTTCAGTGAACGACGCCGAGACA 367
|||||
RESULT 2
HUMIL13A 1270 bp mRNA PRI 22-JUL-1993
LOCUS HUMIL13A Homo sapiens interleukin 13 mRNA, complete cds.
DEFINITION L06801
ACCESSION L06801
VERSION L06801.1 GI:186275
KEYWORDS cytokine; growth factor; interleukin 13; regulatory protein.
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1270)
AUTHORS McKenzie, A.N.J., Culpepper, J.A., de Waal Malefyt, R., Briere, F.,
Punnonen, J., Aversa, G., Sato, A., Dang, W., Cocks, B.G., Menon, S., de
Vries, J.E., Banchereau, J. and Zurawski, G.R.
TITLE Interleukin-13, a T cell-derived cytokine that regulates human
monocyte and B cell function
Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)
JOURNAL 93234572
MEDLINE
FEATURES
Location/Qualifiers
1..1270
/organism="Homo sapiens"
/db_xref="taxon:9606"
45..443
/codon_start=1
/product="interleukin 13"
/protein_id="AAA36107.1"
/db_xref="GI:186276"
/translation="MALLTITVIALTCGLGFASPGVPVPTALRELIELVNTQNOK
HVLDTKIEVAQFVKDLLLHLKLFREGFN"
polyA_site 1270
BASE COUNT 288 a 335 c 336 g 311 t
ORIGIN
Query Match 64.9%; Score 176.4; DB 93; Length 1270;
Best Local Similarity 80.3%; Pred. No. 7e-34; Indels 3; Gaps 1;
Matches 220; Conservative 0; Mismatches 51;
QY 2 ggccctgctcccgagccctgtgactccctcccaacccctcaagagctcattgagga 61

```

*
Db 90 GGCTTTGGCTCCCGAGCCCTGTGCTCTACAGCCCTCAGGGAGCTATTGAGGAG 149
Qy 62 ctggtcaacatcacccagaatc---aggcatccctctgcaacgagcagcatggtgtgagc 118
Db 150 CTGGTCAACATCACCCAGAACCCAGAGGCTCGGCTCTGCAATGGCAGCATGGTATGGAGC 209
Qy 119 gtcaactgaccgcccggatgactgagcagctctagaatctctgataatgtctccgac 178
Db 210 ATCAACCTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCTGATCAACAGTGTCAAGC 269
Qy 179 tgcagcgccatcaaaaggacccagagagatctgaaacactgtgctctcaaaagcccg 238
Db 270 TGCAGTGGCATTCAGAGAGACCCAGAGAGTGTGAGCGGATTCGCCGCCACAGGTTCTCA 329
Qy 239 gaggcgagattccagtgaaacgagcagcgagaca 272
Db 330 GCTGGCGAGTTTCCAGCTTGCATGTCCGAGACA 363

RESULT 3
HSNC30 1282 bp mRNA PRI 17-FEB-1997
LOCUS HsNC30 1282 bp mRNA PRI 17-FEB-1997
DEFINITION H. sapiens interleukin-13 mRNA.
ACCESSION X69079
VERSION X69079.1 GI:297787
KEYWORDS lymphokine.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1282)
Minty,A.J.
Direct Submission
Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches,
Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
2 (bases 1 to 1282)
Minty,A.J., Chalton,P., Derocq,J.M., Dumont,X., Guillemot,J.C.,
Kaghad,M., Labit,C., Lepiatols,P., Liauzun,P., Miloux,B., Minty,C.,
Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and
Caput,D.
Interleukin-13 is a new human lymphokine regulating inflammatory
and immune responses
Nature 362 (6417), 248-250 (1993)
93211479
Location/Qualifiers
1..1282
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosomes="5q 23-31"
/cell_type="peripheral blood lymphocytes"
15..455
/gene="NC30"
15..116
/gene="NC30"
/product="NC30; alternative"
15..455
/gene="NC30"
/notes="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1
/evidence=experimental
/protein_id="CAA48823.1"
/db_xref="GI:580330"
/db_xref="SWISS-PROT:P35225"
/translation="MHPLNPLLLALGLMALLTTVTALTCGLGFASPGVPFPSTALR
ELIEELVNITQKAPLCNGMWSINLTAGMYCAALESINLNSGCSAIEKTRQLMSG
FPHKVSAGQFSSLHVRDTKIEVAQFVKDLLHLKLFREGFN"
57..455
/gene="NC30"
/notes="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1

```

```

/evidence=experimental
/protein_id="CAA48824.1"
/db_xref="GI:673420"
/db_xref="SWISS-PROT:P35225"
/translation="MALLTTVTALTCGLGFASPGVPFPSTALRELIELVNITQK
APLCNGMWSINLTAGMYCAALESINLNSGCSAIEKTRQLMSGCFPHKVSAGQFSSL
HVRDTKIEVAQFVKDLLHLKLFREGFN"
57..116
/gene="NC30"
/product="NC30; alternative"
117..452
/gene="NC30"
/evidence=experimental
238
/gene="NC30"
/replacement="a"
856..860
/notes="ATTTA motif"
873..877
/notes="ATTTA motif"
1134..1138
/notes="ATTTA motif"
1153..1157
/notes="ATTTA motif"
1264..1269
polyA_signal 341 c 337 g 311 t
BASE COUNT 293 a 341 c 337 g 311 t
ORIGIN

Query Match 64.9%; Score 176.4; DB 92; Length 1282;
Best Local Similarity 80.3%; Pred. No. 7e-34;
Matches 220; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

Qy 2 ggccttgctcccgagccctgtgactccctcccaacccctcaagagctcattgaggag 61
Db 102 GCCTTGGCTCCCGAGCCCTGTGCTCTACAGCCCTCAGGGAGCTATTGAGGAG 161
Qy 62 ctggtcaacatcacccagaatc---aggcatccctctgcaacgagcagcatggtgtgagc 118
Db 162 CTGGTCAACATCACCCAGAACCCAGAGGCTCGGCTCTGCAATGGCAGCATGGTATGGAGC 221
Qy 119 gtcaactgagcggcgagctgactgagcagctctagaatctctgataatgtctccgac 178
Db 222 ATCAACCTGACAGCTGGCATGTACTGTGAGGCCCTGGAATCCCTGATCAACGTTGTCAGGC 281
Qy 179 tgcagcgccatcaaaaggacccagagagatgtgaaagcactgtgctctcaaaagcccg 238
Db 282 TGCAGTGGCATTCGAGAGACCCAGAGAGTGTGAGCGGATTCGCCGCCACAGGTTCTCA 341
Qy 239 gaggcgagattccagtgaaacgagcagcgagaca 272
Db 342 GCTGGCGAGTTTCCAGCTTGCATGTCCGAGACA 375

RESULT 4
I34548 1290 bp DNA PAT 06-FEB-1997
LOCUS I34548 1290 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5596072.
ACCESSION I34548
VERSION I34548.1 GI:1825339
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
FEATURES Location/Qualifiers
1..1290
/source
/organism="unknown"
BASE COUNT 308 a 335 c 336 g 311 t
ORIGIN

```

Query Match 64.9%; Score 176.4; DB 10; Length 1290;
Best Local Similarity 80.3%; Pred. No. 6.9e-34;
Matches 220; Conservative 0; Mismatches 51; Indels 3; Gaps 1;

QY 2 ggccttgccctcccagaccctgtgactccttcctcccccaacctccaaggagcatttgaggag 61
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
DB 90 ggcttggctcccagagccctgtgctccctctacagccctcagaggagctcatttgaggag 149
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 62 ctggtcaacaatcacccagaatc---aggcatccctctgcaacgccagcatggtgtggagc 118
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
DB 150 CTGTCACATCACCAGAACCCAGAAAGCTCGGTCTCATATGGCAGCATGGTATGGAGC 209
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 119 gtcaacctgaccgcccgcgatgtactgcgagctctatgaatactctgatcaatgtctccgac 178
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
DB 210 ATCAACTGCAGCTGGCATGCTACTGTGCAGCCCTTGGAATCCCTGATCAACGTGTCAGGC 269
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 179 tgcagcgccatccaaaggaccagagtagctgtgaaagcaactgtctctcaaaaagcccgcg 238
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
DB 270 TGCAGTGCATCGAGAGACCCAGAGGATGCTGAGCGGATTCTGCCGCACAAGGTCTCA 329
||| ||||||||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
QY 239 gcaaggcagatttccagtgaacgcagccagaca 272
||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||
DB 330 GCTGGGCAGTTTTCCAGCTTCATGTCGAGACA 363
||| ||||||||| ||||||||| ||||||||| ||||||||| |||||||||

RESULT 5
AF043334
LOCUS AF043334 417 bp mRNA PRI 21-FEB-1998
DEFINITION Homo sapiens Interleukin 13 precursor (IL13) mRNA, complete cds.
ACCESSION AF043334
VERSION AF043334.1 GI:2905619
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS Jang,J.S. and Kim,B.E.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of
Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong,
Sosa-gu, Bucheon 422-231, Korea
COMMENT
Nested PCR:
1) first PCR :
forward primer (5'-ctcaaatcctctctctgttgcaa-3') -
reverse primer (5'-tagtcaggtcctgtctctgc-3')
2) second PCR :
forward primer (5'-ctcatgctgccttttgttgaccagc-3')
reverse primer (5'-gatgcttggaagtttcaagttaa-3').
Location/Qualifiers
source 1..417
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="PHA-treated peripheral blood leukocyte"
gene 1..417
/gene="IL13"
primer_bind 1..24
/gene="IL13"
/note="second PCR"
PCR_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles;
Deltacycler II from Ericomp"
CDS 4..402
/gene="IL13"
/codon_start=1
/product="interleukin 13 precursor"
/protein_id="AAC03535.1"
/db_xref="GI:2905620"
/translation="MALLTTVTALCLGFSGPVPPTALRELIEELVNTQNOK
APLCNSGMWSINLTAGMTCAALESINVSIGCSAIEKTRMLGGFCPHKYVSAGQFSFL
HVDRTKIEVAQFYKDLLLLHLKLIFREGFRN"
sig_peptide 4..63

```

QY 2' ggcctgtctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggag 61
Db 102 GGTCTTGGCTCCCGAGCCCTGTGCTTCCCTCTACAGCCCTCAGGGAGCTATTGGAGG 161

QY 62 ctggtcaacatcacccagaatc---aggcatccctctgcaacgagcagcatggtgaggc 118
Db 162 CTGGTCAACATCACCCAGAACACCAAGGCTCCGCTCTGCAATGCCAGCATGGTATGGAGC 221

QY 119 gtaacctgaccccgccgactgtactgcgcagctctagaaatctctgataatgtctccgac 178
Db 222 ATCAACCTGACAGCTGACATGTACTGTGCAGCCCTGGAATCCCTGATCAAGCTGCAGGC 281

QY 179 tgcagcgccatcacaaggaccagagagatgtgaaagcaactgtgtctcctcaaaagcccgcg 238
Db 282 TGCAGTGCCTCAGAGAGACCCAGAGGATGCTGAGCGGATCTGCCCGCACAAAGGTCTCA 341

QY 239 gcagggcagatttccagtgaaacgcagccgagaca 272
Db 342 GCTGGGCAGTTTCCAGCTTGCATGTCCGAGACA 375

RESULT 7
LOCUS I58488 1297 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 15 from patent US 5652123.
ACCESSION I58488
VERSION I58488.1 GI:2477726
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Gullelot,J., Kaghad,M., Labit-Le
Bouteiller,C., Lepiatols,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 15 29-JUL-1997;
FEATURES
SOURCE
1. 1297
Location/Qualifiers
/organism="unknown"
BASE COUNT 309 a 341 c 336 g 311 t
ORIGIN

Query Match 64.3%; Score 174.8; DB 10; Length 1297;
Best Local Similarity 79.9%; Pred. No. 1.7e-33;
Matches 219; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 2' ggcctgtctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggag 61
Db 102 GGTCTTGGCTCCCGAGCCCTGTGCTTCCCTCTACAGCCCTCAGGGAGCTATTGGAGG 161

QY 62 ctggtcaacatcacccagaatc---aggcatccctctgcaacgagcagcatggtgaggc 118
Db 162 CTGGTCAACATCACCCAGAACACCAAGGCTCCGCTCTGCAATGCCAGCATGGTATGGAGC 221

QY 119 gtaacctgaccccgccgactgtactgcgcagctctagaaatctctgataatgtctccgac 178
Db 222 ATCAACCTGACAGCTGACATGTACTGTGCAGCCCTGGAATCCCTGATCAAGCTGCAGGC 281

QY 179 tgcagcgccatcacaaggaccagagagatgtgaaagcaactgtgtctcctcaaaagcccgcg 238
Db 282 TGCAGTGCCTCAGAGAGACCCAGAGGATGCTGAGCGGATCTGCCCGCACAAAGGTCTCA 341

QY 239 gcagggcagatttccagtgaaacgcagccgagaca 272
Db 342 GCTGGGCAGTTTCCAGCTTGCATGTCCGAGACA 375

RESULT 8
LOCUS AF072807
DEFINITION Bos taurus interleukin-13 precursor (IL-13) mRNA, partial cds.

```

```

ACCESSION AF072807
VERSION AF072807.1 GI:4558813
KEYWORDS cow.
SOURCE Bos taurus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 343)
AUTHORS Trigona,W.L., Brown,W.C. and Estes,D.M.
TITLE Functional implications for signaling via the IL4R/IL13R complex on
bovine cells
JOURNAL Vet. Immunol. Immunopathol. 72 (1-2), 73-79 (1999)
MEDLINE 20080132
PUBMED 10614495
REFERENCE 2 (bases 1 to 343)
AUTHORS Trigona,W.T., Hirano,A. and Estes,D.M.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-1998) Veterinary Pathobiology, University of
Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO
65211, USA
FEATURES
Location/Qualifiers
1. 343
source
/organism="Bos taurus"
/db_xref="taxon:9913"
/cell_type="activated peripheral T lymphocytes"
1. >343
/gene="IL-13"
1. >343
/gene="IL-13"
/codon_start=1
/product="interleukin-13 precursor"
/protein_id="AAD22748.1"
/db_xref="GI:4558814"
/translation="MALLLTAVILVLCRGLTSPSPVSATALKELIELVNIQNQK
VPLCKGSMVSNLTSSNYCAALDSLISNCVSIQRTKRLNALCPHKPSAKQVSSE
YVRDKIEVAQF"
BASE COUNT 78 a 101 c 85 g 79 t
ORIGIN

Query Match 64.0%; Score 174.2; DB 7; Length 343;
Best Local Similarity 79.6%; Pred. No. 2.9e-33;
Matches 219; Conservative 0; Mismatches 53; Indels 3; Gaps 1;

QY 1 tggccttgcctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggag 60
Db 45 TGGCCTCACCCTCCCAAGCCCTGTGCTTCTGCTACAGCCCTCAAGGAGCTATTGAAGA 104

QY 61 gctgtcaacatcacccagaatc---aggcatccctctgcaacgagcagcatggtgaggag 117
Db 105 GCTGGTAAATATACACCCAGAACCAAGGTCGGCTGTGCAATGGCAGCATGGTGTGGAG 164

QY 118 cgtcaacctgaccgcgcgcatgtactgcgcagctctagaaatctctgataatgtctccgag 177
Db 165 CCTCAACCTGACGAGCAGCATGTACTGTGCAGCCCTGGACTCCCTGATCAGCATCTCCAA 224

QY 178 ctgagcgccatcacaaggaccagagatgctgaaagcaactgtgtctcctcaaaagcccg 237
Db 225 CTGCAGTGTCTATCCAAAGGACCAAGAGGATGCTGAATGCACCTCTGTCTCTCACAAGCCCTC 284

QY 238 ggcagggcagatttccagtgaaacgcagccgagaca 272
Db 285 AGCTAAGCAGGTTTCCAGTGAGTACGTCGAGACA 319

RESULT 9
LOCUS A29950 384 bp DNA PAT 23-JUN-1995
DEFINITION Nucleic acid fragment B.
ACCESSION A29950
VERSION A29950.1 GI:1249030
KEYWORDS

```

SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE artificial sequence.
1 (bases 1 to 384)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le.
Boutellier,C., Lepoint,P., Magazin,M. and Minty,A.
TITLE protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 23 30-SEP-1992;
ELF SANOFI
FEATURES Location/Qualifiers
source 1..384
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 97 a 104 c 99 g 84 t
ORIGIN

Query Match 61.0%; Score 165.8; DB 9; Length 384;
Best Local Similarity 79.2%; Pred. No. 3.5e-31;
Matches 210; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

Qy 11 tccccgagccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaac 70
Db 16 TCCCCAGGCCCTGTGCTCCCTCTACGGCCCTCAGGAGCTCATTGAGGAGCTGGTCAAC 75

Qy 71 atcaccagaatc---aggatccctctgcaacgagcagcatggtgtggagcgtcaacctg 127
Db 76 ATCACCAGAACCAAGAGGCTCCGCTGCAATGGCAGCATGTGTGAGCATCAACCTG 135

Qy 128 accgagcagctgactgagcagcttagaattctctgataatgctccgactgagcagcc 187
Db 136 ACAGCTGACATGTACTGTGACGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCCATGCC 195

Qy 188 atccaaagaccagagatgctgaaagcactgtgctctcaaaagcccgagcagggcag 247
Db 196 ATCGAAGAACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGGCGAG 255

Qy 248 atttcagtgaaacgagcagcagagaca 272
Db 256 TTTTCCAGCTTGATGTCGCGAGACA 280

RESULT 10
LOCUS I58489 384 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 17 from patent US 5652123.
ACCESSION I58489
VERSION I58489.1 GI:2477727
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 384)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-le.
Boutellier,C., Lepoint,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 17 29-JUL-1997;
FEATURES Location/Qualifiers
source 1..384
/organism="unknown"
BASE COUNT 97 a 104 c 99 g 84 t
ORIGIN

Query Match 61.0%; Score 165.8; DB 10; Length 384;
Best Local Similarity 79.2%; Pred. No. 3.5e-31;
Matches 210; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

Qy 11 tccccgagccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaac 70
Db 16 TCCCCAGGCCCTGTGCTCCCTCTACGGCCCTCAGGAGCTCATTGAGGAGCTGGTCAAC 75

Qy 71 atcaccagaatc---aggatccctctgcaacgagcagcatggtgtggagcgtcaacctg 127
Db 76 ATCACCAGAACCAAGAGGCTCCGCTGCAATGGCAGCATGTGTGAGCATCAACCTG 135

Qy 128 accgagcagctgactgagcagcttagaattctctgataatgctccgactgagcagcc 187
Db 136 ACAGCTGACATGTACTGTGACGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCCATGCC 195

Qy 188 atccaaagaccagagatgctgaaagcactgtgctctcaaaagcccgagcagggcag 247
Db 196 ATCGAAGAACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGGCGAG 255

Qy 248 atttcagtgaaacgagcagcagagaca 272
Db 256 TTTTCCAGCTTGATGTCGCGAGACA 280

RESULT 11
LOCUS A29931 336 bp DNA PAT 23-JUN-1995
DEFINITION Sequence coding for the mature cytokine like protein.
ACCESSION A29931
VERSION A29931.1 GI:1249019
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le.
Boutellier,C., Lepoint,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 3 30-SEP-1992;
ELF SANOFI
FEATURES Location/Qualifiers
source 1..336
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN

Query Match 60.7%; Score 165.2; DB 9; Length 336;
Best Local Similarity 80.2%; Pred. No. 5e-31;
Matches 207; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

Qy 18 gcctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 77
Db 2 GCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 61

Qy 78 agatc---aggatccctctgcaacgagcagcatggtgtggagcgtcaacctgagcagccg 134
Db 62 AGAACAGAGAGGCTCCGCTGCAATGGCAGCATGTGTGAGCATCAACCTGACAGCTG 121

Qy 135 gcatgtactgagcagcttagaattctctgataatgctccgactgagcagcagccatcaaa 194
Db 122 GCATGTACTGTGAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCCATCCAGA 181

Qy 195 ggaccagagagatgctgaaagcactgtgctctcaaaagcccgagcagggcagattccca 254
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGGCGAGTTTCCA 241

Qy 255 gtgaacgagcagcagagaca 272
Db 242 GCTTGATGTCGCGAGACA 259

RESULT 12
LOCUS I58494 336 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 24 from patent US 5652123.
ACCESSION I58494

VERSION I58494.1 GI:2477732
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput, D., Ferrara, P., Guillemot, J., Kaghad, M., Labit-Le
Routiller, C., Leplatois, P., Magazin, M., and Minty, A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 24 29-JUL-1997;
FEATURES Location/Qualifiers
source
1..336
/organism="unknown"
BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN

Query Match 60.7%; Score 165.2; DB 10; Length 336;
Best Local Similarity 80.2%; Pred. No. 5e-31;
Matches 207; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

Qy 18 gcccgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 77
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGCTCAACATCACCC 61

Qy 78 agaate---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcg 134
Db 62 AGAACGAGAAGGCTCGCTCTGCAATGGCAGCATGTTGAGGAGCATCAACCTGACAGCTG 121

Qy 135 gcatgtactgcagctctagaatctctgataatctctccgactgcagcgccatccaaa 194
Db 122 GCATGTACTGTGCAGCCCTCGAATCCCTGATCAACGCTGCAGCTGCAGTGCCTCAGGA 181

Qy 195 ggaccagaggtgctgaaagcactgtctctcaaaagccgcggcaggcagatttcca 254
Db 182 AGACCCAGAGGATGCTGACGGGATTTGCCCGCACAAAGTCTCAGCTGGCGAGTTTCCA 241

Qy 255 gtgaacgcagcgcgagaca 272
Db 242 GCTTGATGTCGAGACA 259

RESULT 13
LOCUS AR027065 425 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5956142.
ACCESSION AR027065
VERSION AR027065.1 GI:5937905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux, R., Maldonado, P., and Salome, M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5856142-A 4 05-JAN-1999;
FEATURES Location/Qualifiers
source
1..425
/organism="unknown"
BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 60.3%; Score 164; DB 9; Length 425;
Best Local Similarity 78.4%; Pred. No. 9.6e-31;
Matches 210; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

Qy 8 gctccccgagccctgtactccctcccaaccctcaaggagctcattgaggagctggtc 67
Db 55 GCCTGCTGGCCCTGTGCTCCCACTACTGCCCTCAGGAGCTCATTCAGGAGCTGGTC 114

Qy 68 aacatcacccagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaac 124
Db 115 AACATCACCCAGAACGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174

Qy 125 ctgaccgcggcagctgactgcgagcgtctagaatctctgataatctctccgactgcagc 184
Db 175 CTGACAGTGGCATGTACTGTGTCAGCCCTTGGAAATCCCTGATCAACGCTGTCAGCTG 234

Qy 185 gccatccaaagaccagagatgctgaaagcactgctcctcaaaagccgcggcaggg 244
Db 235 GCCATCGAGAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGG 294

Qy 245 cagatttccagtgaacgcgagcagaca 272
Db 295 CAGTTTTCAGCTTGCATGTCGAGACA 322

RESULT 14
LOCUS I86198 425 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5700665.
ACCESSION I86198
VERSION I86198.1 GI:3205916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux, R., Maldonado, P., and Salome, M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5700665-A 4 23-DEC-1997;
FEATURES Location/Qualifiers
source
1..425
/organism="unknown"
BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 60.3%; Score 164; DB 10; Length 425;
Best Local Similarity 78.4%; Pred. No. 9.6e-31;
Matches 210; Conservative 0; Mismatches 55; Indels 3; Gaps 1;

Qy 8 gctccccgagccctgtactccctcccaaccctcaaggagctcattgaggagctggtc 67
Db 55 GCCTGCTGGCCCTGTGCTCCCACTACTGCCCTCAGGAGCTCATTCAGGAGCTGGTC 114

Qy 68 aacatcacccagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaac 124
Db 115 AACATCACCCAGAACGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174

Qy 125 ctgaccgcggcagctgactgcgagcgtctagaatctctgataatctctccgactgcagc 184
Db 175 CTGACAGTGGCATGTACTGTGTCAGCCCTTGGAAATCCCTGATCAACGCTGTCAGCTG 234

Qy 185 gccatccaaagaccagagatgctgaaagcactgctcctcaaaagccgcggcaggg 244
Db 235 GCCATCGAGAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGG 294

Qy 245 cagatttccagtgaacgcgagcagaca 272
Db 295 CAGTTTTCAGCTTGCATGTCGAGACA 322

RESULT 15
LOCUS A52326 4410 bp DNA PAT 12-DEC-1997
DEFINITION Sequence 1 from Patent EP0725140.
ACCESSION A52326
VERSION A52326.1 GI:2851987
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.

unclassified.
1 (bases 1 to 4410)
REFERENCE Legoux,R., Maldonado,P. and Salome,M.
AUTHORS Process of extraction of periplasmic proteins from prokaryotic
TITLE microorganisms in the presence of arginine
JOURNAL Patent: EP 0725140-A 1 07-AUG-1996;
COMMENT SANOFI SA (FR)
Other publication SK 10696 960904
Other publication CZ 9600290 960814
Other publication JP 8242879 960924
Other publication FI 960427 960801
Other publication PL 312543 960805
Other publication NO 960396 960801
Other publication FR 2729972 960802
Other publication CA 2168382 960801
Other publication AU 4224496 960808.
FEATURES
 Location/Qualifiers
 1..4410
 /organism="unidentified"
 /db_xref="taxon:32644"
 promoter
 1..282
 5'UTR
 283..337
 /note="SEQUENCE DE LA REGION 5' NON TRADUITE DU MESSAGE"
 338..762
 /note="SEQUENCE CODANT POUR LE PRECURSEUR DE L'IL-13"
 763..812
 /note="TERMINATEUR DU GENE 10 DU PHAGE T7"
 813..1012
 /note="TERMINATEUR DU PHAGE FD"
 1013..1253
 /note="GENE CODANT POUR LE REPRESSEUR DE L'OPERON LACTOSE"
 1254..2505
 /note="SEQUENCE DE PBR 327"
 2506..4410
 /note="SEQUENCE DE PBR 327"
BASE COUNT 1078 a 1142 c 1096 g 1094 t
ORIGIN

Query Match 60.3%; Score 164; DB 9; Length 4410;
Best Local Similarity 78.4%; Pred. NO. 7e-31;
Matches 210; Conservative 0; Mismatches 55; Indels 3; Gaps 1;
Qy 8 gcctcccgagccctgtactccctcccaaccctcaaggagctcattgaggagctggtc 67
Db 392 GCCTTCGCTGGCCCTGTGCTCCCTCCAGTACTGCCCTCAGGAGCTCATTGAGGAGCTGGTC 451
Qy 68 aacatcacccagaatc---aggcatccctctgcaacgcagcatggtgtggagcgtcaac 124
Db 452 AACATCACCCAGAACCAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511
Qy 125 ctgaccgcggcagtgtactgcgagctctagaatctctgatcaatgtctccgactgcagc 184
Db 512 CTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGT 571
Qy 185 gccatcaagagaccagagatgctgaagcaactgtctctcaaaagcccgccgaggg 244
Db 572 GCCATCGAAGAGACCCAGAGGATGCTGAGCGGATTTGCCCGCACAGGCTCTCAGCTGGG 631
Qy 245 cagatttcagtgagcagcagcgagaca 272
Db 632 CAGTTTCCACGCTTGCATGTCGAGACA 659

Search completed: May 13, 2001, 14:16:09
Job time: 18849 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 09:02:00 ; Search time 9342.78 Seconds
(without alignments)
262.036 Million cell updates/sec

Title: US-09-451-527-88
Perfect score: 166
Sequence: 1 ctcagcttagccagcctac.....caacctcaaggagctcatt 166

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues 2566470
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_om:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pl1:*
- 13: gb_pl2:*
- 14: gb_pl3:*
- 15: gb_pl4:*
- 16: em_ba1:*
- 17: em_ba2:*
- 18: em_fun:*
- 19: em_htgo_hum:*
- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
- 32: em_htg_other:*
- 33: em_htg_rod:*
- 34: em_hum1:*
- 35: em_hum2:*
- 36: em_hum3:*
- 37: em_hum4:*
- 38: em_hum5:*
- 39: em_hum6:*
- 40: em_hum7:*
- 41: em_in:*
- 42: em_om:*
- 43: em_or:*

44: em_ov:*

45: em_pat:*

46: em_ph:*

47: em_pl:*

48: em_ro:*

49: em_sts:*

50: em_sy:*

51: em_un:*

52: em_v1:*

53: gb_sts1:*

54: gb_sts2:*

55: gb_sts3:*

56: gb_sy:*

57: gb_un:*

58: gb_v11:*

59: gb_v12:*

60: gb_htg1:*

61: gb_htg2:*

62: gb_htg3:*

63: gb_htg4:*

64: gb_htg5:*

65: gb_htg6:*

66: gb_htg7:*

67: gb_htg8:*

68: gb_htg9:*

69: gb_htg10:*

70: gb_htg11:*

71: gb_htg12:*

72: gb_htg13:*

73: gb_htg14:*

74: gb_htg15:*

75: gb_htg16:*

76: gb_htg17:*

77: gb_htg18:*

78: gb_htg19:*

79: gb_htg20:*

80: gb_htg21:*

81: gb_htg22:*

82: gb_htg23:*

83: gb_htg24:*

84: gb_htg25:*

85: gb_pr1:*

86: gb_pr2:*

87: gb_pr3:*

88: gb_pr4:*

89: gb_pr5:*

90: gb_pr6:*

91: gb_pr7:*

92: gb_pr8:*

93: gb_pr9:*

94: gb_rol:*

95: gb_rol2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
c 1	166	100.0	213343	78	AF276990	Canis fam
2	150	90.4	1302	7	AF244915	Canis fam
3	88.4	53.3	1270	93	HUM113A	Homo sapien
4	88.4	53.3	1282	92	HSNC30	H. sapiens 1
5	88.4	53.3	1290	10	I34548	Sequence 1
6	88.4	53.3	1297	9	A29948	Coding sequ
7	88.4	53.3	1297	10	I58488	Sequence 15
8	88.4	53.3	3714	93	HUM11DC99Z	Homo sapien
9	88.4	53.3	4600	93	HUM113B	Human inter
10	88.4	53.3	4740	93	HSU10307	Human inter
11	88.4	53.3	5670	93	HSU31120	Human inter

1 (bases 1 to 1270)
McKenzie, A.N.J., Culpepper, J.A., de Waal Malefyt, R., Briere, F.

Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function
Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)
93234572

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
45. .443
/codon_start=1
/product="interleukin 13"
/protein_id="AAA36107.1"
/db_xref="GI:186276"
/translation="MALILTTVIALTCLGFGASGPVPPSTALRIELVLNITQNK
APVDCIKMVAQSLNLTAGMYCAALSLINVSGCSAIEKTMQLSGFCPHKVSAGQFSL
HLRDPFKIWAQVQKDLLHLKLLFREGRN"

```

	288 a	335 c	336 g	311 t
ch	53.38;	Score 88.4;	DB 93;	Length 1270;
Similarity	80.0%;	pred	NC 1	3e-13.

ctcgctccctcctgcattggctctggctccatggcgctctggtgactctggctattgc 96
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
TCAATCCTCCTCTTGGCACTGGGCGCTCATGGGCGCTTTGTTGACCACGGTCAATGC 73

agatcatt 166
TTCACCTGCCCTGGGGCTTGCCTCCCGAGGCCCTGTCCTCTACAGCCCTCAG 133

Accession	Length	Source	Accession	Length	Source
HSNC30	1282 bp	mRNA	PRI	17-FEB-1997	
H.sapiens	interleukin-13 mRNA.				
x69079					
x69079.1	GI:297787				

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominoidea; Homo.
1 (bases 1 to 1282)
Minty, A.J.
Direct Submission

Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
2 (bases 1 to 1282)
Minty, A. J.; Chalou, P.; Derocq, J. M.; Dumont, X.; Guillemot, J. C.

Caseasas, P., Wilson, G., Dupker, J., Snire, D., Ferrara, P. and Caput, D.
Interleukin-13 is a new human lymphokine regulating inflammatory and immune responses
Nature 362 (6417), 248-250 (1993)
93211479

Location/Qualifiers

1. 1282
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5q 23-31"
/cell_type="peripheral blood lymphocytes"

```
gene
sig_peptide
CDS
15. .455
/gene="NC30"
15. .116
/gene="NC30"
/product="NC30; alternative"
15. .455
/gene="NC30"
/note="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1
/evidence=experimental
/protein_id="CAA48823.1"
/db_xref="GI:580330"
/db_xref="SWISS-PROT:P35225"
/translation="MHPLNPLLLALGLMALLTTVTALTCLGFGFASGPGVPPSTALR
ELIELVNITQNKAPLCNGSMWSINLTAGMYCAALESINVSQCSAIEKQRMLSG
FCPHKVSAGQFSSLHVDRTKIEVAQFVKDLLHLKLFREGFNF"
57. .455
/gene="NC30"
/note="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1
/evidence=experimental
/protein_id="CAA48824.1"
/db_xref="GI:573420"
/db_xref="SWISS-PROT:P35225"
/translation="MALLTTVTALTCLGFGFASGPGVPPSTALRELIELVNITQNK
APLCNGSMWSINLTAGMYCAALESINVSQCSAIEKQRMLSGFCPHKVSAGQFSS
LHVDRTKIEVAQFVKDLLHLKLFREGFNF"
57. .116
/gene="NC30"
/product="NC30; alternative"
117. .452
/gene="NC30"
/evidence=experimental
238
/gene="NC30"
/replace="a"
856. .860
/note="ATTTA motif"
873. .877
/note="ATTTA motif"
1134. .1138
/note="ATTTA motif"
1153. .1157
/note="ATTTA motif"
1264. .1269
/polyA_signal
293 a 341 c 337 g 311 t
BASE COUNT
ORIGIN

Query Match 53.3%; Score 88.4; DB 92; Length 1282;
Best Local Similarity 80.0%; Pred. No. 1.3e-13;
Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 37 cctcgctcctcgatggtcgtggctccatggcgcctgtggtgactgtggtcattgc 96
Db 26 CCTCAATCCTCTCCTGTGGCACTGGGCGCTCATGGCGCTTTTGTGACACGGTCATTGC 85
Qy 97 tctcactgcctcgtggtcgtcctcccgagccctgtgactcctcccaaccctcaa 156
Db 86 TCTCATTGCGCTGGGCGCTTTGGCTCCCGAGGCGCTGCTCCCTCTACAGCCCTCAG 145
Qy 157 ggagctcatt 166
Db 146 GGAGCTCATT 155

Query Match 53.3%; Score 88.4; DB 9; Length 1297;
Best Local Similarity 80.0%; Pred. No. 1.3e-13;
Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 37 cctcgctcctcgatggtcgtggctccatggcgcctgtggtgactgtggtcattgc 96
Db 146 GGAGCTCATT 155
```

```
VERSION I34548.1 GI:1825339
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
FEATURES
source
location/Qualifiers
1. .1290
/organism="unknown"
BASE COUNT 308 a 335 c 336 g 311 t
ORIGIN

Query Match 53.3%; Score 88.4; DB 10; Length 1290;
Best Local Similarity 80.0%; Pred. No. 1.3e-13;
Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 37 cctcgctcctcgatggtcgtggctccatggcgcctgtggtgactgtggtcattgc 96
Db 14 CCTCAATCCTCTCCTGTGGCACTGGGCGCTCATGGCGCTTTTGTGACACGGTCATTGC 73
Qy 97 tctcactgcctcgtggtcgtcctcccgagccctgtgactcctcccaaccctcaa 156
Db 74 TCTCATTGCGCTGGGCGCTTTGGCTCCCGAGGCGCTGCTCCCTCTACAGCCCTCAG 133
Qy 157 ggagctcatt 166
Db 134 GGAGCTCATT 143

RESULT 6
LOCUS A29948 1297 bp DNA PAT 23-JUN-1995
DEFINITION Coding sequence for protein with cytokine like activity.
ACCESSION A29948
VERSION A29948.1 GI:1249028
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kagehad,M., Labit-le
Bouteiller,C., Lepiatois,P., Magazin,M. and Minty,A.
TITLE Protein having cytokine type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 21 30-SEP-1992;
FEATURES
location/Qualifiers
1. .1297
/organism="synthetic construct"
/db_xref="taxon:32630"
15. .455
/codon_start=1
/transl_table=11
/product="protein with cytokine like activity"
/protein_id="CAA01982.1"
/db_xref="GI:1249029"
/translation="MHPLNPLLLALGLMALLTTVTALTCLGFGFASGPGVPPSTALR
ELIELVNITQNKAPLCNGSMWSINLTAGMYCAALESINVSQCSAIEKQRMLSG
FCPHKVSAGQFSSLHVDRTKIEVAQFVKDLLHLKLFREGFNF"
BASE COUNT 309 a 341 c 336 g 311 t
ORIGIN

Query Match 53.3%; Score 88.4; DB 9; Length 1297;
Best Local Similarity 80.0%; Pred. No. 1.3e-13;
Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 37 cctcgctcctcgatggtcgtggctccatggcgcctgtggtgactgtggtcattgc 96
Db 146 GGAGCTCATT 155
```

Db	26	CCTCAATCCCTCTCCTGTTGGCACTGGGCCCTATGAGCCGCTTTTGTGTGACACAGGCTCAATTGC	85
Qy	97	tctcaactgctcgtggtgcttgctcctcccgagccctgtgactcctccccaacctcaa	156
Db	86	TCTCATTTGCTTGGCGGCTTTCCTCCCGAGGCCCTGTGCCTCCCTCTACAGCCCTCAG	145
Qy	157	ggagctcatt	166
Db	146	GGAGCTCATT	155

RESULT	7			
I58488				
LOCUS	I58488	1297 bp	DNA	PAT
DEFINITION	Sequence 15 from patent US 5652123.			
ACCESSION	I58488			
VERSION	I58488.1	GI:2477726		
				07-OCT-1997

SOURCE	UNKNOWN.			
ORGANISM	Unclassified.			
REFERENCE	1 (bases 1 to 1297)			
AUTHORS	Caput, D., Ferrara, P., Guillemot, J., Boucellier, C., Lepiattois, P., Magazin protein having interleukin 13 activi this protein, transformed cells and Patent: US 5652123-A 15 29-JUL-1997;			
TITLE	Location/Qualifiers			
JOURNAL	1. .1297			
FEATURES	/organism="unknown"			
source	309 a	341 c	336 g	311 t
BASE COUNT				
ORIGIN				

RESULT	8				
HUM11DC99Z/c					
LOCUS	HUM11DC99Z	3714 bp	DNA		
DEFINITION	Homo sapiens	(subclone 3_f2 from P1 H11)		PRI	10-MAY-1995
ACCESSION	L42080				
VERSION	L42080.1	GI:804720			
KEYWORDS	Interleukin growth hormone cluster on chromosome 5 (5q31).				
SOURCE	Homo sapiens (tissue library: Subclones in Homo sapiens from P1 clone H11) DNA.				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.				
REFERENCE	1 (bases 1 to 3714)				
AUTHORS	Martin,C.H., Bondoc,M.M., Chiang,A., Cloutier,T., Davis,C.A., Ericsson,C.L., Jaklevic,M.A., Kim,R.J., Lee,M.T., Li,M., Mayeda,C.A., Steiert-El Keir,A. and Palazzolo,M.J.				
TITLE	Sequencing of the interleukin growth hormone cluster on chromosome 5 (5q31) of homo sapiens				
JOURNAL	Unpublished (1995)				
COMMENT	Sequence submitted by: Human Genome Center and Drosophila Genome Center				

Lawrence Berkeley Laboratory
Berkeley, CA 94720
e-mail: seq@genome.lbl.gov
This subclone overlaps H11_8.a1.
The P1, from which this subclone is derived, is adjacent to P1
(none).

FEATURES	Location/Qualifiers
source	1. .3714 /organism="Homo sapiens" /db_xref="taxon:9606" /tissue_lib="Subclones in Homo sapiens from P1 clone H11" 744 a 1018 c 1109 g 843 t
BASE COUNT	
ORIGIN	

	Query Match	53.3%	Score 88.4	DB 93	Length 3714
	Best Local Similarity	80.0%	Pred. No. 1.le-13		
	Matches 104	Conservative 0	Mismatches 26	Indels 0	Gaps 0
Qy	37	cctggctcctcctgcatgtgctctgggctccatggcctctggttgactgtggtcattgc	96		
Db	1963	CCTCAATCCTCTCGTTGGCAGCTGGGCCTCATGGCGCTTTGTGTACACAGGTCATTGC	1904		
Qy	97	tctcacctgcctcctggctgctcctcccgagccctgtgactccctcccaaccctcaa	156		
Db	1903	TCTCATTGCGCTTGGCGGCTTTGGCTCCCCAGGCCCTTGCTCCCTCTCTACAGCCCTCAG	1844		
Qy	157	ggagctcaatt	166		
Db	1843	GGAGCTCATT	1834		

RESULT	9	
HUMIL13B		
LOCUS	HUMIL13B	4600 bp DNA
DEFINITION	Human interleukin-13 gene sequence with four exons.	27-JUL-1993
ACCESSION	LI3029	
VERSION	LI3029.1	GI:307044
KEYWORDS	interleukin 13.	
SOURCE	Homo sapiens (library: EMBL-3 SP6/T7) female placenta DNA.	
ORGANISM	Homo sapiens	
REFERENCE	McKenzie,A.N.J., Li,X., Largaespada,D.A., Sato,A., Kaneda,A., Zurawski,S.M., Doyle,E.L., Milatovich,A., Francke,U., Copeland,N.G., Jenkins,N.A. and Zurawski,G. Structural comparison and chromosomal localization of the human and mouse IL-13 genes	
AUTHORS	J. Immunol. 150, 5436-5444 (1993)	
TITLE		
JOURNAL		

Query Match 53.3%; Score 88.4; DB 93; Length 4600;
Best Local Similarity 80.0%; Pred. No. 1.1e-13;


```
repeat_region /rpt_family="Alu"
19137..19458
/rpt_family="Alu"
19830..20187
/rpt_family="Alu"
20125..20149
/note="(A)25"
/rpt_type=tandem
/rpt_unit=A
complement(20820..21191)
/rpt_family="Alu"
complement(21888..22352)
/rpt_family="L1MB7"
complement(22324..22658)
/rpt_family="Alu"
complement(22633..22884)
/rpt_family="L1MB7"
22919..22998
/note="(AC)40"
/rpt_type=tandem
/rpt_unit=AC
complement(23934..24400)
/note="IL-4 interleukin 4"
complement(24145..24243)
/note="IL-4 interleukin-4"
24730..24807
/rpt_family="MIR"
complement(26824..27018)
/note="IL-4 interleukin 4"
28035..28144
/rpt_family="MERS"
complement(30482..30598)
/rpt_family="MIR"
30773..30798
/note="(AC)13"
/rpt_type=tandem
/rpt_unit=AC
30851..30878
/note="(AC)14"
/rpt_type=tandem
/rpt_unit=AC
30887..31176
/rpt_family="Alu"
complement(32223..32273)
/note="IL-4 interleukin 4"
complement(32534..32678)
/note="IL-4 interleukin 4"
complement(33412..33715)
/rpt_family="Alu"
complement(34058..34363)
/rpt_family="Alu"
34062..34081
/note="(T)20"
/rpt_type=tandem
/rpt_unit=T
complement(34468..34747)
/rpt_family="Alu"
complement(34893..35240)
/rpt_family="Alu"
35107..35585
/rpt_family="L1"
35847..35923
/rpt_family="MER21"
36163..36238
/rpt_family="MER21b"
37403..37481
/rpt_family="MIR"
37646..37777
/rpt_family="MIR"
39322..39395
/rpt_family="MER41"
41201..41288
/rpt_family="MIR2"

misc_feature complement(44670..50282)
/note="IL-13 interleukin-13"
complement(45620..46000)
/note="99% identity"
/db_xref="dbSTS:G06679"
complement(46450..46554)
/note="IL-3 exon"
complement(46616..46756)
/rpt_family="MIR"

STS
complement(45620..46000)
/note="99% identity"
/db_xref="dbSTS:G06679"
complement(46450..46554)
/note="IL-3 exon"
complement(46616..46756)
/rpt_family="MIR"

repeat_region complement(46616..46756)
/rpt_family="MIR"

Query Match 53.3%; Score 88.4; DB 85; Length 50282;
Best Local Similarity 80.0%; Pred. No. 7.4e-14;
Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

QY 37 cctcgctcctcgtgcttggccttgcctcccgagccctgtgactccctcccaaccctcaa 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 48531 CCTCAATCCTCTCTCTGTGGCACTGGGCGCTTCATGGCGCTTTGTGACCACTGTC 48472

QY 97 tctcacctgcctcgtgcttggccttgcctcccgagccctgtgactccctcccaaccctcaa 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 48471 TCTCACTTGCCTTGGCGGCTTTCCTCCCGAGGCGCTGCTCCCTCTACAGCCCTCAG 48412

QY 157 ggaqctcatt 166
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 48411 GGAGCTCAAT 48402

RESULT 13
AC074127
LOCUS AC074127 78469 bp DNA HTG 15-JUL-2000
DEFINITION Homo sapiens chromosome 5 clone CTD-2025J21, WORKING DRAFT
ACCESSION AC074127
VERSION AC074127.1 GI:9211237
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 78469)
AUTHORS DOE Joint Genome Institute.
TITLE Sequencing of Human Chromosome 5
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 78469)
AUTHORS DOE Joint Genome Institute.
TITLE Direct Submission
JOURNAL Submitted (15-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
COMMENT
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 637386
Center clone name: CITB-HI_2025J21
-----
Summary Statistics
Consensus quality: 64691 bases at least Q40
Consensus quality: 72151 bases at least Q30
Consensus quality: 73718 bases at least Q20
Estimated insert size: 137500; agarose-fp estimation
Quality coverage: 7.05 in Q20 bases; sum-of-contigs estimation
Quality coverage: 12.65 in Q20 bases; agarose-fp estimation
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
```



```
* 1 1478: contig of 1478 bp in length
* 1479: gap of unknown length
* 1579: contig of 1027 bp in length
* 2606: gap of unknown length
* 2705: gap of unknown length
* 3993: contig of 1288 bp in length
* 3994: gap of unknown length
* 4094: contig of 1191 bp in length
* 5285: gap of unknown length
* 5385: contig of 2864 bp in length
* 8249: gap of unknown length
* 8349: contig of 1676 bp in length
* 10025: gap of unknown length
* 10125: contig of 1743 bp in length
* 11868: gap of unknown length
* 11968: contig of 1298 bp in length
* 13265: gap of unknown length
* 13366: contig of 2845 bp in length
* 16211: gap of unknown length
* 16311: contig of 3015 bp in length
* 19325: gap of unknown length
* 19425: contig of 2034 bp in length
* 21426: gap of unknown length
* 21460: contig of 3010 bp in length
* 21560: gap of unknown length
* 24570: contig of 3041 bp in length
* 24670: gap of unknown length
* 27711: contig of 2328 bp in length
* 30139: gap of unknown length
* 30239: contig of 4201 bp in length
* 34439: gap of unknown length
* 34539: contig of 7114 bp in length
* 34654: gap of unknown length
* 41754: contig of 7797 bp in length
* 49551: gap of unknown length
* 49651: contig of 10021 bp in length
* 59672: gap of unknown length
* 59772: contig of 18698 bp in length.

FEATURES
  source
    1. 78469
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /chromosome="5"
      /clone="CTD-2025J21"
      /clone_lib="CalTech human BAC library D"
BASE COUNT 18889 a 18951 c 18948 g 19879 t 1802 others
ORIGIN

Query Match 53.3%; Score 88.4; DB 75; Length 78469;
Best Local Similarity 80.0%; Pred. No. 6.9e-14;
Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;

Qy 37 cctcgctcctcgtatggctctgggtccatggcgtctctgggtgactgtggtcattgc 96
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40677 CCTCAATCCTCTCCCTGTTGGCACTGGCGCTCATGGCGCTTTGTTGACCACGGTCATTGC 40736
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 97 tctcacctgcctcgtgccttgcctcccgagccctgtgactcctccccaacctcaaa 156
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 40737 TCTCACTTGGCTTGGCGCTTTGGCTCCCGAGGCCCTGTGCTCTCCCTCTACAGCCCTCAG 40796
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 157 ggagctcatt 166
||||| |||||
Db 40797 GGAGCTCATT 40806

RESULT 14
AC074127/c
LOCUS
DEFINITION Homo sapiens chromosome 5 clone CTD-2025J21, WORKING DRAFT
ACCESSION AC074127
VERSION AC074127.1 GI:9211237
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.

SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

human.
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 78469)
DOE Joint Genome Institute.
Sequencing of Human Chromosome 5
Unpublished
DOE Joint Genome Institute.
2 (bases 1 to 78469)
Direct Submission
Submitted (15-JUL-2000) Production Sequencing Facility, DOE Joint
Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA
-----Genome Center
Center: Joint Genome Institute
Center Code: JGI
Web site: http://www.jgi.doe.gov
-----
Project Information
Center Project Name: 637386
Center clone name: CITB-HI_2025J21
-----
Summary Statistics
Consensus quality: 64691 bases at least Q40
Consensus quality: 72151 bases at least Q30
Consensus quality: 73718 bases at least Q20
Estimated insert size: 137500; agarose-fp estimation
Estimated insert size: 76669; sum-of-contigs estimation
Quality coverage: 7.05 in Q20 bases; agarose-fp estimation
Quality coverage: 12.65 in Q20 bases; sum-of-contigs estimation.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 19 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.
* 1 1478: contig of 1478 bp in length
* 1479: gap of unknown length
* 1579: contig of 1027 bp in length
* 2606: gap of unknown length
* 2705: gap of unknown length
* 3993: contig of 1288 bp in length
* 3994: gap of unknown length
* 4094: contig of 1191 bp in length
* 5285: gap of unknown length
* 5385: contig of 2864 bp in length
* 8249: gap of unknown length
* 8349: contig of 1676 bp in length
* 10025: gap of unknown length
* 10125: contig of 1743 bp in length
* 11868: gap of unknown length
* 11968: contig of 1298 bp in length
* 13265: gap of unknown length
* 13366: contig of 2845 bp in length
* 16211: gap of unknown length
* 16311: contig of 3015 bp in length
* 19325: gap of unknown length
* 19425: contig of 2034 bp in length
* 21426: gap of unknown length
* 21460: contig of 3010 bp in length
* 21560: gap of unknown length
* 24570: contig of 3041 bp in length
* 24670: gap of unknown length
* 27711: contig of 2328 bp in length
* 30139: gap of unknown length
* 30239: contig of 4201 bp in length
* 34439: gap of unknown length
* 34539: contig of 7114 bp in length
* 34654: gap of unknown length
* 41754: contig of 7797 bp in length
* 49551: gap of unknown length
* 49651: contig of 10021 bp in length
* 59672: gap of unknown length
* 59772: contig of 18698 bp in length
```

```
*      * 59672 59771: gap of unknown length
*      * 59772 78469: contig of 18698 bp in length.
FEATURES
    source          Location/Qualifiers
        1..78469
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /chromosome="5"
            /clone="CND-2025J21"
            /clone_lib="CalTech human BAC library D"
BASE COUNT      18889 a 18951 c 18948 g 19879 t 1802 others
ORIGIN
Query Match      53.3%; Score 88.4; DB 75; Length 78469;
Best Local Similarity 80.0%; Pred. No. 6.9e-14;
Matches 104; Conservative 0; Mismatches 26; Indels 0; Gaps 0;
QY   37 cctgcgtcctctgcatggctctgggtccatcgagcgtctggttgactggtgcatgac 96
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   73681 CCTCAATCTCTCTCTGGCACGTGGCCCTCATGGCGCTTTGTTGACCAGCGTCAATTGC 73622
QY   97 tctcacctgcgtggtgacctgcccccgcgcgcgtgactcccccaaccctcaa 156
     ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
DB   73621 TCTCACTTGCTTGGCGCTTGCTCCCCAGGCCCTTCCTCCCTCTACAGCCCTCAG 73562
QY   157 ggagtcatt 166
     ||||| |||||
DB   73561 GGAGCTCATT 73552

RESULT 15
BTA132441
LOCUS       BTA132441 3520 bp DNA MAM 10-SEP-1999
DEFINITION Bos taurus il13 gene, exons 1-4.
ACCESSION  AJ132441
VERSION     AJ132441.1 GI:5420144
KEYWORDS   il13 gene; interleukin-13.
SOURCE      Bos taurus.
ORGANISM   Bos taurus
           Eukaryota; Chordata; Craniata; Vertebrata; Mammalia;
           Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
           Bovinae; Bos.
REFERENCE   1 (bases 1 to 3520)
AUTHORS    Buittkamp,J., Jann,O. and Fries,R.
TITLE      The cattle interleukin-13 gene: genomic organization, chromosomal
           location, and evolution of the promoter
JOURNAL    Immunogenetics 49 (10), 872-878 (1999)
MEDLINE    99367396
REFERENCE   2 (bases 1 to 3520)
AUTHORS    Buittkamp,J.
TITLE      Direct Submission
JOURNAL    Submitted (19-JAN-1999) Buittkamp J., Tierzucht, TU-Muenchen, Alte
           Akademie 12, 85350 Freising, GERMANY
FEATURES
    source          Location/Qualifiers
        1..3520
            /organism="Bos taurus"
            /db_xref="taxon:9913"
            /chromosome="4"
            /dev_stage="adult"
            /map="4q23-31"
            /clone="IS16b"
            /join(588..789,1742..1795,2038..2142,2484..2591)
gene       join(588..789,1742..1795,2038..2142,2484..2591)
           588..2591
exon       /gene="il13"
           588..789
           /number=1
sig_peptide 657..717
           /gene="il13"
CDS        /join(658..789,1742..1795,2038..2142,2484..2591)
           /gene="il13"
           /codon_start=1
```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:28:50 ; Search time 472.02 Seconds

(without alignments)

336.402 Million cell updates/sec

Title: US-09-451-527-89

Perfect score: 272

Sequence: 1 tggccttgctcccgagcc.....cagtgaacgagccgagaca 272

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*
1: /cgnl_8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	272	100.0	272	21	Canine interleukin
2	272	100.0	393	21	Canine interleukin
3	272	100.0	393	21	Canine interleukin
4	272	100.0	1302	21	Canine interleukin
5	272	100.0	1302	21	Canine interleukin
6	256	94.1	333	21	Canine mature inte
7	256	94.1	333	21	Canine mature inte
8	256	94.1	330	21	Canine interleukin
9	256	94.1	330	21	Canine interleukin
10	256	94.1	1269	21	Canine interleukin
11	256	94.1	1269	21	Canine interleukin

c	12	240	88.2	330	21	Z55565
	13	240	88.2	330	21	Z55566
	14	234	86.0	278	21	Z55554
	15	176.4	64.9	1270	21	F21334
	16	176.4	64.9	1270	21	A35212
	17	176.4	64.9	1282	21	F21332
	18	176.4	64.9	1282	21	A35210
	19	176.4	64.9	1290	15	Q56692
	20	176.4	64.9	6952	21	F21333
	21	176.4	64.9	6952	21	A35211
	22	176.4	64.9	14978	21	F21338
	23	176.4	64.9	14978	21	A35216
	24	174.8	64.3	1297	13	Q28947
	25	165.2	60.7	336	13	Q28944
	26	163.6	60.1	336	13	Q28943
	27	128	47.1	1212	15	Q56693
	28	71	26.1	5670	21	F21331
	29	71	26.1	5670	21	F21337
	30	71	26.1	5670	21	A35209
	31	71	26.1	5670	21	A35215
	32	55	20.2	166	21	Z55552
	33	37.2	13.7	66	20	Z32227
	34	35.2	12.9	2249	18	T74283
	35	35.2	12.9	2300	18	T74282
	36	35.2	12.9	3187	17	T10922
	37	35.2	12.9	3192	18	T72106
	38	35.2	12.9	3192	18	T63318
	39	35.2	12.9	3192	21	Z24236
	40	34	12.5	479	21	C38383
	41	34	12.5	1896	21	Z48297
	42	33.6	12.4	772	19	V48405
	43	33.2	12.2	2712	20	Z06825
	44	33.2	12.2	77536	21	A14651
	45	32.4	11.9	717	21	A93373

ALIGNMENTS

RESULT 1
Z55553
ID Z55553 standard; cDNA; 272 BP.
XX
AC Z55553;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.
XX
KW Interleukin-13; IL-13; antibody; canine; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
PS Claim 11; Page 228; 264pp; English.
XX

OS Canis familiaris.
XX
PN WO9961618-A2.
XX
XX
PD 02-DEC-1999.
XX
XX
PF 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
PR (HESK-) HESKA CORP.
XX
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR P-PSDB; Y58221.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX
PS Claim 11; Page 233; 264pp; English.
XX
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match 100.0%; Score 272; DB 21; Length 393;
Best Local Similarity 100.0%; Pred. No. 5.3e-67;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggccttgctcccgagccctgtgactccctcccaaccctcaaggagctcattgagga 60
Db 349 TGGCCTTGCTCCCGAGCCCTGTGACTCCCTCCCAACCCTCAAGGAGCTCAATTGAGGA 290

Qy 61 gctggtcaacatcacccagaatcaggcatccctctgcaacggcgagcatggtgtggagcgt 120
Db 289 GCTGGTCAACATCACCCAGCAATCAGGCATCCCTCTGCAACGGCGAGCATGTTGGAGCGT 230

Qy 121 caactgacccgcgcgcatgtactgacgacgtctatgataatctctgataatgtctccgactg 180
Db 229 CAACCTGACCCGCGGCATGACTGCGCAGCTCTAGATAATCTCTGATCAATGCTCCGACTG 170

Qy 181 cagcgcacatccaaagaccagagatgctgaaagcactgtgctctcaaaagccacgac 240
Db 169 CAGCGCCATCCAAAGGACCCAGAGGATGCTGAAGACACATGTGTCTCAAAAGCCCGCGC 110

Qy 241 agggcagatcttcagtgaaacgacgcgagaca 272
Db 109 AGGGCAGATTTTCCAGTGAACGACGACGCGAGACA 78

RESULT 4
25555

255555 standard; cDNA; 1302 BP.
255555;
14-MAR-2000 (first entry)
Canine interleukin-13 (IL-13) clone 80 cDNA.
Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
Canis familiaris.
Key Location/Qualifiers
CDS 52..447
FT /*tag= a
FT /product= "Canine IL-13 clone 80"
XX
PN WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR P-PSDB; Y58221.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 229-230; 264pp; English.
XX
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 272; DB 21; Length 1302;
Best Local Similarity 100.0%; Pred. No. 7.3e-67;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 tggccttgctcccgagccctgtgactccctcccaaccctcaaggagctcattgagga 60
Db 96 tggccttgctcccgagccctgtgactccctcccaaccctcaaggagctcattgagga 155

Qy 61 gctggtcaacatcacccagaatcaggcatccctctgcaacggcgagcatggtgtggagcgt 120
Db 156 gctggtcaacatcacccagaatcaggcatccctctgcaacggcgagcatggtgtggagcgt 215

CC	and in drug targetting.
XX	
SQ	Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;
Query Match	100.0%; Score 272; DB 21; Length 1302;
Best Local Similarity	100.0%; Pred. No. 7.3e-67;
Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps	
QY	1 tggccttgctccccgagccctgtgactccctcccaaccctcaagagcgtcattgagga 60
DB	1207 TGGCTTGCCTTCCCGAGCCCTGTGACTCCTCCCAACCCCTCAAGGAGCTCATTCAGGA 114
QY	61 gctggtcaacatcacccaggaatcaggcatccctctgcaacggcagcatggtgtggagcgt 120
DB	1147 GCTGGTCAACATCACCCAGAATCAGGCATCCCTCTGCAACGGCAGCATGCTGTGGAGCGT 108
QY	121 caacctgacgcggcgatgtactgcygcagctctagaaatctctgataatctctccgactg 180
DB	1087 CAACCTGACCCCGCGCATGTACTCCGAGCTCTAGAAATCTCTGATCAATGCTCTCCGACTG 102
QY	181 cagcgccatcaaaagaccagaggatgctgaaagcactgtgctctcaaaagccgcgcgc 240
DB	1027 CAGCGCCATCCAAAGGACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCCGCGC 968
QY	241 agggcagatttcagtgaaacgcagccgagaga 272
DB	967 AGGSCAGATTTCAGTGAACGACGACGAGACA 936
RESULT	6
ID	255559 standard; cDNA; 333 BP.
XX	
AC	255559;
XX	
DT	14-MAR-2000 (first entry)
XX	
DE	Canine mature interleukin-13 (IL-13); clone 80 cDNA.
XX	
KW	Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX	
OS	Canis familiaris.
XX	
PN	WO9961618-A2.
XX	
PD	02-DEC-1999.
XX	
PF	28-MAY-1999; 99WO-US11942.
XX	
PR	29-MAY-1998; 98US-0087306.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX	
DR	WPI: 2000-072623/06.
DR	P-PSDB; Y58222.
XX	
PT	Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT	useful for treating or preventing e.g. tumors or autoimmune disease
XX	
PS	Claim 11; Page 233-234; 264pp; English.
XX	
CC	Sequences 255552-255560 and 255561-255566 represent cDNA
CC	sequences encoding canine interleukin-13 (IL-13) clones 80
CC	and 78 respectively. The invention relates to canine
CC	IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC	feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC	interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC	colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC	immunoregulatory proteins. The proteins, their associated

CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 333;
 Best Local Similarity 100.0%; Pred. No. 1.5e-62;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 17 agccctgtgactccctcccaaccctcaaggagctcattgagagctgtgtcaacatcacc 76
 Db 1 agccctgtgactccctcccaaccctcaaggagctcattgagagctgtgtcaacatcacc 60
 Qy 77 cagaatcaggatccctctgcaacggcagcagctggtgtgagagctcaacctgacgcgcgc 136
 Db 61 cagaatcaggatccctctgcaacggcagcagctggtgtgagagctcaacctgacgcgcgc 120
 Qy 137 atgtactgcgcagctcagaatctctgataatgtctccgactgcagcgcacccaagg 196
 Db 121 atgtactgcgcagctcagaatctctgataatgtctccgactgcagcgcacccaagg 180
 Qy 197 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcagagttccagt 256
 Db 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcagagttccagt 240
 Qy 257 gaacgcagccgagaca 272
 Db 241 gaacgcagccgagaca 256

RESULT 7
 255560/c
 ID 255560 standard; cDNA; 333 BP.
 AC
 XX
 XX 255560;
 DT 14-MAR-2000 (first entry)
 DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.
 DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 XX WO9961618-A2.
 PN
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 PR
 PR 29-MAY-1998; 98US-0087306.
 XX
 XX (HESK-) HESKA CORP.
 PA
 XX
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 PI
 XX
 XX WPI: 2000-072623/06.
 DR
 DR P-PSDB; Y58222.
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 useful for treating or preventing e.g. tumors or autoimmune disease

XX Claim 11; Page 235; 264pp; English.
 XX
 CC Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (G-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;
 Query Match 94.1%; Score 256; DB 21; Length 333;
 Best Local Similarity 100.0%; Pred. No. 1.5e-62;
 Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 17 agccctgtgactccctcccaaccctcaaggagctcattgagagctgtgtcaacatcacc 76
 Db 333 AGCCCTGTGACTCCCTCCCAACCTCAAGGAGCTCAATTGAGGAGCTGTCAACATCACC 274
 Qy 77 cagaatcaggatccctctgcaacggcagcagctggtgtgagagctcaacctgacgcgcgc 136
 Db 273 CAGAATCAGGATCCCTCTGCAAGCGCAGCATGCTGTGAGCGTCAAGCTGACCGCGC 214
 Qy 137 atgtactgcgcagctcagaatctctgataatgtctccgactgcagcgcacccaagg 196
 Db 213 ATGTACTGCGCAGCTCTAGAAATCTGTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 154
 Qy 197 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcagagttccagt 256
 Db 153 ACCCAGAGGATGCTGAAAGCAGCTGTGCTCTCAAAAGCCGCGGAGGAGGATTTCCAGT 94
 Qy 257 gaacgcagccgagaca 272
 Db 93 GAACGCAGCCGAGACA 78
 RESULT 8
 255563
 ID 255563 standard; cDNA; 390 BP.
 AC
 XX 255563;
 XX
 DT 14-MAR-2000 (first entry)
 DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.
 DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 XX WO9961618-A2.
 PN
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX


```

PR 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI: 2000-072623/06.
XX P-PSDB; Y58223.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 238-239; 264pp; English.
XX
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha), and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX can also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for
XX modulators of activity, while the antibodies may be used in detection,
XX and in drug targeting.
XX
XX Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 390;
Best Local Similarity 98.9%; Pred. No. 1.5e-62;
Matches 269; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 tggccttgctccccgagccctgtgactccctccccaacctcaaggagctattgagga 60
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
45 tggccttgctccccgagccctgtgactccctccccaacctcaaggagctattgagga 104
QY 61 gctggtcaacatcacccagagatcagcctctctgcaacgagcagcatggtgagcgt 120
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 105 gctggtcaacatcacccagagatcagcctctctgcaacgagcagcatggtgagcgt 164
QY 121 caacctgacgcgcgcatgtactgcgagctctagaatctctgataatgtctccgactg 180
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 165 caacctgacgcgcgcatgtactgcgagctctagaatctctgataatgtctccgactg 224
QY 181 cagcgccatccaaagagccagagatgctgaagcactgctctcaaaagcccgaggc 240
DB ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 225 cagcgccatccaaagagccagagatgctgaagcactgctctcaaaagcccgaggc 284
QY 241 agggcagatttccagtgaacgagccgagaca 272
DB ||||| ||||||| ||||||| ||||||| ||||||| ||||||| ||||||| |||||||
DB 285 agg--gatttccagtgaacgagccgagaca 313

RESULT 9
Z55564/c
ID Z55564 standard; cDNA; 390 BP.
XX
AC Z55564;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI: 2000-072623/06.
XX P-PSDB; Y58223.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 239; 264pp; English.
XX
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha), and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX can also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for
XX modulators of activity, while the antibodies may be used in detection,
XX and in drug targeting.
XX
XX Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 390;
Best Local Similarity 98.9%; Pred. No. 1.5e-62;
Matches 269; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 tggccttgctccccgagccctgtgactccctccccaacctcaaggagctattgagga 60
DB 346 tggccttgctccccgagccctgtgactccctccccaacctcaaggagctattgagga 287
QY 61 gctggtcaacatcacccagagatcagcctctctgcaacgagcagcatggtgagcgt 120
DB 286 GCTGTCAACATCACCCAGCATCCCTCTCTCAACGGCAGCATGGTGTGGAGCGT 227
QY 121 caacctgacgcgcgcatgtactgcgagctctagaatctctgataatgtctccgactg 180
DB 226 CAACCTGACCGCGGCATGTACTGCCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTG 167
QY 181 cagcgccatccaaagagccagagatgctgaagcactgctctcaaaagcccgaggc 240
DB 166 CAGCGCCATCCAAAGAGACCCAGAGGATGCTGAAGCACTGTGCTCTCAAAAGCCCGCGC 107
QY 241 agggcagatttccagtgaacgagccgagaca 272
DB 106 AGG---GATTTCCAGTGAACGAGCGGAGACA 78
```


CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX SQ Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 94.1%; Score 256; DB 21; Length 1269;
 Best Local Similarity 98.9%; Pred. No. 2.1e-62;
 Matches 269; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 tggccttgctcccccagccctgtgactccctcccccacccctcaaggagctcattgagga 60
 Db 1169 TGGCCTTGCTCCCGACCCCTGTGACTCCCTCCCAACCTCAAGAGCTCATTTGAGA 1110

QY 61 gctggtcaacatcacccagaatcaggcatcctctgcaacgagcatggtgtgagcgt 120
 Db 1109 GCTGCTCAACATCACCCAGATCAGGCATCCCTCTGCAACGCGCATGGTGTGAGCGT 1050

QY 121 caactgaccccgccatgactgactgcaagctctagaatctctgatcaatgtctccgactg 180
 Db 1049 CAACCTGACCCCGCGCATGTACTGCGCAGCTCTAGAACTCTGATCAATGTCTCGACTG 990

QY 181 cagcgccatccaaaggacccagagatgctgaagcactgtgctctcaaaagcccgccgc 240
 Db 989 CAGCGCCATCCAAAGGACCCAGAGATGCTGAAGCACTGTGCTCTCAAAAGCCCGCGGC 930

QY 241 agggcagatttccagtaaacgagcccgagaca 272
 Db 929 AGG---GATTTCAGTGAACGCGCGAGACA 901

RESULT 12

ID 255565 standard; cDNA; 330 BP.

XX AC 255565;

XX DT 14-MAR-2000 (first entry)

XX DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.

XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

XX KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US11942.

XX PR 29-MAY-1998; 98US-0087306.

XX PA (HESK-) HESKA CORP.

XX PI Slim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; Y58224.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumors or autoimmune disease

XX PS Claim 11; Page 239-240; 264pp; English.

XX CC Sequences 255552-255560 and 255561-255566 represent cDNA

XX CC sequences encoding canine interleukin-13 (IL-13) clones 80

XX CC and 78 respectively. The invention relates to canine

XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 88.2%; Score 240; DB 21; Length 330;
 Best Local Similarity 98.8%; Pred. No. 4.3e-58;
 Matches 253; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 17 agccctgtgactccctcccccacccctcaaggagctcattgagagctgtcaacatcac 76
 Db 1 agccctgtgactccctcccccacccctcaaggagctcattgagagctgtcaacatcac 60

QY 77 cagaatcaggcatccctctgcaacgagcagcagctgtgtgagcgtcaacctgacccgcgc 136
 Db 61 cagaatcaggcatccctctgcaacgagcagcagctgtgtgagcgtcaacctgacccgcgc 120

QY 137 atgtactgcgagctctagaatctctgataatgtctccgactgcagcgcattccaaag 196
 Db 121 atgtactgcgagctctagaatctctgataatgtctccgactgcagcgcattccaaag 180

QY 197 accagagatgctgaagcactgtgtctcaaaagcccgagcagcgagattccagt 256
 Db 181 accagagatgctgaagcactgtgtctcaaaagcccgagcagcgagattccagt 237

QY 257 gaacgcagccgagaca 272

Db 238 gaacgcagccgagaca 253

RESULT 13

255566/c

XX ID 255566 standard; cDNA; 330 BP.

XX AC 255566;

XX DT 14-MAR-2000 (first entry)

XX DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.

XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

XX KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US11942.

XX PR 29-MAY-1998; 98US-0087306.

XX PA (HESK-) HESKA CORP.

XX PI Slim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; Y58224.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,

XX useful for treating or preventing e.g. tumors or autoimmune disease

XX PS Claim 11; Page 239-240; 264pp; English.

XX CC Sequences 255552-255560 and 255561-255566 represent cDNA

XX CC sequences encoding canine interleukin-13 (IL-13) clones 80

XX CC and 78 respectively. The invention relates to canine

XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:45 ; Search time 226.02 Seconds
(without alignments)
210.123 Million cell updates/sec

Title: US-09-451-527-89
Perfect score: 272
Sequence: 1 tggccttgctcccgagcc.....cagtgaacgcagccgagaca 272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents.NA.*
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq.*
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq.*
3: /cgnl_7/ptodata/1/ina/6A_COMB.seq.*
4: /cgnl_7/ptodata/1/ina/6B_COMB.seq.*
5: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgnl_7/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	176.4	64.9	1290	1 US-08-012-543-1	Sequence 1, Appli
2	176.4	64.9	1290	5 PCT-US93-07645A-1	Sequence 1, Appli
3	176.4	64.9	1290	5 PCT-US93-07645-1	Sequence 1, Appli
4	174.8	64.3	1297	1 US-08-371-121-15	Sequence 15, Appl
5	165.8	61.0	384	1 US-08-371-121-17	Sequence 17, Appl
6	165.2	60.7	336	1 US-08-371-121-24	Sequence 24, Appl
7	164	60.3	425	1 US-08-594-469-4	Sequence 4, Appli
8	164	60.3	425	2 US-08-906-957-4	Sequence 4, Appli
9	164	60.3	4410	1 US-08-594-469-1	Sequence 1, Appli
10	164	60.3	4410	2 US-08-906-957-1	Sequence 1, Appli
11	163.6	60.1	336	1 US-08-371-121-2	Sequence 2, Appli
12	128	47.1	447	1 US-08-371-121-26	Sequence 26, Appl
13	128	47.1	1212	1 US-08-012-543-3	Sequence 3, Appli
14	128	47.1	1212	5 PCT-US93-07645A-3	Sequence 3, Appli
15	128	47.1	1212	5 PCT-US93-07645-3	Sequence 3, Appli
16	35.2	12.9	2249	3 US-08-814-052-19	Sequence 19, Appl
17	35.2	12.9	2300	3 US-08-814-052-18	Sequence 18, Appl
18	35.2	12.9	3183	2 US-08-939-218A-1	Sequence 1, Appli
19	35.2	12.9	3187	5 PCT-US95-06815-1	Sequence 1, Appli
20	35.2	12.9	3192	1 US-08-706-037-26	Sequence 26, Appl
21	35.2	12.9	3192	1 US-08-940-661A-1	Sequence 1, Appli
22	35.2	12.9	3192	2 US-09-083-485-1	Sequence 1, Appli
23	35.2	12.9	3192	2 US-09-005-397-26	Sequence 26, Appl
24	33.6	12.4	1322	4 US-09-128-450-27	Sequence 27, Appl
25	33.2	12.2	2712	3 US-09-025-691-4	Sequence 4, Appli
26	32.4	11.9	720	4 US-09-094-359-3	Sequence 3, Appli
27	32.4	11.9	720	4 US-09-094-359-7	Sequence 7, Appli

28 32.4 11.9 720 4 US-09-172-063-11 Sequence 11, Appl
29 32.4 11.9 720 4 US-09-172-063-13 Sequence 13, Appl
30 32.4 11.9 762 1 US-08-532-390-40 Sequence 40, Appl
31 32.4 11.9 762 4 US-08-717-294-40 Sequence 40, Appl
32 32.4 11.9 768 4 US-09-094-359-11 Sequence 11, Appl
33 32.4 11.9 850 4 US-09-062-102-2 Sequence 2, Appli
34 32.4 11.9 972 4 US-09-172-063-27 Sequence 27, Appl
35 32.4 11.9 972 4 US-09-172-063-29 Sequence 29, Appl
36 32.4 11.9 1095 4 US-09-085-305-5 Sequence 5, Appli
37 32.4 11.9 1929 2 US-08-818-253-1 Sequence 1, Appli
38 32.4 11.9 1929 2 US-08-818-253-5 Sequence 5, Appli
39 32.4 11.9 1929 4 US-08-818-252-1 Sequence 1, Appli
40 32.4 11.9 1929 4 US-08-818-252-5 Sequence 5, Appli
41 32.4 11.9 1959 2 US-08-818-253-3 Sequence 3, Appli
42 32.4 11.9 1959 4 US-08-818-252-7 Sequence 7, Appli
43 32.4 11.9 1971 2 US-08-818-252-7 Sequence 7, Appli
44 32.4 11.9 1971 4 US-08-818-252-7 Sequence 7, Appli
45 32.4 11.9 7938 4 US-09-331-581-14 Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banhereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

```

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
US-08-012-543-1

```

Query Match	64.9%	Score 176.4;	DB 1;	Length 1290;
Best Local Similarity	80.3%	Pred. No. 8.9e-45;		
Matches 220;	Conservative	0;	Mismatches 51;	Indels 3;
			Gaps 1;	

Qy	2	ggccttgctccccgagccctgtgactccctccccaaacctcaagagagctcatctgaggag	61
Db	90	GGCTTTGCCCTCCCGAGCCCTGTGCTCCCTACAGCCCTCAGGAGGCTCATTGAGGAG	149
Qy	62	ctggtcaacatcacccagaatc--aggcatccctctgaacggcagcatggtgtgagac	118
Db	150	CTGGTCAACATCACCAGAACCCAGAGGCTCCGCTCTGCATAATGGCAGCATGCTATGGAGC	209
Qy	119	gtcaacctgaccgcggcgatgactgcgcgagctctagaatctctgatatcgtctccgac	178
Db	210	ATCAACCTGCAGCTGGCATGTACTGTGCAGCCCTCGAATCCCTGTATCAACGTGTCAAGC	269
Qy	179	tgaagcgcctatcaaaagaccagagagatgctgaagacactgtgctctcaaaagccgcg	238
Db	270	TGCAGTCCCATCGAGAGACCCAGAGGATGCTGAGCGGATTTGCCCGCACAGAGTTCTCA	329
Qy	239	gcagggcagatattccagtgcaacgcagcgagaca	272
Db	330	GC'TGGGCAGT'TTTTCCAGT'TGCATGTCCGAGACA	363

```

RESULT      2
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

```

Query Match	64.9%	Score 176.4;	DB 5;	Length 1290;
Best Local Similarity	80.3%	Pred. No. 8.9e-45;		
Matches 220;	Conservative	0;	Mismatches 51;	
			Indels 33;	Gaps 1;

QY 2 GGCTGGCTCCCGAGGCGCTGTGAATCCTCCCCAACCTCAAGAGTcattgaggag 61
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 90 GGCTTTGCCTCCCACAGGCCGTGCTTCCTCACAGCCCTACGGAGGCTCATTTAGGAG 149

QY 62 cttctcaatcatccccaagaatc---aaqcatcctctgcacaacgccacatgaatgaaac 118

Db	150	CTGTCAACATCACCGAAGAGGCTCGCTCTGCAATGSCAGCATGATGAGC	209
Qy	119	gtcaacctgaaccgcgcatgtactgcgcagctcgaatactctgatcaatgtctccgac	178
Db	210	ATCAACCTTGACAGTGGCATGTCTGTGACGCCCTGGAACTCCGTATCAACGTTGACGC	269
Qy	179	tgcagcccatccaaaggaccagaggaatgctgaagcactgtgctctcaaaagccgcg	238
Db	270	TGCAGTGCATTCGAGAAGACCCAGAGGATGCTGAGCGGATTCTCCCGCACAAGGTTCTCA	329
Qy	239	gcaaggcgagatttcagtgaaacgcagccgagaca	272
Db	330	GCTGGCGAGTTTCCAGCTTCAGCTGTCAGTCCGAGACA	363

```

RESULT      3
PCT-US93-07645-1
; Sequence 1, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-1

```

Query Match	64.9%	Score	176.4	DB 5	Length	1290
Best Local Similarity	80.3%	Pred. No.	8.9e-45			
Matches	220	Conservative	0	Mismatches	51	Indels
					3	Gaps
					1	

Qy	2	ggccttgccctcccgcagaccctgtgactccctcccccacccctcaagagagctcatgtgaggag	61
Db	90	ggccttgccctcccgcagaccctgtgactccctcccccacccctcaagagagctcatgtgaggag	149
Qy	62	ctggtgcaacatcacccagaatc---aggcatccctctgcaacgcgcagcatggtgtgagac	118
Db	150	ctggtgcaacatcacccagaacccaagagcctcgctctgcaatggcagcatggatggagc	209
Qy	119	gtcaactgacccgcgcagcatgtactgcgcagcgtctagaatctctgtatcaatgctctccac	178
Db	210	atcaactgtgacagctggcatgtactgtgcagaccctggaaatccctgtatcaacgctgtcaggc	269
Qy	179	tgcagcgccatccaaagaccagagatgctgaaagcactgtgctctcaaaaagcccgcg	238
Db	270	tgcagtgccatcgagagaccagagcatgctgagcggatttgcctccgcacagagcttca	329
Qy	239	gcaggcgagatttccagtgacgcgagcccgagaca	272
Db	330	gctgggagagttttccagcttgcattgtcccgagaca	363

```

RESULT 4
US-08-371-121-15
; Sequence 15, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE ROUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938.161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..452
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 117..452
; US-08-371-121-15

Query Match 64.3%; Score 174.8; DB 1; Length 1297;
Best Local Similarity 79.9%; Pred. No. 2.7e-44;
Matches 219; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

RESULT 5
US-08-371-121-17
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE ROUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938.161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..452
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 117..452
; US-08-371-121-15

Query Match 64.3%; Score 174.8; DB 1; Length 1297;
Best Local Similarity 79.9%; Pred. No. 2.7e-44;
Matches 219; Conservative 0; Mismatches 52; Indels 3; Gaps 1;


```

```

QY 2 ggcttgctcccccagagcctgtgactccctcccaaacctcaaggagctcattgaggag 61
Db 102 GGCTTTGCCCTCCCGAGGCCCTGTGCCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAG 161
QY 62 ctggtcaacatcacccagaatc---aggcatccctctgcaacggcagcagcatggtggaqc 118
Db 162 CTGGTCAACATCACCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGC 221
QY 119 gtcaacctgaccgcggcagctagtctgctgagctctagaatctctgataatgtctccgac 178
Db 222 ATCAACCTGACAGTGACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGCAGGC 281
QY 179 tgagcgccatccaaagaccagagatgctgaaagcactgtgtctctcaaaagccgcgc 238
Db 282 TGAGTGCCTCGAGAACCCAGAGGATGCTGAGCGATTCTGCCCGCACAAAGGTCTCA 341
QY 239 gcagggcagatttccagtgaaacgcagcagagaca 272
Db 342 GCTGGGCGAGTTTCCAGCTTGCATGTCGAGACA 375

RESULT 5
US-08-371-121-17
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE ROUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938.161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..452
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 117..452
; US-08-371-121-15

Query Match 64.3%; Score 174.8; DB 1; Length 1297;
Best Local Similarity 79.9%; Pred. No. 2.7e-44;
Matches 219; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

```


INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match
Best Local Similarity 61.0%; Score 165.8; DB 1; Length 384;
Matches 210; Conservative 0; Mismatches 52; Indels 3; Gaps 1;

QY 11 tccccagccctgtgactccctcccccacccctcaagagctcattgaggagctggtcaac 70
DB 16 TCCCCAGGCCCTGTGCTCCCTCTACGCCCTCAGGAGCTCATTTAGGAGCTGTCAAC 75
QY 71 atcaccagatc---aggcatccctctgcaacgagcagctggtgagagctcaactg 127
DB 76 ATACCCAGAACAGAGAGCTCCCTCTGCANTGGCAGCATGGTATGAGCATCAACCTG 135
QY 128 accgcccggctactgctgagcagctgagatctctgacatctctccgactgcagcgcc 187
DB 136 ACAGCTGACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTTGAGGCTGCC 195
QY 188 atccaaagaccagagagatgctgaaagcactgtgctctcaaaaagccgagcgagcag 247
DB 196 ATGAGAAGACCCAGAGAGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGCGAG 255
QY 248 atttcagtgaaacgagcagcgagaca 272
DB 256 TTTTCCAGCTTGATGTCCGAGACA 280

RESULT 6
US-08-371-121-24
Sequence 24, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMET, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTEILLER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992

PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match
Best Local Similarity 60.7%; Score 165.2; DB 1; Length 336;
Matches 207; Conservative 0; Mismatches 48; Indels 3; Gaps 1;

QY 18 gccctgtgactccctcccccacccctcaagagctcattgaggagctggtcaacatcaccc 77
DB 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTAGGAGCTGTCAACATCACCC 61
QY 78 agaatc---aggcatccctctgcaacgagcagctggtgagagctcctccgactgcagcgccg 134
DB 62 AGAACCAAGAGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121
QY 135 gcattactgagcagctctagaaatctctgacatctctccgactgcagcgccatccaaa 194
DB 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGTCAAGCTGTGAGTGCATCGAGA 181
QY 195 ggaaccagagagatgctgaaagcactgtctcctcaaaaagccgagcgagcgagatttcca 254
DB 182 AGACCCAGAGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGTGGCGAGTTTCCA 241
QY 255 gtgaacgagcagcgagaca 272
DB 242 GCTTGCATGTCCGAGACA 259

RESULT 7
US-08-594-469-4
Sequence 4, Application US/08594469
Patent No. 5700665
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

COMPUTER: IBM PC compatible

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FIGHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; TOPOLOGY: single
; STANDEDNESS: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-594-469-1

```

Query Match 60.3%; Score 164; DB 1; Length 4410;

	Best Local Similarity	Mismatches	Conservative	% 4s	Pied: NO: 7:0e 41:	Indels	Gaps
Qy	8	gcctccccgagccctgtgactccctcccccacccctcaaggagctcaattgaggagctggtc	67				
Db	392	GCCTTGCTGCCCTGTGCCCTCCAGTACTGCCCTCAGGGAGCTCATTTGAGGAGCTGTGTC	451				
Qy	68	aacatcacccagaatc---aagcatccctctgcaacggcagcatggttgtgagggtcaac	124				
Db	452	AACATACCCCAAGAACCAAGAGGCCTCCGCTCTGCAATGGCAGCATGGTATGAGGACATCAAC	511				
Qy	125	ctgaccgcggcaltgactgcgcagctctagaactctctgataactgtctccgactgcagc	184				
Db	512	CTGACAGCTGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGCAGGCTGCAGT	571				
Qy	185	gcaatcaaaaggacccagagagatgctgaagcactgtgtctctcaaaagcccgcgaggg	244				
Db	572	GCCATCAGAGAAGACCCAGAGGATGCTGAGCGGATTTCTCCCGCAAGGCTCTCAGCTGGG	631				
Qy	245	cagattccagtgaacgcagccgagaca	272				
Db	632	CAGTTTTCCAGCTTGCATGTCCCGAGACA	659				

RESULT 10

```

US-08-906-957-1
: Sequence 1, Application US/08906957
: Patent No. 5856142
: GENERAL INFORMATION:
: APPLICANT: LEGOUX, Richard
: APPLICANT: MALDONADO, Paul
: APPLICANT: SALOME, Marc
: TITLE OF INVENTION: Method for
: TITLE OF INVENTION: periplasmic
: TITLE OF INVENTION: presence of
: NUMBER OF SEQUENCES: 9
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Bacon & Thomas
: STREET: 625 Slaters Lane - Fo
: CITY: Alexandria
: STATE: Virginia
: COUNTRY: USA
: ZIP: 22314
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible

```

```

; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
;
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
;
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E.
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
; US-08-906-957-1

```

Query Match 60.38: Score 164: DB 2: Length 4410:

	Best Local Similarity	78.4%;	Pred. No. 7.86-4.1;
Matches	210; Conservative	0;	Mismatches 55;
			Gaps 3; Indels 1;
Qy	8	gcctccccgagccctgtgaactccctcccacacctcaaggagcgtcatlgaggagctggtc	67
Db	392	GCCTTCGCTGCCCTGTGSCCTCCCAAGTACTGCCCTCAGGGAGCTATTGAGGAGCTGTC	451
Qy	68	aacatcacccagaatc---aggatccctctgcaaacggcagcatgtgtgagagctaac	124
Db	452	AACATCACCCAGAACCAAGAAGCGTCGCTCTGCAATGGCAGCATGGTATGAGCATCAAC	511
Qy	125	ctgaccgccggcatgtactgcgagctctgaatactctgatactctccgactgcagc	184
Db	512	CTGACAGCTGSCATGTACTGTGCGAGCCCTGGAATCCCTTGATCAACGTCTCAGGCTGCAGT	571
Qy	185	gccatcaaaagagccccagagagatgctaagaacactgtgctctcaaaaaccgcgcgaggg	244
Db	572	GCCATCGAAGAGACCAGAGAGATGCTGAGCGGATTCGCCCGCACAAGGTCTCAGCTGGG	631
Qy	245	cagatttcagtgaacgcagccgagaca	272
Db	632	CAGTTTTCCAGCTTTGCATGTCTCCGAGACA	659

RESULT 11

US-08-371121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascal
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match 60.1%; Score 163.6; DB 1; Length 336;
Best Local Similarity 79.8%; Pred. No. 4.4e-41;
Matches 206; Conservative 0; Mismatches 49; Indels 3; Gaps 1;
QY 18 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 77
Db 2 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGTCACATCACCC 61
QY 78 agaatc---aggatccctctgcaacgagcagcagctggtgagcgtcaacctgaccgcg 134
Db 62 AGAACCAAGGCTCCGCTCTGCATGCGAGCATGGTATGGAGCATCAACCTGACAGCTG 121
QY 135 gcattactgcgagctctagaatctctgataatgtctccgactgagcagcgcacataaa 194
Db 122 ACATGTACTGTGCAGCCCTCGAATCCCTGTATCAACGTGTGAGGCTGCGATCGCATCGA 181
QY 195 ggaaccagagatgctgaaagcagctgtctctcaaaagcccgagcgagatttcca 254
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTCCCGCAACAGGCTCTCAGCTGGCGAGTTTCCA 241
QY 255 gtgaacgcagcgcagaca 272
Db 242 GCTTGCATGTCGAGACA 259
RESULT 12
US-08-371-121-26
Sequence 26, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel

APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTEILLER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM: disk
MEDIUM TYPE: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-371-121-26
Query Match 47.1%; Score 128; DB 1; Length 447;
Best Local Similarity 73.2%; Pred. No. 3.3e-30;
Matches 164; Conservative 0; Mismatches 60; Indels 0; Gaps 0;
QY 14 ccagacccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatc 73
Db 118 CCAAGATCTGTCTCTCTCCCTCTGACCCCTTAAGAGCTTATTGAGGAGCTGAGCAACATC 177
QY 74 accagaatcaggcatccctctctgcaacgagcagcagctggtgagcgtcaacctgaccgcc 133
Db 178 ACACAAGACCAGACTCCCTCTGTGCAACGGCAGCATGTTATGAGTGTGGACCTGGCGCT 237
QY 134 gcatgtactgcgagctctagaaatctctgataatgtctccgactgagcagcgcacataaa 193
Db 238 GCGGGTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCCAATTCATGCGCATCTAC 297
QY 194 aggaccagagatgctgaaagcagctgtgctctctcaaaagccgcg 237

Dbb 298 AGGACCCAGAGGATATTGCATGGCCCTCTGTAAACCGCAAGGCCCC 341

RESULT 13
US-08-012-543-3

```

1 / SECRET NO: 5550972
2 /
3 / GENERAL INFORMATION:
4 /
5 / APPLICANT: Culpepper, Janice
6 / APPLICANT: McKenzie, Andrew
7 /
8 / APPLICANT: Dang, Warren
9 / APPLICANT: de Waal Malefyt, Rene
10 /
11 / APPLICANT: Heath, Andrew
12 /
13 / APPLICANT: Aversa, Gregorio
14 / APPLICANT: Briere, Francine
15 / APPLICANT: Banchereau, Jacques
16 / APPLICANT: de Vries, Jan
17 / APPLICANT: Zurawski, Gerard
18 /
19 / TITLE OF INVENTION: Human Interleukin-13
20 /
21 / NUMBER OF SEQUENCES: 27
22 / CORRESPONDENCE ADDRESS:
23 /

```

Query Match	47.1%	Score 128;	DB 1;	Length 1212;
Best Local Similarity	73.2%;	Pred. No. 4.5e-30;		
Matches 164;	Conservative	0;	Mismatches 60;	Indels 0;
				Gaps 0;

	Best bound similarity	Identical	Indels	Gaps
Matches 164; Conservative	95.24%	0	60	0
14	CGAGCGCTGTGACTCCTCCCAACCTCAAGAGCTATTGAGGAGCTGTTCAACATC	73		
139	CCAAGATCTGTCTCTCCCTCTGACCCCTTAAGAGAGCTTATTGAGGAGCTGAGCAACATC	198		
74	ACCAGAATCAGGCATCCCTCTCTGCAACGCGAGCATGTTGGAGCGTCAACCTGACCGCC	133		
199	ACACAGACCAAGACTCCCTCTGTCAGACGGCAGCATGTATGGAGTGTGGACCTGGCCGCT	258		
134	GGGATGACTGCGAGCTGTAGATCTCTGATCAATGTCTCCGACTGAGCGCCATCCAA	193		

Db 259 GCGGGTCTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAATGCCATCTAC 318
QY 194 aggaccagagatgctgaagcactgtgctctcaaaagccgc 237
Db 319 AGACCCAGAGATATTGGATGCCCTCTGTAAACCGCAAGCCGCC 362

```

RESULT 14
PCT-US93-07645A-3
; Sequence 3, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-3

```

Query Match	47.1%	Score 128;	DB 5;	Length 1212;
Best Local Similarity	73.2%	Pred. No. 4.5e-30;		
Matches 164;	Conservative	0;	Mismatches 60;	Indels 0;
			Gaps	0;

	Best bound similarity	Identical	Indels	Gaps
Matches 164; Conservative	95.24%	0	60	0
14	CGAGCGCTGTGACTCCTCCCAACCTCAAGAGCTATTGAGGAGCTGTTCAACATC	73		
139	CCAAGATCTGTCTCTCCCTCTGACCCCTTAAGAGAGCTTATTGAGGAGCTGAGCAACATC	198		
74	ACCAGAATCAGGCATCCCTCTCTGCAACGCGAGCATGTTGGAGCGTCAACCTGACCGCC	133		
199	ACACAGACCAAGACTCCCTCTGTCAGACGGCAGCATGTATGGAGTGTGGACCTGGCCGCT	258		
134	GGGATGACTGCGAGCTGTAGATCTCTGATCAATGTCTCCGACTGAGCGCCATCCAA	193		

```
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-3
```

```
Query Match          47.1%; Score 128; DB 5; Length 1212;
Best Local Similarity 73.2%; Pred. No. 4.5e-30;
Matches 164; Conservative 0; Mismatches 60; Indels 0; Gaps 0;

QY 14 ccgagccctgtgactccctcccccacccctcaaggagctcattgaggagctgggtcaacatc 73
   || || || || || || || || || || || || || || || || || || || || || ||
Db 139 CCAAGATCTGTGTCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTGAGCAACATC 198

QY 74 acccagaatcaggcatccctctgtcgaacgcagcatggtgtggagcgtcaacctgaccgcc 133
   || || || || || || || || || || || || || || || || || || || || || ||
Db 199 ACACAAGACGAGACTCCCTGTGCAACGGCAGCATGTTATGGAGTGTGGACCTGGCCGCT 258

QY 134 ggcattgactgcgacgtctagaatctctgatcaatgtctccgactgcagcgccatccaa 193
   || || || || || || || || || || || || || || || || || || || || || ||
Db 259 GCGGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAATGCCATCTAC 318

QY 194 aggaccagaggatgctgaagcactgtgctctcaaaagccgc 237
   || || || || || || || || || || || || || || || || || || || || || ||
Db 319 AGGACCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGCCCC 362
```

Search completed: May 13, 2001, 14:20:49
Job time: 17800 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:39:33 ; Search time 5997.24 Seconds
(without alignments)
396.219 Million cell updates/sec

Title: US-09-451-527-89
Perfect score: 272
Sequence: 1 tggccttgctcccgagcc.....cagtgaacgcagccgagaca 272

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : EST:

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*
- 12: gb_est12.*
- 13: gb_est13.*
- 14: gb_est14.*
- 15: gb_est15.*
- 16: gb_est16.*
- 17: gb_est17.*
- 18: gb_est18.*
- 19: gb_est19.*
- 20: gb_est20.*
- 21: gb_est21.*
- 22: gb_est22.*
- 23: gb_est23.*
- 24: gb_est24.*
- 25: gb_est25.*
- 26: gb_est26.*
- 27: gb_est27.*
- 28: gb_est28.*
- 29: gb_est29.*
- 30: gb_est30.*
- 31: gb_est31.*
- 32: gb_est32.*
- 33: gb_est33.*
- 34: gb_est34.*
- 35: gb_est35.*
- 36: gb_est36.*
- 37: gb_est37.*
- 38: gb_est38.*
- 39: gb_est39.*
- 40: gb_est40.*
- 41: gb_est41.*
- 42: gb_est42.*
- 43: gb_est43.*
- 44: gb_est44.*
- 45: gb_est45.*
- 46: gb_est46.*
- 47: gb_est47.*

- 44: em_esthum10.*
- 45: em_esthum11.*
- 46: em_esthum12.*
- 47: em_esthum13.*
- 48: em_esthum14.*
- 49: em_esthum15.*
- 50: em_esthum16.*
- 51: em_esthum17.*
- 52: em_esthum18.*
- 53: em_esthum19.*
- 54: em_esthum20.*
- 55: em_esthum21.*
- 56: em_esthum22.*
- 57: em_esthum23.*
- 58: em_esthum24.*
- 59: em_esthum25.*
- 60: em_esthum26.*
- 61: em_esthum27.*
- 62: em_esthum28.*
- 63: em_estin1.*
- 64: em_estin2.*
- 65: em_estin3.*
- 66: em_estin4.*
- 67: em_estin5.*
- 68: em_estom1.*
- 69: em_estom2.*
- 70: em_estov1.*
- 71: em_estov2.*
- 72: em_estpl1.*
- 73: em_estpl2.*
- 74: em_estpl3.*
- 75: em_estpl4.*
- 76: em_estpl5.*
- 77: em_estpl6.*
- 78: em_estpl7.*
- 79: em_estpl8.*
- 80: em_estpl9.*
- 81: em_estpl10.*
- 82: em_estro1.*
- 83: em_estro2.*
- 84: em_estro3.*
- 85: em_estro4.*
- 86: em_estro5.*
- 87: em_estro6.*
- 88: em_estro7.*
- 89: em_estro8.*
- 90: em_estro9.*
- 91: em_estro10.*
- 92: em_estro11.*
- 93: em_estro12.*
- 94: em_estro13.*
- 95: em_estro14.*
- 96: em_estro15.*
- 97: em_estro16.*
- 98: em_estro17.*
- 99: em_estro18.*
- 100: em_estro19.*
- 101: em_estro20.*
- 102: gb_est25.*
- 103: gb_est26.*
- 104: gb_est27.*
- 105: gb_est28.*
- 106: gb_est29.*
- 107: gb_est30.*
- 108: gb_est31.*
- 109: gb_est32.*
- 110: gb_est33.*
- 111: gb_est34.*
- 112: gb_est35.*
- 113: gb_est36.*
- 114: gb_est37.*
- 115: gb_est38.*
- 116: gb_est39.*

```
117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*
```

```
190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	36.4	13.4	277	137	BE593226	BS593226 WSL_99_B0
2	36.4	13.4	537	166	BE357229	BE357229 DG1_147_B
3	36	13.2	462	143	BF039993	BF039993 RP250023B
C 4	35.6	13.1	537	29	AV387571	AV387571 AV387571
C 5	35.6	13.1	1070	136	BE536034	BE536034 601062471
6	35.4	13.0	498	150	BF606532	BF606532 273595 MA
7	34.8	12.8	507	138	BE705147	BE705147 SC02_08f0
8	34.6	12.7	576	141	BE907816	BE907816 601501924
C 9	34.6	12.7	965	217	AZ201624	AZ201624 SP_0053_A
10	34.4	12.6	570	24	AT746678	AT746678 ul06b05_Y
11	34.2	12.6	535	161	BE032541	BE032541 131940 MA
12	34.2	12.6	546	161	BE032543	BE032543 131942 MA
13	34	12.5	341	163	BE127683	BE127683 DEPA1432
14	34	12.5	370	166	BE363650	BE363650 WSL_64_G1
15	34	12.5	562	166	BE361027	BE361027 DG1_69_A0
C 16	34	12.5	925	229	CNS0091P	AL053013 Drosophila
C 17	33.6	12.4	177	103	A1909438	A1909438 IL-BT208-
18	33.6	12.4	544	13	AA880435	AA880435 VW89f07.r


```

Db 249 CCCATGGAGAGGCTCGGGAGCCGCGGACATCGCGCGGTGCTCGGTTCTCTGCAC 308
QY 100 cgcagcatgtgtgagcgtcaacctgaccgcgcgcatgtactgagcagctctagaatc 159
Db 309 CGACGGCGCGAGTGGGTCAACGGCAGGTCACTCCGCCCAACGGCGGCTACGTGTGATG 368
QY 160 tctgatcaatgtctccgactgc 181
Db 369 TCTGATCTTTAGCTTCTACAGC 390

RESULT 3
LOCUS BF039993 462 bp mRNA EST 10-OCT-2000
DEFINITION BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA
clone BP250023B10D12 5', mRNA sequence.
ACCESSION BF039993
VERSION BF039993.1 GI:10757048
KEYWORDS EST.
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 462)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333-5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTACCTCACTAAG
Insert Length: 462 Std Error: 0.00
Plate: BP250023B10 row: D column: 12
Seq primer: ACGGTATACATTTTCACACGGA
High quality sequence stop: 462.
FEATURES
source
location/Qualifiers
1..462
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250023B10D12"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/note="Organ: placenta; Vector: pT73pac; Site_1: ECORI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 110 a 153 c 123 g 73 t 3 others
ORIGIN

Query Match 13.2%; Score 36; DB 143; Length 462;
Best Local Similarity 47.9%; Pred. No. 9.1;
Matches 102; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 41 ctcaagagactcattgaggagcgtggtcaacatcaccacagatcaggcatccctctgaac 100

```

```

Db 113 CTGATGGAGTTTCAGTGAGCACCTGGCCATCATCTCTGGAGGACCGCTCCGACATCAGC 172
QY 101 ggcagcatggtgtgagcgtcaacctgaccgcgcgcatgtactgagcagctctagaatct 160
Db 173 TCCACTCGCGCAACCAACATCAACCAACACACGAGCTGCTCCCATCGAGTGGACACC 232
QY 161 ctgatcaatgtctcgcactgcagcccatcccaaaagaccagagatctgaaagcactg 220
Db 233 CTGGTGGCAAGGGCGCTTCCCGAGNTCTACAAGGCCAAGCTGAAGCAGAACGCTCT 292
QY 221 tgcctcaaaagcccgcgaggcgaggttcctcc 253
Db 293 GAGCAGTTCGAGACCGTGGCGCTCAAGATCTTC 325

RESULT 4
LOCUS AV387571 537 bp mRNA EST 29-SEP-2000
DEFINITION AV387571 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
cDNA clone CM026e03_r, mRNA sequence.
ACCESSION AV387571
VERSION AV387571.1 GI:6541787
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
REFERENCE 1 (bases 1 to 537)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
TITLE A large scale structural analysis of cDNAs in a unicellular green
alga, Chlamydomonas reinhardtii. I. Generation of 3433
non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)
MEDLINE 20152988
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.
FEATURES
source
location/Qualifiers
1..537
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="CM026e03_r"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI"
BASE COUNT 62 a 220 c 166 g 89 t
ORIGIN

Query Match 13.1%; Score 35.6; DB 29; Length 537;
Best Local Similarity 47.0%; Pred. No. 12;
Matches 110; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 3 gccttgctcccgagccctgtgactccctcccaacctcaaggagctcattgaggagc 62
Db 497 GCCAGGCATCACCCCTCGACACATTCATCCGCAAGTTGAGGTGCTGAGGCGCCCA 438
QY 63 tgggtcaacatcaccagaaatcaggcatccctctgcaacggcagcatggtgtgagcgtca 122
Db 437 AGTTCGACATCACCAAGCTCATGGAGGTGCACGGTGTACTACAGCGAGGAGGTGGCGCCA 378
QY 123 acctgaccgcgcgcatgtactgagcagctctagatctctgataatgtctccgactgca 182
Db 377 AGATCGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 318
QY 183 gcgcatcacaagagaccagagagtgctgaaagcactgtgctctcaaaagccg 236
Db 317 GCAGCCGTCACGCTCCGCGGAGGAGGGAATGCGCTGCTGGGAAGTCCG 264

```

RESULT 5
BE536034/c LOCUS
DEFINITION BE536034 1070 bp mRNA EST 09-AUG-2000
601062471f1 NIH_MGC_10 Homo sapiens cDNA clone IMAGE:3448912 5', mRNA sequence.
ACCESSION BE536034
VERSION BE536034.1 GI:9764679
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1070)
AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: Incyte Genomics, Inc.
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Plate: L1AM8424 row: n column: 17
High quality sequence start: 3
High quality sequence stop: 5.
FEATURES
source
1. .1070
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3448912"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/note="Organ: Cervix; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.5 kb. Library prepared by Life Technologies."
BASE COUNT 197 a 247 c 315 g 311 t
ORIGIN
Query Match 13.1%; Score 35.6; DB 136; Length 1070;
Best Local Similarity 55.7%; Pred. No. 14;
Matches 68; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
Qy 4 ccttgctccccgagccctgtgactccctcccccacccctcaaggagctcattgaggagct 63
Db 1047 CCGCGCCCCCGCGCGGTATTAAGGCCCTCTTAACAGCGGGGCCCATAGAGGTCCC 988
Qy 64 ggtcaacatcacccagaatcaggcctccctctgcacgcagcagcagcagcagcagc 123
Db 987 GCCCACACTTCCACAGTAAGCGCCGCCCTCCACAGGGTCCACTACTCTGGCACTCAA 928
Qy 124 cc 125
Db 927 TC 926
RESULT 6
BF606532 LOCUS
DEFINITION BF606532 498 bp mRNA EST 13-DEC-2000
273595 MARC 3BOV Bos taurus cDNA 5', mRNA sequence.
ACCESSION BF606532
VERSION BF606532.1 GI:11707239
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovoidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 498)
AUTHORS Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Laegreid W.W. and Keefe,J.W.
TITLE Design and use of four pooled tissue normalized cDNA libraries for EST discovery in cattle
JOURNAL Unpublished (2000)
COMMENT Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
Plate: 61 row: H column: 2
Seq primer: ATTAGTGACACTATAG.
FEATURES
source
1. .498
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone_lib="MARC 3BOV"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from marrow, alveolar macrophage, ovary, fetal semitendinosus muscle, and fetal longissimus muscle."
BASE COUNT 117 a 162 c 137 g 82 t
ORIGIN
Query Match 13.0%; Score 35.4; DB 150; Length 498;
Best Local Similarity 47.9%; Pred. No. 14;
Matches 102; Conservative 0; Mismatches 111; Indels 0; Gaps 0;
Qy 41 ctcaaggagctcattgaggagctggtcaacatcacccagaatcaccctctgtgcaac 100
Db 162 CTGATGGAGTTCAGTGAGCACCTGGCCATCATCTGGAGGACGACCGCTCCGACATCAGC 221
Qy 101 ggagcagtggtgagcgtcaacctgacgcgcgcgcgcgcgcgcgcgcgcgcgcgc 160
Db 222 TCCACCTCGCCCAACAACATCAACACACGAGGTGCTGCCCATCGAGCTGGACACC 281
Qy 161 ctgatcaatgtctccgactcagcgccatccaaaggaccagagatgctgaaagcactg 220
Db 282 CTGTTGGGCAAGGGCGCTTCGCGGAGGTCTACAAAGGCCAAGCTGAAGCAACACGCTCT 341
Qy 221 tgcctctcaaaagccgc 253
Db 342 GAGCAGTTCGAGACCGTGGCGGTCAAGATCTTC 374
RESULT 7
BE705147 LOCUS
DEFINITION BE705147 507 bp mRNA EST 12-SEP-2000
Sc02_08f05_A Sc02_AAFC_EC0RC_cold_stressed_winter_rye_seedlings Secale cereale cDNA clone Sc02_08f05, mRNA sequence.
ACCESSION BE705147
VERSION BE705147.1 GI:10093412
KEYWORDS EST.
SOURCE rye.
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Secale.
REFERENCE 1 (bases 1 to 507)

AUTHORS	Singh, J.A., Piche, C., Couroux, P., De Moors, A., Harris, L.J., Hattori, J.I., Ouellet, T., Robert, L.S., Spratt, D. and Tinker, N.A.
TITLE	Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
JOURNAL	Unpublished (2000)
COMMENT	Contact: Singh, J.A. Eastern Cereal and Oilseed Research Centre Agriculture and Agri-food Canada 960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada Tel: (613) 759-1662 Fax: (613) 759-1701 Email: singhja@em.agr.ca.

```

FEATURES
  Location/Qualifiers
    1..507
      /organism="Secale cereale"
      /cultivar="Puma (winter rye)"
      /db_xref="taxon:4550"
      /clone="Sc02_08f05"
      /clone_lib="Sc02_AAFC_cold_stressed_winter_rye_seedlings"
      /tissue_type="leaf, crown"
      /dev_stage="seedling three-leaf stage"
      /note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI; Site_2: Xho I; Sampled three-leaf seedlings treated for one week at 20C, 12 hrs light/day. Library made with Stratagene UNIZAP XR kit/(not packaged). cDNA is directly ligated into SK+/XhoI-EcoRI, then electroporated into TOP10 cells (Invitrogen)."
    115 a 169 c 148 g 65 t 10 others
BASE COUNT
ORIGIN

```

Query Match	12.8%;	Score 34.8;	DB 138;	Length 507;
Best Local Similarity	53.3%;	Pred. No. 20;		
Matches 64;	Conservative	4;	Mismatches 52;	Indels 0;
				Caps 0;

	8	gcccctccagagcctcgtagactccctcccccaaccctcaaggagactcatgtagagagtgtgc	67
Qy			
	147	GCTGCAGTCGATGTGCACGGCGTCCAGCACCAARACCCCACCAGGAGGAGCGG	206
Db		: :	
	68	acatcacccagaatacagtcacctcttgcacggcagcagtgtgtggagcgtcaacctg	127
Qy			
	207	AACAGCAACAARAACACGCGTCCGCCGACTCCGGCGACCTGGATGAAGAAGAHCATG	266
Db			

RESULT	8			
BE907816				
LOCUS	BE907816	576 bp	mrna	EST
DEFINITION	601501924F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903965 5',			
				mrna sequence.

ACCESSION BE907816
VERSION BE907816.1 GI:10401759
KEYWORDS EST.
SOURCE human.

ORGANISM	Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	

REFERENCE
1 (bases 1 to 576)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL
COMMENT

Email: Robert_Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arranged by: The T M A C E Consortium (TIN)

DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
CUNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

round through the I.M.A.G.E. CONSULTUM/LEML ac;
http://image.llnl.gov
Plate: LLAM9708 row: 0 column: 06
High quality sequence stop: 571.

FEATURES	Location/Qualifiers
1. General Information	
2. Geographic Location	
3. Physical Description	
4. Historical Significance	
5. Current Status	
6. Ownership	
7. Access	
8. Preservation	
9. Research	
10. Publications	
11. References	
12. Notes	
13. Appendices	
14. Index	
15. Summary	
16. Conclusion	
17. Recommendations	
18. Final Remarks	
19. Signatures	
20. Attachments	
21. Other Information	
22. Comments	
23. Revisions	
24. Approval	
25. Final Review	
26. Publication	
27. Distribution	
28. Archiving	
29. Accession	
30. Inventory	
31. Condition	
32. Value	
33. Importance	
34. Uniqueness	
35. Completeness	
36. Authenticity	
37. Reliability	
38. Accuracy	
39. Consistency	
40. Clarity	
41. Conciseness	
42. Coherence	
43. Cohesion	
44. Style	
45. Format	
46. Layout	
47. Design	
48. Appearance	
49. Condition	
50. Value	
51. Importance	
52. Uniqueness	
53. Completeness	
54. Authenticity	
55. Reliability	
56. Accuracy	
57. Consistency	
58. Clarity	
59. Conciseness	
60. Coherence	
61. Cohesion	
62. Style	
63. Format	
64. Layout	
65. Design	
66. Appearance	
67. Condition	
68. Value	
69. Importance	
70. Uniqueness	
71. Completeness	
72. Authenticity	
73. Reliability	
74. Accuracy	
75. Consistency	
76. Clarity	
77. Conciseness	
78. Coherence	
79. Cohesion	
80. Style	
81. Format	
82. Layout	
83. Design	
84. Appearance	
85. Condition	
86. Value	
87. Importance	
88. Uniqueness	
89. Completeness	
90. Authenticity	
91. Reliability	
92. Accuracy	
93. Consistency	
94. Clarity	
95. Conciseness	
96. Coherence	
97. Cohesion	
98. Style	
99. Format	
100. Layout	
101. Design	
102. Appearance	
103. Condition	
104. Value	
105. Importance	
106. Uniqueness	
107. Completeness	
108. Authenticity	
109. Reliability	
110. Accuracy	
111. Consistency	
112. Clarity	
113. Conciseness	
114. Coherence	
115. Cohesion	
116. Style	
117. Format	
118. Layout	
119. Design	
120. Appearance	
121. Condition	
122. Value	
123. Importance	
124. Uniqueness	
125. Completeness	
126. Authenticity	
127. Reliability	
128. Accuracy	
129. Consistency	
130. Clarity	
131. Conciseness	
132. Coherence	
133. Cohesion	
134. Style	
135. Format	
136. Layout	
137. Design	
138. Appearance	
139. Condition	
140. Value	
141. Importance	
142. Uniqueness	
143. Completeness	
144. Authenticity	
145. Reliability	</

```

source
1. .576
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3903965"
/clone_lib="NIH_MGC_70"
/tissue_type="epithelioid carcinoma"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NoI1;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.1 kb. Library constructed by Life
Technologies."
108 a 174 c 147 g 147 t
BASE COUNT
ORIGIN

```

Query Match	12.7%	Score 34.6;	DB 141;	Length 576;
Best Local Similarity	47.8%;	Pred. No. 23;		
Matches 100;	Conservative	0;	Mismatches 109;	Indels 0;
				Gaps 0;

Qy	1	tggccttgctccccgagccctgtgactccctccccacccctcaaggagctcattgagga	60
Db	231	TGTCCATGAGCCGCTGCTACTCTCTGATTCTGCGCTCACTATCAGCTCGACATCGCCCA	290
Qy	61	gcctgtcaacatcaccagaaatcaggacatccctctgcaacggcagcatatggttgagcgt	120
Db	291	GCTGGGCTTCAATACCGCTGATCAGCGCTGGTATTATTGCGGCATTTGGGCTCCAAGC	350
Qy	121	caacctgacgcgcggcgtgtactgcgagctctlagaatctctgatcaatgtctccgactg	180
Db	351	CGCCTCCGTTTTCGCCAGTGTGTCTTCCANGGCAGCTTTCATGCTCAGCTGTCACTG	410
Qy	181	cagcgcaatccaaagaccagaggatgc	209
Db	411	CAGCTCAATCTCAAGACCTTGAAGGGTGC	439

RESULT 9
AZ201624/C

LOCUS	DEFINITION	AZ201624	965 bp	DNA	GSS	31-AUG-2000
SP_0053_A2_B12	SP053_A2_B12_SPOE Strongylocentrotus purpuratus, purple sea urchin, sperm genomic BAC library Strongylocentrotus purpuratus genomic clone Plate-53 Col-24 Row-C, DNA sequence.					

ACCESSION
 AZ201624
 VERSION
 AZ201624.1
 KEYWORDS
 GI:8396538
 GSS.

RELATIVES	SOURCE	ORGANISM
355.		
		Strongylocentrotus purpuratus.
		Strongylocentrotus purpuratus
		Eukaryota; Metazoa; Echinodermata; Eleutherozoa; Echinozoa;
		Echinoidea; Euechinoidea; Echinacea; Echinoida;
		Strongylocentrotidae; Strongylocentrotus.

REFERENCE
1 (bases 1 to 965)
AUTHORS
Cameron, R.A., Mahairas, G., Rast, J.P., Martinez, P., Biondi, T.R., Swartzell, S., Wallace, J.C., Poustka, A.J., Livingston, B.T., Wray, G.A., Ettensohn, C.A., Lehrach, H., Britten, R.J., Davidson, E.H. and Hood, L.
strongly oncogenic; strongly oncogenic.

TITLE A sea urchin genome project: Sequence scan, virtual map, and additional resources

JOURNAL Proc. Natl. Acad. Sci. U. S. A. 97 (17), 9514-9518 (2000)

MEDLINE	COMMENT
20402566	Contact: Cameron, RA, Davidson, EH, Hood, L Division of Biology 156-29 California Institute of Technology Pasadena California 91125, USA Tel: (626) 395-8421 Fax: (626) 793-3047

Fax: (020) 753-3047
Email: acameron@caltech.edu
Plate: 53 row: C column: 24
Seq primer: sp6
Class: BAC ends

```

FEATURES
  source
    Location/Qualifiers
      High quality sequence stop: 965.
      Class. BAC ends

```

```
source
1: 303
/organism="Strongylocentrotus purpuratus"
```


ORIGIN

	Query Match	12.68;	Score 34.2;	DB 161;	Length 535;
	Best Local Similarity	55.5%;	Pred. No. 30;		
	Matches 66;	Conservative 0;	Mismatches 53;	Indels 0;	Gaps 0;
QY	20	cctgtgactccctcccaacccctcaagagagctcattgaggagctgggtcaacatcaccacag	79		
Db	227	CCTGTGACCACACGGTGTACGATGACAAGGGCAATGAGAAAGAGCATCACCGTGGCCACG	286		
QY	80	aatcaggcatccctctgcacaacgcgcagcatggtgtggagcgtcaacctgacacgcgcgggaat	138		
Db	287	GATGAGGCATTCGCCCCCAACACACCATGAGGGCCCTGGCCAAACTGAACCCCTGCCTT	345		

RESULT	12
LOCUS	BE032543
DEFINITION	131942 MARC 1Pig Sus scrofa cDNA 5', mRNA sequence.
ACCESSION	BE032543
VERSION	BE032543.1 GI:8327552
KEYWORDS	EST,
SOURCE	pig.
ORGANISM	Sus scrofa
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus. 1 (bases 1 to 546)
AUTHORS	Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E., Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W. and Keeler,J.W.
TITLE	Design and use of two pooled tissue normalized cDNA libraries for EST discovery in swine
JOURNAL	Unpublished (2000)
COMMENT	Contact: Smith TPL USDA, ARS, US Meat Animal Research Center PO Box 166, Clay Center, NE 68933-0166, USA Tel.: 402 762 4366 Fax: 402 762 4390 Email: smith@email.marc.usda.gov Single pass sequencing. Bases called and alt-trimmed with phred v0.980904.e. Vector identified by cross_match with the -minscore 18 and -minmatch 12 options.

BASE COUNT	125 a	152 c	169 g	98 t	2 others
ORIGIN					
<hr/>					
Query Match	12.6%; Score 34.2; DB 161; Length 546;				
Best Local Similarity	55.8%; Pred. No. 30;				
Matches	66; Conservative	0; Mismatches	53; Indels	0; Gaps	0;
<hr/>					
QY	20	cctgtgactcctccccaacccctaagaggctcatcttgaggagtctgttcaacatcacccag	79		
Db	227	CCTGTGACCACCGGGTCTAGCATGACAAAGGCCAATGAGRAGACATCACCGTGCCCGCAG	286		
<hr/>					
QY	80	aatacaggcatacctctctgcacaagcgagcatggttgtaggcgtcaaccttcagcccggcat	138		
Db	287"	GATTGAGGGCATTCGCGCCCAACACACCACTGAGGGCCCTGGCCAACCTGAAGCCCTGCCTT	345		

RESULT	13
BE127683	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	
AUTHORS	
TITLE	
JOURNAL	
COMMENT	
FEATURES	
SOURCE	
BASE COUNT	
ORIGIN	
Query Map	
Best Loc	
Matches	
Qy	4
Db	151
Qy	64
Db	211
Qy	124
Db	271
RESULT	14
BE363650	
LOCUS	
DEFINITION	
ACCESSION	
VERSION	
KEYWORDS	
SOURCE	
ORGANISM	
REFERENCE	

RESULT 14
BE363650
LOCUS BE363650 370 bp mRNA EST 20-JUL-2000
DEFINITION WSL_64-G10-gl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BE363650
VERSION BE363650.1 GI:9305207
KEYWORDS EST.
SOURCE sorghum.
ORGANISM sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
1 (bases 1 to 370)
REFERENCE

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:16:09 ; Search time 9342.78 Seconds
(without alignments)
438.831 Million cell updates/sec

Title: US-09-451-527-90
Perfect score: 278
Sequence: 1 atggcgctctgtgactgt.....gcactgtgtctcaaaagcc 278

Scoring table: IDENTITY_NDC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues 2566470

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
- 1: gb_ba1.*
 - 2: gb_ba2.*
 - 3: gb_ba3.*
 - 4: gb_in1.*
 - 5: gb_in2.*
 - 6: gb_in3.*
 - 7: gb_om.*
 - 8: gb_ov.*
 - 9: gb_pat1.*
 - 10: gb_pat2.*
 - 11: gb_ph.*
 - 12: gb_pl1.*
 - 13: gb_pl2.*
 - 14: gb_pl3.*
 - 15: gb_pl4.*
 - 16: gb_ba1.*
 - 17: gb_ba2.*
 - 18: em_fun.*
 - 19: em_htgo_hum.*
 - 20: em_htgo_inv.*
 - 21: em_htgo_rod.*
 - 22: em_htg_hum1.*
 - 23: em_htg_hum2.*
 - 24: em_htg_hum3.*
 - 25: em_htg_hum4.*
 - 26: em_htg_hum5.*
 - 27: em_htg_hum6.*
 - 28: em_htg_hum7.*
 - 29: em_htg_hum8.*
 - 30: em_htg_inv1.*
 - 31: em_htg_inv2.*
 - 32: em_htg_other.*
 - 33: em_htg_rod.*
 - 34: em_hum1.*
 - 35: em_hum2.*
 - 36: em_hum3.*
 - 37: em_hum4.*
 - 38: em_hum5.*
 - 39: em_hum6.*
 - 40: em_hum7.*
 - 41: em_in.*
 - 42: em_om.*
 - 43: em_or.*

- 44: em_ov.*
- 45: em_pat.*
- 46: em_ph.*
- 47: em_pl.*
- 48: em_ro.*
- 49: em_sts.*
- 50: em_sy.*
- 51: em_un.*
- 52: em_vi.*
- 53: gb_sts1.*
- 54: gb_sts2.*
- 55: gb_sts3.*
- 56: gb_sy.*
- 57: gb_un.*
- 58: gb_vil.*
- 59: gb_v12.*
- 60: gb_htg1.*
- 61: gb_htg2.*
- 62: gb_htg3.*
- 63: gb_htg4.*
- 64: gb_htg5.*
- 65: gb_htg6.*
- 66: gb_htg7.*
- 67: gb_htg8.*
- 68: gb_htg9.*
- 69: gb_htg10.*
- 70: gb_htg11.*
- 71: gb_htg12.*
- 72: gb_htg13.*
- 73: gb_htg14.*
- 74: gb_htg15.*
- 75: gb_htg16.*
- 76: gb_htg17.*
- 77: gb_htg18.*
- 78: gb_htg19.*
- 79: gb_htg20.*
- 80: gb_htg21.*
- 81: gb_htg22.*
- 82: gb_htg23.*
- 83: gb_htg24.*
- 84: gb_htg25.*
- 85: gb_pr1.*
- 86: gb_pr2.*
- 87: gb_pr3.*
- 88: gb_pr4.*
- 89: gb_pr5.*
- 90: gb_pr6.*
- 91: gb_pr7.*
- 92: gb_pr8.*
- 93: gb_pr9.*
- 94: gb_ro1.*
- 95: gb_ro2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	278	100.0	1302	7 AF244915	AF244915 Canis fam
2	191	68.7	1270	93 HUM113A	L06801 Homo sapien
3	191	68.7	1282	92 HSN30	X69079 H.sapiens 1
4	191	68.7	1290	10 I34548	I34548 Sequence 1
5	189.4	68.1	417	88 AF043334	AF043334 Homo sapi
6	189.4	68.1	1297	9 A29948	A29948 Coding sequ
7	189.4	68.1	1297	10 I58488	I58488 Sequence 15
8	183.4	66.0	343	7 AF072807	AF072807 Bos tauru
9	148.2	53.3	384	9 A29950	A29950 Nucleic aci
10	148.2	53.3	384	10 I58489	I58489 Sequence 17
11	147.6	53.1	336	9 A29931	A29931 Sequence co


```

Db 45 ATGGCGCTTTTGTGACACAGGTCACTGCTCACTTGCCTTGGCGCTTGCCTCCCA 104
Qy 61 agccctgtactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
Db 105 GGCCCTGTGCCCTCCTCTACAGCCCTCAGGAGGCTCATTTAGGAGCTGCTCAACATCAC 164
Qy 121 cagaatc---aggatccctctgaacggcagcatggtgtgaggagctgaacctgaccgcc 177
Db 165 CAGAACCAAGAGGATCCCTCTGCAATGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
Qy 178 ggcgtactgcgagctctagaatctctgatcaatgctctcgcagctgcagcccatccaa 237
Db 225 GCCATGTACTGTGAGCCCTCGAATCCCTGATCAACGTGTGAGGCTGCAGTGCCTCGAG 284
Qy 238 aggaccagagagtgctgaagcagctgtgctctcaaaag 276
Db 285 AAGACCAGAGGATGCTGAGCGGATTCTGCCCGCACAG 323

RESULT 3
HSNC30 1282 bp mRNA PRI 17-FEB-1997
LOCUS H.sapiens interleukin-13 mRNA.
DEFINITION X69079
ACCESSION X69079
VERSION X69079.1 GI:297787
KEYWORDS lymphokine.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1282)
Minty,A.J.
Direct Submission
Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches,
Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
2 (bases 1 to 1282)
Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C.,
Kaghad,M., Labit,C., Leplatois,P., Liausun,P., Miloux,B., Minty,C.,
Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and
Caput,D.
TITLE Interleukin-13 is a new human lymphokine regulating inflammatory
and immune responses
JOURNAL Nature 362 (6417), 248-250 (1993)
MEDLINE 93211479
FEATURES
source Location/Qualifiers
1..1282
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5q 23-31"
/cell_type="peripheral blood lymphocytes"
15..455
/gene="NC30"
15..1116
/gene="NC30"
/product="NC30; alternative"
15..455
/gene="NC30"
/note="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1
/evidence=experimental
/protein_id="CAA48823.1"
/db_xref="GI:580330"
/db_xref="SWISS-PROT:P35225"
/translation="MHLLPLPLALGLMALLTTVIALTCLGGFASPGVPVPSTALRELIEELVNTQK
ELIEELVNTQKAPLCNGSMVWSINLTAGMYCAALESINVSGCSAIEKQRLMSG
FCPHKVSAGQFSSLVHROTKIEVAQFVKDLLHLKLLFREGFN"
57..455
/gene="NC30"
/note="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1

```

```

/evidence=experimental
/protein_id="CAA48824.1"
/db_xref="GI:673420"
/translation="MALLTTVIALTCLGGFASPGVPVPSTALRELIEELVNTQK
APLCNGSMVWSINLTAGMYCAALESINVSGCSAIEKQRLMSGFCPHKVSAGQFSSL
HYRDKIEVAQFVKDLLHLKLLFREGFN"
57..1116
/gene="NC30"
/product="NC30; alternative"
117..452
/gene="NC30"
/evidence=experimental
variation
238
/gene="NC30"
/replacement="a"
856..860
/note="ATTTA motif"
873..877
/note="ATTTA motif"
1134..1138
/note="ATTTA motif"
1153..1157
/note="ATTTA motif"
polyA_signal 1264..1269 337 g 311 t
BASE COUNT 293 a 341 c 337 g 311 t
ORIGIN

Query Match 68.7%; Score 191; DB 92; Length 1282;
Best Local Similarity 82.8%; Pred. No. 4.7e-36;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;

Qy 1 atggcgtctgtgactgtggtcattgctctcaccctgcctgcctgcctcccg 60
Db 57 ATGGCGCTTTTGTGACACAGGTCACTGCTCACTTGCCTTGGCGCTTGCCTCCCA 116
Qy 61 agccctgtactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
Db 117 GGCCCTGTGCCCTCCTCTACAGCCCTCAGGAGGCTCATTTAGGAGCTGCTCAACATCAC 176
Qy 121 cagaatc---aggatccctctgaacggcagcatggtgtgaggagctgaacctgaccgcc 177
Db 177 CAGAACCAAGAGGATCCCTCTGCAATGCAGCATGGTATGGAGCATCAACCTGACAGCT 236
Qy 178 ggcgtactgcgagctctagaatctctgatcaatgctctcgcagctgcagcccatccaa 237
Db 237 GCCATGTACTGTGAGCCCTCGAATCCCTGATCAACGTGTGAGGCTGCAGTGCCTCGAG 296
Qy 238 aggaccagagagtgctgaagcagctgtgctctcaaaag 276
Db 297 AAGACCAGAGGATGCTGAGCGGATTCTGCCCGCACAG 335

RESULT 4
LOCUS 134548 1290 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5596072.
ACCESSION 134548
VERSION 134548.1 GI:1825339
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
FEATURES Location/Qualifiers
source 1..1290
/organism="unknown"
BASE COUNT 308 a 335 c 336 g 311 t
ORIGIN

```


QY 1 atggcgctgtgtgactgtggtcattgtctcaactgctcggtgacctgtgctccccc 60
Db 57 ATGGCGCTTTGTTGACACAGGTCATTGCTCACTTGGCTTGGCGCTTGGCTCCCCA 116
QY 61 agcctgtgactcctcccccaaccctcaaggagctcattgagagctggtgcaacatcac 120
Db 117 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGAGCTGCTCAACATCAC 176
QY 121 cagaatc---aggatccctctgcaacggcagcatgggtgagagctgcaacctgaccgc 177
Db 177 CAGAACCAAGAGGCTCCGCTCTGCAATGCGACATGGTATGGAGCATCAACCTGACAGCT 236
QY 178 ggcgtgactgcagctctagaatctctgatcaatgtctcgcactgagcgcacccaa 237
Db 237 GACATGTAAGTGTGCGCCCTGGAATCCCTGATCAAGTGTGAGGCTGCGATCGAG 296
QY 238 aggacccagagatgctgaaagcactgtgctctcaaaag 276
Db 297 AAGACCCAGAGATGCTGAGCGGATTCTGCCCGCACAG 335
RESULT 7
I58488 1297 bp DNA PAT 07-OCT-1997
LOCUS I58488 Sequence 15 from patent US 5652123.
DEFINITION I58488
ACCESSION I58488
VERSION I58488.1 GI:2477726
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le
Boutiller,C., Lepiatols,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 15 29-JUL-1997;
FEATURES
Location/Qualifiers
source 1..1297
BASE COUNT 309 a 341 c 336 g 311 t
ORIGIN
Query Match 68.1%; Score 189.4; DB 10; Length 1297;
Best Local Similarity 82.4%; Pred. No. 1.1e-35;
Matches 230; Conservative 0; Mismatches 46; Indels 3; Gaps 1;
QY 1 atggcgctgtgtgactgtggtcattgtctcaactgctcggtgacctgtgctccccc 60
Db 57 ATGGCGCTTTGTTGACACAGGTCATTGCTCACTTGGCTTGGCGCTTGGCTCCCCA 116
QY 61 agcctgtgactcctcccccaaccctcaaggagctcattgagagctggtgcaacatcac 120
Db 117 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGAGCTGCTCAACATCAC 176
QY 121 cagaatc---aggatccctctgcaacggcagcatgggtgagagctgcaacctgaccgc 177
Db 177 CAGAACCAAGAGGCTCCGCTCTGCAATGCGACATGGTATGGAGCATCAACCTGACAGCT 236
QY 178 ggcgtgactgcagctctagaatctctgatcaatgtctcgcactgagcgcacccaa 237
Db 237 GACATGTAAGTGTGCGCCCTGGAATCCCTGATCAAGTGTGAGGCTGCGATCGAG 296
QY 238 aggacccagagatgctgaaagcactgtgctctcaaaag 276
Db 297 AAGACCCAGAGATGCTGAGCGGATTCTGCCCGCACAG 335
RESULT 8
AF072807 343 bp mRNA MAM 21-JAN-2000
LOCUS AF072807 Bos taurus interleukin-13 precursor (IL-13) mRNA, partial cds.
DEFINITION

AF072807 1 GI:4558813
VERSION AF072807.1
KEYWORDS
SOURCE COW.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 343)
AUTHORS Trigona,W.L., Brown,W.C. and Estes,D.M.
TITLE Functional implications for signaling via the IL4R/IL13R complex on
bovine cells
JOURNAL Vet. Immunol. Immunopathol. 72 (1-2), 73-79 (1999)
MEDLINE 20080132
PUBMED 10614495
REFERENCE 2 (bases 1 to 343)
AUTHORS Trigona,W.T., Hirano,A. and Estes,D.M.
TITLE Direct Submission
JOURNAL Submitted (16-JUN-1998) Veterinary Pathobiology, University of
Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO
65211, USA
FEATURES
Location/Qualifiers
source 1..343
/organism="Bos taurus"
/db_xref="taxon:9913"
gene 1..>343
/cell_type="activated peripheral T lymphocytes"
CDS 1..>343
/gene="IL-13"
/gene="IL-13"
/codon_start=1
/product="interleukin-13 precursor"
/protein_id="AAD22748.1"
/db_xref="GI:4558814"
/translation="MALLLTAVILVLCFGLTSPSPVPSATALKELIEELVNTQNK
VPLNGSMWSLNLTSMTCAALDSLISNCSVIQTKRMLNALCPHKPSAKOVSS
VYNDTKIEVAQF"
BASE COUNT 78 a 101 c 85 g 79 t
ORIGIN
Query Match 66.0%; Score 183.4; DB 7; Length 343;
Best Local Similarity 80.8%; Pred. No. 3.8e-34;
Matches 227; Conservative 0; Mismatches 51; Indels 3; Gaps 1;
QY 1 atggcgctgtgtgactgtggtcattgtctcaactgctcggtgacctgtgctccccc 60
Db 1 ATGGCGCTTCTATTGACCGCGCTCATTTGCTTTATCTGCTTTGCTGGCTCACCTCCCCA 60
QY 61 agcctgtgactcctcccccaaccctcaaggagctcattgagagctggtgcaacatcac 120
Db 61 AGCCCTGTGCTTCTGTGTACAGCCCTCAGGAGCTCATTTGAGAGCTGTTAATATCAC 120
QY 121 cagaatc---aggatccctctgcaacggcagcatgggtgagagctgcaacctgaccgc 177
Db 121 CAGAACCAAGAGTGTGCGCTGTGCAATGGCAGCATGGTGTGAGCTTCAACCTGACGAGC 180
QY 178 ggcgtgactgcagctctagaatctctgatcaatgtctcgcactgagcgcacccaa 237
Db 181 AGCATGTACTGTGCGAGCCCTGGACTCCCTGATCATCAGCATCTCCAACTGCAGTGTATCA 240
QY 238 aggacccagagatgctgaaagcactgtgctctcaaaag 278
Db 241 AGGACCAAGAGGATGCTGAATGCACCTCTGCTCTCACAAGCC 281
RESULT 9
A29950 384 bp DNA PAT 23-JUN-1995
LOCUS A29950 Nucleic acid fragment B.
DEFINITION A29950
ACCESSION A29950
VERSION A29950.1 GI:1249030
KEYWORDS

SOURCE synthetic construct.
 ORGANISM synthetic construct
 REFERENCE 1 (bases 1 to 384)
 AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-Le
 Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
 TITLE Protein having cytokin type activity, recombinant DNA coding for
 this protein, transformed cells and microorganisms
 JOURNAL Patent: EP 056574-A 23 30-SEP-1992;
 FEATURES
 source Location/Qualifiers
 1..384 /organism="synthetic construct"
 BASE COUNT 97 a 104 c 99 g 84 t /db_xref="taxon:32630"
 ORIGIN
 Query Match 53.3%; Score 148.2; DB 9; Length 384;
 Best Local Similarity 81.8%; Pred. No. 1e-25;
 Matches 184; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
 QY 55 tccccgagccctgtgactccctccccaaccctcaaggagctcattgaggagctggtcaac 114
 Db 16 TCCCCAGGCCCTGTGCCCTCCCTCTACGGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAAC 75
 QY 115 atcaccagaatc---aggcaatccctctgcacgcgcagcatgggtgagcgctcaacctg 171
 Db 76 ATACCCAGACACGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135
 QY 172 acgcgcggcatgtactgcgcgctctagaaatctctgatcaatgtctccgcagctcagcgcc 231
 Db 136 ACAGTGCATGTACTGTGCAGCCCTGGATCCCTGATCAACGCTGCAGGCTGCAGTGCC 195
 QY 232 atccaaggacccagaggaatcgtgaagcactgtgctctcaaaag 276
 Db 196 ATCAGAGAAGCCAGAGGATGCTAGCGGATTCGCCGCCACAAG 240
 RESULT 10
 I58489
 LOCUS I58489 384 bp DNA PAT 07-OCT-1997
 DEFINITION Sequence 17 from patent US 5652123.
 ACCESSION I58489
 VERSION I58489.1 GI:2477727
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unclassified.
 REFERENCE 1 (bases 1 to 384)
 AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le
 Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
 TITLE Protein having interleukin 13 activity, recombinant DNA coding for
 this protein, transformed cells and microorganisms
 JOURNAL Patent: US 5652123-A 17 29-JUL-1997;
 FEATURES
 source Location/Qualifiers
 1..384 /organism="unknown"
 BASE COUNT 97 a 104 c 99 g 84 t
 ORIGIN
 Query Match 53.3%; Score 148.2; DB 10; Length 384;
 Best Local Similarity 81.8%; Pred. No. 1e-25;
 Matches 184; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
 QY 55 tccccgagccctgtgactccctccccaaccctcaaggagctcattgaggagctggtcaac 114
 Db 16 TCCCCAGGCCCTGTGCCCTCCCTCTACGGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAAC 75
 QY 115 atcaccagaatc---aggcaatccctctgcacgcgcagcatgggtgagcgctcaacctg 171
 Db 76 ATACCCAGACACGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135

Qy 172 accgcccagatgtactgcgcagcttagaatactctgatcaattgtctcgcagtgcagcgcc 231
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 136 ACAGCTGACATGTACTGTGCAGCCCGTGGAAATCCCTGATCAACGTTGTCAGGCTGCAGTGCC 195
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Qy 232 atcaaaagaccagagatgactgaagaacacactgtgctctcaaaa 276
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 196 ATCGAAGAACCAGAGGATGCTGAGCGGATTCTGCCCGCACAAG 240
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 11

A29931		336 bp	DNA	PAT	23-JUN-1995
DEFINITION	Sequence coding for the mature cytokine like protein.				
ACCESSION	A29931				
VERSION	A29931.1 GI:1249019				
KEYWORDS	synthetic construct.				
SOURCE	synthetic construct				
ORGANISM	artificial sequence.				
REFERENCE	1 (bases 1 to 336)				
AUTHORS	Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.				
TITLE	Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms				
JOURNAL	Patent: EP 0506574-A 30-SEP-1992;				
FEATURES	ELF SANOFI				
source	Location/Qualifiers				
	1..336				
	/organism="synthetic construct"				
	/db_xref="taxon:32630"				
BASE COUNT	80 a 95 c 90 g 71 t				
ORIGIN					

Query Match 53.1%; Score 147.6; DB 9; Length 336;
 Best Local Similarity 83.0%; Pred. No. 1.5e-25;
 Matches 181; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

Qy 62 gccctgtgactccctccccacctcaaaggagctcattgaggagctggtaacatcaccc 121
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 2 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGGCTCATTCAGGAGCTGGTCAACATCACCC 61
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 122 agaattc---aggcatcccttgcaacggcagcatggtgtggagcgtaaacctgaccgccg 178
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 62 AGAACCCAGGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 179 gcattgactgcgcagcttagaattctctgataatgtctccgactgcagcgccatccaaa 238
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 122 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGTCAGGCTGCAGTGCCATCGAGA 181
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Qy 239 ggaccagagatgctgtaaagacactgtgctctcaaaa 276
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
 Db 182 AGACCCAGAGATGCTGAGCGGATTCTGCCCGCACAAG 219
 ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 12

I58494		336 bp	DNA	PAT	07-OCT-1997
LOCUS	I58494				
DEFINITION	Sequence 24 from patent US 5652123.				
ACCESSION	I58494				
VERSION	I58494.1 GK:2477732				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 336)				
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.				
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms				
JOURNAL	Patent: US 5652123-A 24 29-JUL-1997;				
FEATURES	Location/Qualifiers				

```

source
1. .336
/organism="unknown"
BASE COUNT      80 a      95 c      90 g      71 t
ORIGIN

Query Match      53.1%; Score 147.6; DB 10; Length 336;
Best Local Similarity 83.0%; Pred. No. 1.5e-25;
Matches 181; Conservative 0; Mismatches 34; Indels 3; Gaps 1;

Qy 62 gccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 121
Db 2 GCCCTGTGCTCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGTTCAACATCACCC 61

Qy 122 agaattc---aggcatccctctctcaacaggcagcatggtggtggaagcgtcaacctgaccgcg 178
Db 62 AGAACGAGAAGGCTCGCTCTGCAATGGCAGCATGTTATGGAGCATCAACCTGACAGCTG 121

Qy 179 gcatactatgcgcagctctagaattctctatcaattctccgactcagcgccatccaaa 238
Db 122 GCATGTACTGTGCAGCCCTGGGAATCCCTGATCAACCTGTGAGGCTGCAGTGCATCGAGA 181

Qy 239 ggaccagaggtgctgaaagcactgctgctctcaaaa 276
Db 182 AGACCCAGAGGATGTCGAGCGGATTTCTGCCCGCACAA 219

RESULT 13
AR027065
LOCUS      AR027065      425 bp      DNA      PAT      29-SEP-1999
DEFINITION Sequence 4 from patent US 5856142.
ACCESSION AR027065
VERSION AR027065.1 GI:5937905
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 425)
AUTHORS      Legoux,R., Maldonado,P. and Salome,M.
TITLE      Method for the extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL      Patent: US 5856142-A 4 05-JAN-1999;
FEATURES
source
1. .425
/organism="unknown"
BASE COUNT      100 a      116 c      110 g      99 t
ORIGIN

Query Match      52.7%; Score 146.4; DB 9; Length 425;
Best Local Similarity 80.7%; Pred. No. 2.8e-25;
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 52 gccctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtc 111
Db 55 GCCTTCGTGGCCCTGTGCTGCCAGTACTGCCCTCAGGAGCTCATTTGAGGAGCTGGTC 114

Qy 112 aacatcacccagaatc---aggcatccctctgcaacgcagcatggtgtgagcgtcaac 168
Db 115 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGGAGCATCAAC 174

Qy 169 ctgaccgcggcgtactgctgcagctctagaattctctgataatgtctccgactgcagc 228
Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGCAGGCTGCAGT 234

Qy 229 gccatccaaaggaccagagaggtcgtgaaagcactgtgtctctcaaaa 276
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAA 282

RESULT 14
AR027065
LOCUS      AR027065      425 bp      DNA      PAT      10-JUN-1998
DEFINITION Sequence 4 from patent US 5856142.
ACCESSION AR027065
VERSION AR027065.1 GI:5937905
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 425)
AUTHORS      Legoux,R., Maldonado,P. and Salome,M.
TITLE      Method for the extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL      Patent: US 5856142-A 4 05-JAN-1999;
FEATURES
source
1. .425
/organism="unknown"
BASE COUNT      100 a      116 c      110 g      99 t
ORIGIN

Query Match      52.7%; Score 146.4; DB 9; Length 425;
Best Local Similarity 80.7%; Pred. No. 2.8e-25;
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 52 gccctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtc 111
Db 55 GCCTTCGTGGCCCTGTGCTGCCAGTACTGCCCTCAGGAGCTCATTTGAGGAGCTGGTC 114

Qy 112 aacatcacccagaatc---aggcatccctctgcaacgcagcatggtgtgagcgtcaac 168
Db 115 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGGAGCATCAAC 174

Qy 169 ctgaccgcggcgtactgctgcagctctagaattctctgataatgtctccgactgcagc 228
Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGCAGGCTGCAGT 234

Qy 229 gccatccaaaggaccagagaggtcgtgaaagcactgtgtctctcaaaa 276
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAA 282

RESULT 14
186198
LOCUS
```

```

DEFINITION      Sequence 4 from patent US 5700665.
ACCESSION      186198
VERSION        186198.1 GI:3205916
KEYWORDS
SOURCE      Unknown.
ORGANISM      Unclassified.
REFERENCE      1 (bases 1 to 425)
AUTHORS      Legoux,R., Maldonado,P. and Salome,M.
TITLE      Method for the extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL      Patent: US 5700665-A 4 23-DEC-1997;
FEATURES
source
1. .425
/organism="unknown"
BASE COUNT      100 a      116 c      110 g      99 t
ORIGIN

Query Match      52.7%; Score 146.4; DB 10; Length 425;
Best Local Similarity 80.7%; Pred. No. 2.8e-25;
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

Qy 52 gccctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtc 111
Db 55 GCCTTCGTGGCCCTGTGCTGCCAGTACTGCCCTCAGGAGCTCATTTGAGGAGCTGGTC 114

Qy 112 aacatcacccagaatc---aggcatccctctgcaacgcagcatggtgtgagcgtcaac 168
Db 115 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGGAGCATCAAC 174

Qy 169 ctgaccgcggcgtactgctgcagctctagaattctctgataatgtctccgactgcagc 228
Db 175 CTGACAGCTGGCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGCTGCAGGCTGCAGT 234

Qy 229 gccatccaaaggaccagagaggtcgtgaaagcactgtgtctctcaaaa 276
Db 235 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAA 282

RESULT 15
A52326
LOCUS      A52326      4410 bp      DNA      PAT      12-DEC-1997
DEFINITION      Sequence 1 from Patent EP0725140.
ACCESSION      A52326
VERSION        A52326.1 GI:2851987
KEYWORDS
SOURCE      Unidentified.
ORGANISM      Unidentified.
REFERENCE      1 (bases 1 to 4410)
AUTHORS      Legoux,R., Maldonado,P. and Salome,M.
TITLE      Process of extraction of periplasmic proteins from prokaryotic
            microorganisms in the presence of arginine
JOURNAL      Patent: EP 0725140-A 1 07-AUG-1996;
COMMENT      SANOFI SA (FR)
            Other publication SK 10696 960904
            Other publication CZ 960290 960814
            Other publication JP 8242879 960924
            Other publication FI 960427 960801
            Other publication PL 312543 960805
            Other publication NO 960396 960801
            Other publication FR 2729972 960802
            Other publication CA 2168382 960801
            Other publication AU 4224496 960808.
FEATURES
source
1. .4410
/organism="unidentified"
/db_xref="taxon:32644"
promoter
5'UTR      283. .337
misc_RNA    338. .762
/note="SEQUENCE DE LA REGION 5' NON TRADUITE DU MESSAGE"
```

```
terminator      /note="SEQUENCE CODANT POUR LE PRECURSEUR DE L'IL-13"
terminator      763..812
terminator      813..1012
terminator      /note="TERMINATEUR DU GENE 10 DU PHAGE T7"
terminator      1013..1253
misc_rna        /note="TERMINATEUR DU PHAGE FD"
misc_rna        1254..2505
misc_rna        /note="GENE CODANT POUR LE REPRESSEUR DE L'OPERON LACTOSE"
misc_rna        2506..4410
BASE COUNT     1078 a 1142 c 1096 g 1094 t
ORIGIN
```

```
Query Match      52.7%  Score 146.4;  DB 9;  Length 4410;
Best Local Similarity 80.7%  Pred. No. 2e-25;
Matches 184;  Conservative 0;  Mismatches 41;  Indels 3;  Gaps 1;

QY  52  gccctcccgagcctgtgactccctcccaaccctcaaggagctcattgagagctggtc 111
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  392 GCCTTCGCTGGCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCATTGAGAGCTGGTC 451
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  112 aacatcacccagaaatc---aggcattccctctgcaacggcagcatggtgtgagcgctcaac 168
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  452 AACATCACCACAGAACAGAGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 511
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  169 ctgaccgcccgcgtactgtgcagcgtctagaatctctgataatgctcgcgactgcagc 228
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  512 CTGACAGCTGGCATGTACTGTGTGACGCCCTGGAAATCCCTGATCAACGCTGCAGCTGCAGT 571
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  229 gccatccaaaggaccagagatgctgaaagcactgtgctctcaaaag 276
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
QY  572 GCCATCGAGAAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAG 619
Db   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
```

Search completed: May 13, 2001, 14:16:12
Job time: 18852 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:28:53 ; Search time 472.02 Seconds
(without alignments)
343.823 Million cell updates/sec

Title: US-09-451-527-90
perfect score: 278
Sequence: 1 atggcgctctggttgaactgt.....gcactatgactctcaaaaagcc 278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

post-processing: Minimum Match 0%

Post processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

```
Database : N_Geneseq_0401.*
1: /cgnl_8/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseqn/NA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseqn/NA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseqn/NA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseqn/NA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseqn/NA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseqn/NA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseqn/NA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseqn/NA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseqn/NA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseqn/NA2001.DAT.*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	278	100.0	278	21	255554	Canine interleukin
2	278	100.0	390	21	255563	Canine interleukin
3	278	100.0	390	21	255564	Canine interleukin
4	278	100.0	393	21	255557	Canine interleukin
5	278	100.0	393	21	255558	Canine interleukin
6	278	100.0	1269	21	255561	Canine interleukin
7	278	100.0	1269	21	255562	Canine interleukin
8	278	100.0	1302	21	255555	Canine interleukin
9	278	100.0	1302	21	255556	Canine interleukin
10	234	84.2	272	21	255553	Canine interleukin
11	218	78.4	330	21	255565	Canine mature inte

C	12	218	78.4	330	21	Z55566	Canine mature inte
	13	218	78.4	333	21	Z55559	Canine mature inte
C	14	218	78.4	333	21	Z55560	Canine mature inte
	15	191	68.7	1270	21	F21334	Human low adenosin
	16	191	68.7	1270	21	A35212	Human adenosine re
	17	191	68.7	1282	21	F21332	Human low adenosin
	18	191	68.7	1282	21	A35210	Human adenosine re
	19	191	68.7	1290	15	Z55692	Sequence encoding
	20	191	68.7	6952	21	F21333	Human low adenosin
	21	191	68.7	6952	21	A35211	Human adenosine re
	22	191	68.7	14978	21	F21338	Human low adenosin
	23	191	68.7	14978	21	A35216	Human adenosine re
	24	189.4	68.1	1297	13	Q28947	Cytokine NC30. Q
	25	147.6	53.1	336	13	Q28944	Gly41-Cytokine cod
	26	146	52.5	336	13	Q28943	Asp41-Cytokine cod
	27	142.4	51.2	1212	15	Z55693	Sequence encoding
	28	101.8	36.6	5670	21	F21331	Human low adenosin
	29	101.8	36.6	5670	21	F21337	Human low adenosin
	30	101.8	36.6	5670	21	A35209	Human adenosine re
	31	101.8	36.6	5670	21	A35215	Human adenosine re
	32	99	35.6	166	21	Z55552	Canine interleukin
	33	44.6	16.0	60	13	Q28942	Cytokine signal se
	34	44.6	16.0	102	13	Q28941	Cytokine signal se
	35	40.8	14.7	2460	11	Q08086	Plasmid pZPC13 enc
	36	37.2	13.4	86	20	Z32227	Human interleukin
	37	35.8	12.9	2249	18	T74283	Cellulose binding
	38	35.8	12.9	2300	18	T74282	Cellulose binding
	39	35.8	12.9	3187	17	T10922	Laccase gene. Myc
	40	35.8	12.9	3192	18	T72106	Myeliotrophora the
	41	35.8	12.9	3192	18	T69318	Myeliotrophora the
	42	35.8	12.9	3192	21	Z42436	M. thermophila lac
	43	34.4	12.4	772	19	V48405	Dominant-negative
	44	34.4	12.4	1521	12	Q14288	Human neuronal nic
	45	34.4	12.4	2448	15	V12201	Human neuronal nic

ALIGNMENTS

RESULT	1	
Z55554		
ID	Z55554	standard; cDNA; 278 BP.
XX		
AC	Z55554;	
XX		
XX	14-MAR-2000	(first entry)
XX		
DE	Canine interleukin-13	(IL-13) cDNA probe.
XX		
KW	Interleukin-13; IL-13;	antibody; canine; inhibitor; immune response;
KW	immunoregulation;	tumour; cancer; autoimmune disease; vaccine; ss.
XX		
OS	Canis familiaris.	
XX		
PN	WO9961618-A2.	
XX		
PD	02-DEC-1999.	
XX		
PF	28-MAY-1999;	99WO-US11942.
XX		
PR	29-MAY-1998;	98US-0087306.
XX		
PA	(HESK-) HESKA CORP.	
XX		
PI	Sim G, Yang S, Dreitz MJ,	Wonderling RS;
XX		
DR	WPI; 2000-072623/06.	

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune diseases
 XX
 PS Claim 11; Page 229; 264pp; English.

```
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
SQ Sequence 278 BP; 58 A; 93 C; 69 G; 58 T; 0 other;

Query Match      100.0%; Score 278; DB 21; Length 278;
Best Local Similarity 100.0%; Pred. No. 2e-66;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctcgttggtgactgtggtcattgctctcaccctgcctcgtggtgctcctcccg 60
   |||||||
DB 1 atggcgctcgttggtgactgtggtcattgctctcaccctgcctcgtggtgctcctcccg 60

QY 61 agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 120
   |||||||
DB 61 agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 120

QY 121 cagaatcagcattccctctgcaacggcagcatggtgtgagcgtcaacctgaccgccggc 180
   |||||||
DB 121 cagaatcagcattccctctgcaacggcagcatggtgtgagcgtcaacctgaccgccggc 180

QY 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
   |||||||
DB 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240

QY 241 acccagaggatgctgaaagcactgtgctctcaaaaagcc 278
   |||||||
DB 241 acccagaggatgctgaaagcactgtgctctcaaaaagcc 278

RESULT 2
Z55563
ID Z55563 standard; cDNA; 390 BP.
XX
AC Z55563;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
```

```
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
DR P-PSDB; Y58223.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX Claim 11; Page 238-239; 264pp; English.
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX can also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for
XX modulators of activity, while the antibodies may be used in detection,
XX and in drug targeting.
SQ Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match      100.0%; Score 278; DB 21; Length 390;
Best Local Similarity 100.0%; Pred. No. 2.2e-66;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctcgttggtgactgtggtcattgctctcaccctgcctcgtggtgctcctcccg 60
   |||||||
DB 1 atggcgctcgttggtgactgtggtcattgctctcaccctgcctcgtggtgctcctcccg 60

QY 61 agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 120
   |||||||
DB 61 agccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 120

QY 121 cagaatcagcattccctctgcaacggcagcatggtgtgagcgtcaacctgaccgccggc 180
   |||||||
DB 121 cagaatcagcattccctctgcaacggcagcatggtgtgagcgtcaacctgaccgccggc 180

QY 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
   |||||||
DB 181 atgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240

QY 241 acccagaggatgctgaaagcactgtgctctcaaaaagcc 278
   |||||||
DB 241 acccagaggatgctgaaagcactgtgctctcaaaaagcc 278

RESULT 3
Z55564/c
ID Z55564 standard; cDNA; 390 BP.
XX
AC Z55564;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
```


QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
 |||||
 Db 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
 |||||
 QY 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278
 |||||
 Db 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278
 |||||

RESULT 5
 Z5558/c
 ID Z5558 standard; cDNA; 393 BP.
 XX
 AC Z5558;
 XX
 XX 14-MAR-2000 (first entry)
 DT
 XX Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.
 DE
 XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 XX (HESK-) HESKA CORP.
 PA
 XX
 XX Slim G, Yang S, Dreitz MJ, Wonderling RS;
 PI
 XX WPI: 2000-072623/06.
 DR
 DR P-PSDB; Y58221.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PS
 PS Claim 11; Page 233; 264pp; English.
 XX
 CC Sequences Z5552-Z5556 and Z5551-Z5556 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 XX Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match 100.0%; Score 278; DB 21; Length 393;
 Best Local Similarity 100.0%; Pred. No. 2.2e-66;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctgttgcactgtgttcattgtctctcactgcctgcgtgctgcctccccc 60

Db 393 atggcgctctgttgcactgtgttcattgtctcactgcctgcgtgctgcctccccc 334
 |||||
 QY 61 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtgacatcacc 120
 |||||
 Db 333 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtgacatcacc 274
 |||||
 QY 121 cagaatcaggagcactccctctgcaacgcagcagcatggtgtgagcgtcaacctgaccgccg 180
 |||||
 Db 273 cagaatcaggagcactccctctgcaacgcagcagcatggtgtgagcgtcaacctgaccgccg 214
 |||||
 QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
 |||||
 Db 213 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 154
 |||||
 QY 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278
 |||||
 Db 153 acccagaggatgctgaaagcactgtgctctcaaaagcc 116
 |||||

RESULT 6
 Z55561
 ID Z55561 standard; cDNA; 1269 BP.
 XX
 AC Z55561;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-13 (IL-13) clone 78 cDNA.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 XX Key Location/Qualifiers
 FT CDS 57..449
 FT /*tag= a
 FT /product= "Canine IL-13 clone 78"
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 XX (HESK-) HESKA CORP.
 PI
 XX Slim G, Yang S, Dreitz MJ, Wonderling RS;
 DR
 DR WPI: 2000-072623/06.
 DR P-PSDB; Y58223.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PS
 PS Claim 11; Page 235-236; 264pp; English.
 XX
 CC Sequences Z5552-Z5556 and Z5551-Z5556 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 XX Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 278; DB 21; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 3e-66;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctggtgactgtggtcattgtctcactgcctcctggtggtcctcccccgcg 60
 Db 57 atggcgctctggtgactgtggtcattgtctcactgcctcctggtggtcctcccccgcg 116
 QY 61 agccctgtgactcctccccaacccaagagctcattgagagctggtcaacatcacc 120
 Db 117 agccctgtgactcctccccaacccaagagctcattgagagctggtcaacatcacc 176
 QY 121 cagaatcaggatccctctcgaacggcagcagctggtgtgagcgtcaacctgaccgccgcg 180
 Db 177 cagaatcaggatccctctcgaacggcagcagctggtgtgagcgtcaacctgaccgccgcg 236
 QY 181 atgtactgcgcagctctagaaatctctgatcaatgtctcgcagctcagcgcctccaaagg 240
 Db 237 atgtactgcgcagctctagaaatctctgatcaatgtctcgcagctcagcgcctccaaagg 296
 QY 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278
 Db 297 acccagaggatgctgaaagcactgtgctctcaaaagcc 334

RESULT 7

Z55562/c
 ID Z55562 standard; cDNA; 1269 BP.

XX AC Z55562;

DT 14-MAR-2000 (first entry)

XX Canine interleukin-13 (IL-13) clone 78 cDNA complement.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX Key Location/Qualifiers
 FT CDS complement (821..1213)
 FT /*tag= a
 FT /product= "Canine IL-13 clone 78"

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX P-PSDB; Y58223.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease

XX
 PS
 XX

Claim 11; Page 237-238; 264pp; English.

CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 100.0%; Score 278; DB 21; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 3e-66;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 atggcgctctggtgactgtggtcattgtctcactgcctcctggtggtcctcccccgcg 60
 Db 1213 atggcgctctggtgactgtggtcattgtctcactgcctcctggtggtcctcccccgcg 1154
 QY 61 agccctgtgactcctccccaacccaagagctcattgagagctggtcaacatcacc 120
 Db 1153 agccctgtgactcctccccaacccaagagctcattgagagctggtcaacatcacc 1094
 QY 121 cagaatcaggatccctctcgaacggcagcagctggtgtgagcgtcaacctgaccgccgcg 180
 Db 1093 cagaatcaggatccctctcgaacggcagcagctggtgtgagcgtcaacctgaccgccgcg 1034
 QY 181 atgtactgcgcagctctagaaatctctgatcaatgtctcgcagctcagcgcctccaaagg 240
 Db 1033 atgtactgcgcagctctagaaatctctgatcaatgtctcgcagctcagcgcctccaaagg 974
 QY 241 acccagaggatgctgaaagcactgtgctctcaaaagcc 278
 Db 973 acccagaggatgctgaaagcactgtgctctcaaaagcc 936

RESULT 8

Z55555
 ID Z55555 standard; cDNA; 1302 BP.

XX AC Z55555;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-13 (IL-13) clone 80 cDNA.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX Key Location/Qualifiers

XX CDS 52..447

XX /*tag= a

XX /product= "Canine IL-13 clone 80"

XX WO9961618-A2.

```
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US11942.
XX PR 29-MAY-1998; 98US-0087306.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX DR P-PSDB; Y58221.
XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX PS Claim 11; Page 229-230; 264pp; English.
XX
XX CC Sequences 255552-255560 and 255561-255566 represent cDNA
XX CC sequences encoding canine interleukin-13 (IL-13) clones 80
XX CC and 78 respectively. The invention relates to canine
XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX CC immunoregulatory proteins. The proteins, their associated
XX CC nucleic acids, specific antibodies and inhibitors may be used as
XX CC vaccines for therapeutic or prophylactic regulation of an immune
XX CC response in animals (particularly cats, dogs, horses and humans).
XX CC They may be used to treat autoimmune or infectious diseases including
XX CC allergies, tumors, inflammation and graft rejection, and to increase
XX CC the response from a co-administered antigen. The nucleotide sequences
XX CC can also be used for the recombinant production of a protein, while
XX CC nucleotide fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for
XX CC modulators of activity, while the antibodies may be used in detection,
XX CC and in drug targeting.
XX
XX SQ Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 278; DB 21; Length 1302;
Best Local Similarity 100.0%; Pred. No. 3e-66;
Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 atggcgctctggtgactgtggtcattgctcaccctgctcggtgctgctcccg 60
|||||
Db 52 atggcgctctggtgactgtggtcattgctcaccctgctcggtgctgctcccg 111
|||||
Qy 61 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 120
|||||
Db 112 agccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaacatcacc 171
|||||
Qy 121 cagaatcaggatccctctgcaacgagcagatggtgtggagcgtcaacctgagccgcgcg 180
|||||
Db 172 cagaatcaggatccctctgcaacgagcagatggtgtggagcgtcaacctgagccgcgcg 231
|||||
Qy 181 atgtactgcagactctagaatctgataatgtctccgactgcaagcgcattccaaagg 240
|||||
Db 232 atgtactgcagactctagaatctgataatgtctccgactgcaagcgcattccaaagg 291
|||||
Qy 241 acccagagatgctgaaagcactgtgctctcaaaagcc 278
|||||
Db 292 acccagagatgctgaaagcactgtgctctcaaaagcc 329
|||||

RESULT 9
ID 255556/c
XX 255556 standard; cDNA; 1302 BP.
XX AC 255556;
```

Db 1131 CAGAAATCAGGCATCCTCTGTCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCGGC 1072
 QY 181 atgtactgcgagctctagaatctctgtatgtaoatgtctcagctagcgccatccaaagg 240
 Db 1071 ATGTACTCGCGAGCTCTACAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAGG 1012
 QY 241 accagagatgctgaaagcactgtgctctcaaaagcc 278
 Db 1011 ACCCAGAGATGCTGAAAGCACTGTGCTCTCAAAAGCC 974

RESULT 10
 ID 255553 standard; cDNA; 272 BP.
 XX 255553;
 AC
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 XX 02-DEC-1999.
 XX
 XX 28-MAY-1999; 99WO-US11942.
 XX
 XX 29-MAY-1998; 98US-0087306.
 XX
 XX (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 XX WPI: 2000-072623/06.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim 11; Page 228; 264pp; English.
 XX
 XX Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;
 SQ

Query Match 84.2%; Score 234; DB 21; Length 272;
 Best Local Similarity 100.0%; Pred. No. 1.6e-54;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 45 tggccttgctcccgagccctgactccctcccaacccctcaaggagctcattgagga 104
 Db 1 tggccttgctcccgagccctgactccctcccaacccctcaaggagctcattgagga 60
 QY 105 gctggtcaacatcacccagagcaggtacccctctgcaacggcagcatggtgtgagcgt 164
 Db 61 gctggtcaacatcacccagagcaggtacccctctgcaacggcagcatggtgtgagcgt 120
 QY 165 caacctgaccgcggcgatgtactgcgagctctagaatctctgatcaatgtctccgactg 224
 Db 121 caacctgaccgcggcgatgtactgcgagctctagaatctctgatcaatgtctccgactg 180
 QY 225 cagcgccatccaaagaccagagagtgctgaaagcactgtgctctcaaaagcc 278
 Db 181 cagcgccatccaaagaccagagagtgctgaaagcactgtgctctcaaaagcc 234

RESULT 11
 ID 255565 standard; cDNA; 330 BP.
 XX 255565;
 AC
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 XX 02-DEC-1999.
 XX
 XX 28-MAY-1999; 99WO-US11942.
 XX
 XX 29-MAY-1998; 98US-0087306.
 XX
 XX (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 XX WPI: 2000-072623/06.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim 11; Page 239-240; 264pp; English.
 XX
 CC Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX

SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 78.4%; Score 218; DB 21; Length 330;
Best Local Similarity 100.0%; Pred. No. 3.6e-50;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccaacccaagagagctcattgagagctggtcaacatcacc 120
DB 1 agccctgtgactccctcccaacccaagagagctcattgagagctggtcaacatcacc 60
QY 121 cagaatcaggcattccctctgcaacggcagcatggtgagagctcattgagagctggtcaacatcacc 180
DB 61 cagaatcaggcattccctctgcaacggcagcatggtgagagctcattgagagctggtcaacatcacc 120
QY 181 atgtactgcagctctagaaatctctgatcaatgtctccgactgcagcgcattccaaagg 240
DB 121 atgtactgcagctctagaaatctctgatcaatgtctccgactgcagcgcattccaaagg 180
QY 241 acccagagagctgaaagcactgtgctctcaaaagcc 278
DB 181 acccagagagctgaaagcactgtgctctcaaaagcc 218

RESULT 12
ID 255566 standard; cDNA; 330 BP.
AC 255566;
DT 14-MAR-2000 (first entry)
XX Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX WO9961618-A2.
XX 02-DEC-1999.
XX 28-MAY-1999; 99WO-US11942.
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
DR WPI; 2000-072623/06.
DR P-PSDB; Y58224.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 11; Page 241; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences

CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.

SQ Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 78.4%; Score 218; DB 21; Length 330;
Best Local Similarity 100.0%; Pred. No. 3.6e-50;
Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 61 agccctgtgactccctcccaacccaagagagctcattgagagctggtcaacatcacc 120
DB 330 agccctgtgactccctcccaacccaagagagctcattgagagctggtcaacatcacc 271
QY 121 cagaatcaggcattccctctgcaacggcagcatggtgagagctcattgagagctggtcaacatcacc 180
DB 270 cagaatcaggcattccctctgcaacggcagcatggtgagagctcattgagagctggtcaacatcacc 211
QY 181 atgtactgcagctctagaaatctctgatcaatgtctccgactgcagcgcattccaaagg 240
DB 210 atgtactgcagctctagaaatctctgatcaatgtctccgactgcagcgcattccaaagg 151
QY 241 acccagagagctgaaagcactgtgctctcaaaagcc 278
DB 150 acccagagagctgaaagcactgtgctctcaaaagcc 113

RESULT 13
ID 255559 standard; cDNA; 333 BP.
AC 255559;
XX
DT 14-MAR-2000 (first entry)
XX Canine mature interleukin-13 (IL-13) clone 80 cDNA.
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX WO9961618-A2.
XX 02-DEC-1999.
XX 28-MAY-1999; 99WO-US11942.
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
DR WPI; 2000-072623/06.
DR P-PSDB; Y58222.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 11; Page 233-234; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:49 ; Search time 226.02 Seconds
(without alignments)
214.758 Million cell updates/sec

Title: US-09-451-527-90
Perfect score: 278
Sequence: 1 atggcgctgtgtgactgt.....gcactgtgtctctcaaaagcc 278

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Issued_Patents_NA.*
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq:*
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq:*
3: /cgnl_7/ptodata/1/ina/6A_COMB.seq:*
4: /cgnl_7/ptodata/1/ina/6B_COMB.seq:*
5: /cgnl_7/ptodata/1/ina/PCTRUS_COMB.seq:*
6: /cgnl_7/ptodata/1/ina/backfiles.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	191	68.7	1290	1	US-08-012-543-1
2	191	68.7	1290	5	PCT-US93-07645A-1
3	189.4	68.1	1297	1	US-08-371-121-15
4	148.2	53.3	384	1	US-08-371-121-17
5	147.6	53.1	336	1	US-08-371-121-24
6	146.4	52.7	425	1	US-08-594-469-4
7	146.4	52.7	425	2	US-08-906-957-4
8	146.4	52.7	4410	1	US-08-594-469-1
9	146.4	52.7	4410	2	US-08-906-957-1
10	146.4	52.7	4410	2	US-08-906-957-1
11	146.4	52.7	336	1	US-08-371-121-2
12	142.4	51.2	447	1	US-08-371-121-26
13	142.4	51.2	1212	1	US-08-012-543-3
14	142.4	51.2	1212	5	PCT-US93-07645A-3
15	142.4	51.2	1212	5	PCT-US93-07645-3
16	44.6	16.0	60	1	US-08-371-121-12
17	44.6	16.0	102	1	US-08-371-121-10
18	39.6	14.2	54	1	US-08-371-121-11
19	39.6	14.2	96	1	US-08-371-121-9
20	35.8	12.9	2249	3	US-08-814-052-19
21	35.8	12.9	2300	3	US-08-814-052-18
22	35.8	12.9	3183	2	US-08-939-218A-1
23	35.8	12.9	3187	5	PCT-US95-06815-1
24	35.8	12.9	3192	1	US-08-706-037-26
25	35.8	12.9	3192	1	US-08-940-661A-1
26	35.8	12.9	3192	2	US-09-083-485-1
27	35.8	12.9	3192	2	US-09-005-397-26

RESULT 1
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA

ALIGNMENTS

28	34.4	12.4	1322	4	US-09-128-450-27	Sequence 27, Appl
29	34.4	12.4	1521	1	US-08-496-855A-3	Sequence 3, Appl
30	34.4	12.4	1521	2	US-07-938-154-9	Sequence 9, Appl
31	34.4	12.4	1521	5	PCT-US91-02311-9	Sequence 9, Appl
32	34.4	12.4	2450	2	US-08-466-589-9	Sequence 9, Appl
33	34.4	12.4	2450	2	US-08-700-636-9	Sequence 9, Appl
34	34.4	12.4	2450	3	US-08-467-574-9	Sequence 9, Appl
35	33.2	11.9	2712	3	US-09-025-691-4	Sequence 4, Appl
36	32.4	11.7	720	4	US-09-094-359-3	Sequence 3, Appl
37	32.4	11.7	720	4	US-09-172-063-11	Sequence 7, Appl
38	32.4	11.7	720	4	US-09-172-063-13	Sequence 11, Appl
39	32.4	11.7	762	1	US-08-532-390-40	Sequence 13, Appl
40	32.4	11.7	762	4	US-08-717-294-40	Sequence 40, Appl
41	32.4	11.7	768	4	US-09-094-359-11	Sequence 11, Appl
42	32.4	11.7	850	4	US-09-062-102-2	Sequence 2, Appl
43	32.4	11.7	972	4	US-09-172-063-27	Sequence 27, Appl
44	32.4	11.7	972	4	US-09-172-063-29	Sequence 29, Appl
45	32.4	11.7	972	4	US-09-172-063-29	Sequence 29, Appl

FEATURE:
NAME/KEY: CDS
LOCATION: 45..443
US-08-012-543-1

Query Match 68.7%; Score 191; DB 1; Length 1290;
Best Local Similarity 82.8%; Pred. No. 4.le-46;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
QY 1 atggcgctgtggtgactgtgcttgcctccacccctgcctcgtggtgcttgcctccccc 60
Db 45 ATGGCGCTTTTGTGGACACGGTCATTGCTCTCACTTGGCTTGGCGCTTGGCTCCCCA 104
QY 61 agccctgtgactccctcccccacccctcaaggagctcattgaggtggtgagcgtccacc 120
Db 105 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGGCTCAATTGAGGAGCTGGTCAACATCACC 164
QY 121 cagaatc---aggcatccctctgcaacgcagcagcagcagcagcagcagcagcagc 177
Db 165 CAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
QY 178 ggcattgtactgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 237
Db 225 GGCATGTACTGTGAGCCCTGGATCCCTGATCAACGTGTGAGGCTGCAGTGCCATCGAG 284
QY 238 aggaccagagagatgctgaaagcactgtgctctcaaaag 276
Db 285 AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAG 323

RESULT 2
PCT-US93-07645A-1
; Sequence 1; Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match 68.7%; Score 191; DB 5; Length 1290;
Best Local Similarity 82.8%; Pred. No. 4.le-46;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
QY 1 atggcgctgtggtgactgtgcttgcctccacccctgcctcgtggtgcttgcctccccc 60
Db 45 ATGGCGCTTTTGTGGACACGGTCATTGCTCTCACTTGGCTTGGCGCTTGGCTCCCCA 104
QY 61 agccctgtgactccctcccccacccctcaaggagcagcagcagcagcagcagcagcagc 120

Db 105 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGGCTCAATTGAGGAGCTGGTCAACATCACC 164
QY 121 cagaatc---aggcatccctctgcaacgcagcagcagcagcagcagcagcagcagcagc 177
Db 165 CAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
QY 178 ggcattgtactgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 237
Db 225 GGCATGTACTGTGAGCCCTGGATCCCTGATCAACGTGTGAGGCTGCAGTGCCATCGAG 284
QY 238 aggaccagagagatgctgaaagcactgtgctctcaaaag 276
Db 285 AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAG 323

RESULT 3
PCT-US93-07645-1
; Sequence 1; Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-1

Query Match 68.7%; Score 191; DB 5; Length 1290;
Best Local Similarity 82.8%; Pred. No. 4.le-46;
Matches 231; Conservative 0; Mismatches 45; Indels 3; Gaps 1;
QY 1 atggcgctgtggtgactgtgcttgcctccacccctgcctcgtggtgcttgcctccccc 60
Db 45 ATGGCGCTTTTGTGGACACGGTCATTGCTCTCACTTGGCTTGGCGGCTTGGCTCCCCA 104
QY 61 agccctgtgactccctcccccacccctcaaggagcagcagcagcagcagcagcagcagc 120
Db 105 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGGCTCAATTGAGGAGCTGGTCAACATCACC 164
QY 121 cagaatc---aggcatccctctgcaacgcagcagcagcagcagcagcagcagcagcagc 177
Db 165 CAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
QY 178 ggcattgtactgcgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 237
Db 225 GGCATGTACTGTGAGCCCTGGATCCCTGATCAACGTGTGAGGCTGCAGTGCCATCGAG 284
QY 238 aggaccagagagatgctgaaagcactgtgctctcaaaag 276
Db 285 AAGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAG 323

Query Match ✓ 68.1%; Score 189.4; DB 1; Length 1297;
Best Local Similarity 82.4%; Pred. No. 1.2e-45;
Matches 230; Conservative 0; Mismatches 46; Indels 3;

1:

INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match 53.3%; Score 148.2; DB 1; Length 384;
Best Local Similarity 81.8%; Pred. No. 5.6e-34;
Matches 184; Conservative 0; Mismatches 38; Indels 3; Gaps 1;
QY 55 tccccgagcctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaaac 114
Db 16 TCCCCAGGCCCTGTGCTCCCTCTACGGCCCTCAGGGAGCTCAITGAGGAGCTGGTCAAC 75
QY 115 ataccaccagaaac---aggcctccctctgaacgcgagcagctggtgagcgctcaaacctg 171
Db 76 ATACCCAGAACGAGAGGCTCCGCTCTGCATGCGAGCATGGTATGGAGCATCAACCTG 135
QY 172 acgcgcgctgactgctgagcagctctagaatctctgatcaatgtctccgactgcagcgcc 231
Db 136 ACAGCTGACATGTACTGTGAGCCCTCGAATCCCTGATCAACGCTGTCAGGCTGCAGTGCC 195
QY 232 atccaaaggaccagagatgctgaaagcactgtgctctcaaaaag 276
Db 196 ATCAGAGAAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAG 240

RESULT 6

US-08-371-121-24
Sequence 24, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLENOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTEILLER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match 53.1%; Score 147.6; DB 1; Length 336;
Best Local Similarity 83.0%; Pred. No. 8e-34;
Matches 181; Conservative 0; Mismatches 34; Indels 3; Gaps 1;
QY 62 gccctgtgactccctcccaaccctcaaggagctcattgaggagctgttcaacatcaccc 121
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61
QY 122 agaatc---aggcctccctctgcaacgcgagcagcatggttggagcgtcaacctgacgcgcg 178
Db 62 AGAACGAGAAGGCTCCGCTCTGCATGCGAGCATGGTATGGAGCATCAACCTGACAGCTG 121
QY 179 gcattgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 238
Db 122 GCATGTACTGTGAGCCCTCGAATCCCTGATCAACGCTGTGAGCTGCAGTGCATCGCATCGA 181
QY 239 ggaccagagagatgctgaaagcactgtgctctcaaaaag 276
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAG 219

RESULT 7

US-08-594-469-4
Sequence 4, Application US/08594469
Patent No. 5700665
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-594-469-1

Query Match 52.7%; Score 146.4; DB 1; Length 4410;
Best Local Similarity 80.7%; Pred. No. 3.4e-33;
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 52 gcttccccgagccctgtgactccctcccaaccctcaaggagctcattgagagctgtgtc 111
DB 392 GCTTCTGCTGGCCCTGTGCTCCAGTAGTACCTCCCTCAGGAGCTCATTTGAGAGCTGTC 451
QY 112 aacatccaccagaaatc---aggcatccctctgcaacgagcagcagtggtgagcgtcaac 168
DB 452 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGCGAGCTGATGGAGCATCAAC 511
QY 169 ctgaccgccgagctgactgagcagctctagaatctctgatcaatgtctccgactgcagc 228
DB 512 CTGACAGCTGCGATGTACTGTGCGAGCCCTGCAATCCCTGATCAAGTGTCAAGCTGCAGT 571
QY 229 gccatcaaaaggaccagagagatgctgaaagcactgtgtctctcaaaaag 276
DB 572 GCCATCGAGAGAGCCAGAGATGCTGAGCGGATTCTGCCGCGACAAG 619

RESULT 10

US-08-906-957-1
Sequence 1, Application US/08906957
Patent No. 5856142

GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard

APPLICANT: MALDONADO, Paul

APPLICANT: SALOME, Marc

TITLE OF INVENTION: Method for the extraction of periplasmic proteins of prokaryotic microorganisms in the

TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the

TITLE OF INVENTION: presence of arginine

NUMBER OF SEQUENCES: 9

CORRESPONDENCE ADDRESS:

ADDRESSEE: Bacon & Thomas

STREET: 625 Slaters Lane - Fourth Floor

CITY: Alexandria

STATE: Virginia

COUNTRY: USA

ZIP: 22314

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/906,957

FILING DATE: 06-AUG-1997

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/594,469

FILING DATE:

APPLICATION NUMBER: FR 95 01083

FILING DATE: 31-JAN-1995

ATTORNEY/AGENT INFORMATION:

NAME: FICHTER, Richard E

REGISTRATION NUMBER: 26,382

REFERENCE/DOCKET NUMBER: REF/LEGOUX

TELECOMMUNICATION INFORMATION:

TELEPHONE: (703) 683-0500

TELEFAX: (703) 683-1080

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 4410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-906-957-1

Query Match 52.7%; Score 146.4; DB 2; Length 4410;
Best Local Similarity 80.7%; Pred. No. 3.4e-33;
Matches 184; Conservative 0; Mismatches 41; Indels 3; Gaps 1;

QY 52 gcttccccgagccctgtgactccctcccaaccctcaaggagctcattgagagctgtgtc 111
DB 392 GCTTCTGCTGGCCCTGTGCTCCAGTAGTACCTCCCTCAGGAGCTCATTTGAGAGCTGTC 451
QY 112 aacatccaccagaaatc---aggcatccctctgcaacgagcagcagtggtgagcgtcaac 168
DB 452 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGCGAGCTGATGGAGCATCAAC 511
QY 169 ctgaccgccgagctgactgagcagctctagaatctctgatcaatgtctccgactgcagc 228
DB 512 CTGACAGCTGCGATGTACTGTGCGAGCCCTGGAATCCCTGATCAACGTGTCAAGCTGCAGT 571
QY 229 gccatcaaaaggaccagagagatgctgaaagcactgtgtctctcaaaaag 276
DB 572 GCCATCGAGAGAGCCAGAGATGCTGAGCGGATTCTGCCGCGACAAG 619

RESULT 11

US-08-371-121-2
Sequence 2, Application US/08371121
Patent No. 5652123

GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel

APPLICANT: FERRARA, Pascual

APPLICANT: GUILLEMOT, Jean-Claude

APPLICANT: LEPLATOIS, Pascal

APPLICANT: MINTY, Adrian

APPLICANT: KAGHAD, Mourad

APPLICANT: LABIT-LE BOUTELLER, Christine

APPLICANT: MAGAZIN, Marilyn

TITLE OF INVENTION: Protein having a cytokine type

TITLE OF INVENTION: activity, recombinant DNA coding for this protein,

TITLE OF INVENTION: transformed cells and microorganisms.

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/371,121

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/938,161

FILING DATE: 30-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR92/00280

FILING DATE: 27-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 00137

FILING DATE: 08-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 03904

FILING DATE: 29-MAR-1991

```

; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-371-121-2

Query Match      52.5%; Score 146; DB 1; Length 336;
Best Local Similarity 82.6%; Pred. No. 2.3e-33;
Matches 180; Conservative 0; Mismatches 35; Indels 3; Gaps 1;

QY 62 gccctgtgactccctcccccacccctcaaggagctcatgtgagcgtcgaacatcaccc 121
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATGAGGAGCTGGTCAACATCACCC 61

QY 122 agaatc---aggatccctctgcaacgcagcatgtgtggagcgtcaaacctgacgcgcg 178
Db 62 AGAACCAAGGCTCCGCTCTGCAATGGCAGCATGGTATGAGCATCAACCTGACAGCTG 121

QY 179 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 238
Db 122 ACATGTACTGTGCAGCCCTCGAATCCCTGATCAAGCTGTGAGGCTGCAGTCGATCGAGA 181

QY 239 ggaccagagatgctgaagcactgtctctcaaaag 276
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAG 219

RESULT 12
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
;
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; US-08-371-121-26

Query Match      51.2%; Score 142.4; DB 1; Length 447;
Best Local Similarity 71.4%; Pred. No. 2.7e-32;
Matches 207; Conservative 0; Mismatches 71; Indels 12; Gaps 1;

QY 1 atggcgctctgtgtgactgtgctcctcaccctgcctcgcctgcctgcctgcctccccc 60
Db 49 ATGGCGCTCTGGGTGACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 108

QY 61 agcc-----ctgtgactccctcccccacccctcaaggagcctcattgagagctg 108
Db 109 GGCGCGGTGCCAAGATCTGTGCTCTCCCTCTGACCTTAAGGAGCTTATTGAGGAGCTG 168

QY 109 gtcaaatatccacagaaatcaggatccctctgcaacggcagcatggtgtgagagctaac 168
Db 169 AGCAACATCATCACAAAGACCAAGACTCCCTCTGTGCAACGCAGCATGGTATGAGTGTGAC 228

QY 169 ctgacgcgcgcgcatgtactgcgagctctagaatctctgatcaatgtctcgcgactgcagc 228
Db 229 CTGCGCGCTGGCGGTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 288

QY 229 gccatccaaaggacccagagatgctgaaagcactgtgctctcaaaagcc 278
Db 289 GCCATCTACAGGAGGCCAGAGGATATTGCAATGGCCTCTGTAAACCCGCAAGCC 338

RESULT 13
US-08-012-543-3
; Sequence 3, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Bancheureau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
;
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-371-121-2
```


;
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-3

```

Query Match      51.2%; Score 142.4; DB 5; Length 1212;
Best Local Similarity 71.4%; Pred No. 3.4e-32;
Matches 207; Conservative 0; Mismatches 71; Indels 12; Gaps 1;

Qy 1 atggcgctctgttgactgtggtcattgtctcacctgctcggtggtgcttgcctcccg 60
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 70 ATGGCGCTCTGGGTGACTGCAGTCTGCTTGGCTTGGTGGTCTCGCCGCCCA 129

Qy 61 agcc-----ctgtgactccctcccaaccctcaaggagctcattgaggagctg 108
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 130 GGGCGGCTGCCAAGATCTGTCTCTCCCTCTGAGCCTTAAGGAGCTTATTGAGGAGCTG 189

Qy 109 gtcaacatcacccaggaatcaggcatccctctgcaacggcagcatggtgaggagctcaac 168
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 190 AGCAACATCACACAGACAGACTCCCTCTGTGCAAGCGGAGCATGGTATGGAGTGTGGAC 249

Qy 169 ctgaccgcggcgtgactgcgcagctctagaaatctctgatcaatgtctccgactgcagc 228
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 250 CTGGCCGCTGGGGGTTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT 309

Qy 229 gccatccaaagagaccagagatgctgaaagcactgtgctctcaaaagcc 278
   ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 310 GCCATCTACAGGACCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGC 359

```

Search completed: May 13, 2001, 14:20:52
Job time: 17803 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:39:46 ; Search time 5997.24 Seconds
(without alignments)
404.959 Million cell updates/sec

Title: US-09-451-527-90
Perfect score: 278
Sequence: 1 atggcgctctgttgactgt.....gcactgtgctctcaaaagcc 278

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues 19247034
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_estl1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est33:*
26: gb_est34:*
27: gb_est35:*
28: gb_est36:*
29: gb_est37:*
30: gb_est38:*
31: gb_est39:*
32: gb_est40:*
33: em_estba:*
34: em_estfun:*
35: em_esthum1:*
36: em_esthum2:*
37: em_esthum3:*
38: em_esthum4:*
39: em_esthum5:*
40: em_esthum6:*
41: em_esthum7:*
42: em_esthum8:*
43: em_esthum9:*
44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estin5:*
68: em_estomi:*
69: em_estom2:*
70: em_estov1:*
71: em_estov2:*
72: em_estpl1:*
73: em_estpl2:*
74: em_estpl3:*
75: em_estpl4:*
76: em_estpl5:*
77: em_estpl6:*
78: em_estpl7:*
79: em_estpl8:*
80: em_estpl9:*
81: em_estpl10:*
82: em_estro1:*
83: em_estro2:*
84: em_estro3:*
85: em_estro4:*
86: em_estro5:*
87: em_estro6:*
88: em_estro7:*
89: em_estro8:*
90: em_estro9:*
91: em_estro10:*
92: em_estro11:*
93: em_estro12:*
94: em_estro13:*
95: em_estro14:*
96: em_estro15:*
97: em_estro16:*
98: em_estro17:*
99: em_estro18:*
100: em_estro19:*
101: em_estro20:*
102: gb_est25:*
103: gb_est26:*
104: gb_est27:*
105: gb_est28:*
106: gb_est29:*
107: gb_est30:*
108: gb_est31:*
109: gb_est32:*
110: gb_est41:*
111: gb_est42:*
112: gb_est43:*
113: gb_est44:*
114: gb_est45:*
115: gb_est46:*
116: gb_est47:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	43.4	15.6	581	219	AZ305110	AZ305110 1M005P05
2	40	14.4	463	24	AI712497	AI712497 UT-R-AFI-
3	37.8	13.6	994	231	CNS0402X	AL300678 Tetraodon
4	36.8	13.2	576	141	BE907816	BE907816 601501924
5	36.6	13.2	329	146	BF292210	BF292210 WHE2208_A
6	36.4	13.1	277	137	BE593226	BE593226 WSL_99_B0
7	36.4	13.1	411	201	AQ001086	AQ001086 CIT-HSP-2
8	36.4	13.1	537	166	BE357229	BE357229 DGL_147_B
9	35.6	12.8	230	167	BE498968	BE498968 WHE0969_G
10	35.6	12.8	1070	136	BE536034	BE536034 601062471
11	35.2	12.7	177	103	AI909438	AI909438 IL-BT208-
12	35.2	12.7	570	24	AI746678	AI746678 ul06505_Y
13	35	12.6	359	17	AI209519	AI209519 b0e07a1_f
14	34.8	12.5	507	138	BE705147	BE705147 Sc02_08f0
15	34.6	12.4	965	217	AZ201624	AZ201624 SP_0053_A
16	34.4	12.4	462	143	BF039993	BF039993 BP250023B
17	34.4	12.4	544	13	AA880435	AA880435 vw89f07_r
18	34.4	12.4	553	106	AU075583	AU075583 AU075583

```

19 34.4 12.4 700 113 AW318852
20 34.4 12.4 712 115 AW475303
21 34.4 12.4 1056 144 BF143984
22 34.2 12.3 477 151 BF625277
23 34.2 12.3 535 161 BE032541
24 34.2 12.3 546 161 BE032543
25 34.2 12.3 616 106 AU066538
26 34.2 12.3 691 150 BF620464
27 34 34.2 341 163 BE127683
28 34 34.2 370 166 BE363650
29 34 34.2 562 166 BE361027
30 34 34.2 704 230 CNS02PBO
31 34 34.2 1122 141 BF889888
32 33.8 12.2 498 150 BF606532
33 33.6 12.1 537 29 AV387571
34 33.6 12.1 727 164 BE216356
35 33.6 12.1 891 151 BF685554
36 33.6 12.1 902 106 AL522415
37 33.4 12.0 619 173 BG112663
38 33.4 12.0 669 211 AQ780112
39 33.4 12.0 752 212 AQ849747
40 33.4 12.0 818 212 AQ849972
41 33.2 11.9 462 164 BE228410
42 33.2 11.9 487 22 AT598187
43 33.2 11.9 616 15 AT062250
44 33.2 11.9 621 175 C97983
45 33.2 11.9 683 15 AT064071

```

ALIGNMENTS

```

RESULT 1
AZ305110 581 bp DNA 29-SEP-2000
LOCUS 1M0005P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
DEFINITION clone UUGC1M0005P05 R, DNA sequence.
ACCESSION AZ305110
VERSION AZ305110.1 GI:10341800
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 581)
Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
,M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.
and Wright,D., Weiss,R.
Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
Unpublished (2000)
Contact: Robert B. Weiss
University of Utah Genome Center
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: P column: 05
Seq primer: CACACAGGAAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 581.
Location/Qualifiers
1..581
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0005P05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"

```

FEATURES

source

FEATURES

source

```

/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/note="Vector: PWD42nv; Purified genomic DNA from M. musculus C57BL/6J (male) was obtained from the Jackson Laboratory Mouse DNA Resource (http://www.jax.org/resources/documents/dnares/). The DNA was hydrodynamically sheared by repeated passage through a 0.005 inch orifice at constant velocity. The sheared DNA was blunt end-repaired with T4 DNA polymerase and T4 polynucleotide kinase. Adaptor oligonucleotides were ligated to the blunt ends in high molar excess. The adaptor DNA was purified and size-selected for a 9.5 to 10.5 kb range using preparative agarose gel electrophoresis. Vector DNA was prepared from a derivative of pWD42 (gii4732114|gb|AF129072.1), a copy-number inducible derivative of plasmid RI. The vector was ligated with adaptors complementary to the insert adaptors and purified. The sheared, adaptor mouse DNA was annealed to adaptor vector DNA, and transformed into chemically-competent E. coli XL10-Gold (Stratagene) cells and selected for ampicillin resistance."
BASE COUNT 169 a 139 c 153 g 120 t
ORIGIN

Query Match 15.6%; Score 43.4; DB 219; Length 581;
Best Local Similarity 76.8%; Pred. No. 0.14;
Matches 53; Conservative 0; Mismatches 16; Indels 0; Gaps 0;

QY 1 atggcgctctgttgactgtgctcattgtcctcactgcctcgttggtgcttcctccccc 60
|||||
Db 513 ATGGCGCTCTGGGTGACTGCAGTCTGCTCTGCTTGGTGGTGGTCTCGCCGCCCA 572
|||||

QY 61 agccctgtg 69
|||||
Db 573 GGGCCGGTG 581

RESULT 2
AT1712497 463 bp mRNA EST 08-JUN-1999
LOCUS UI-R-AFI-aap-b-12-0-UI.s1 UI-R-AFI Rattus norvegicus cDNA clone
DEFINITION UI-R-AFI-aap-b-12-0-UI 3', mRNA sequence.
ACCESSION AT1712497
VERSION AT1712497.1 GI:5016297
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 463)
Ronalds,M.F., Lennon,G. and Soares,M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
97044477
Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
Oligo-dt track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-NO. Location/Qualifiers
1..463
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"

```

```
/db_xref="taxon:10116"
/clone="UI-R-AF1-aap-b-12-0-UI"
/clone_lib="UI-R-AF1"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="vector: pT7T3D-Pac (Pharmacia) with a modified
polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-AF1
library is a normalized library constructed from 15 dpc
rat atrioventricular (AV) canal. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dT track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_LIB=UI-R-AF1
TAG_TISSUE=AV canal at 15 dpc
TAG_SEQ=GAAGG"
BASE COUNT      97 a 130 c  92 g 144 t
ORIGIN

Query Match      14.4%; Score 40; DB 24; Length 463;
Best Local Similarity 58.3%; Pred. No. 1.1;
Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 23 tcattgtctcaactgctgctggtgctgctcccccagccctgtgactccctccca 82
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 255 TGATTGCTGCTCCCAACCCCTGTTCTGACCTTCATGATCCCTATGACTTCTTCCCTGC 314
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 83 ccctcaggagctcatgagagctggtggtcaacatcaccagacagcagcctctgca 142
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 315 CCCTTAGTTCATCTGATGATCTGCTCTCAGACACATATGCGCCCTGGGGCTACA 374
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 3
CNS0402X/c
LOCUS      994 bp      DNA      GSS      25-MAY-2000
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone
            125F09 of library G from Tetraodon nigroviridis, genomic survey
            sequence.
ACCESSION  AL300678.1 GI:8177652
VERSION    AL300678.1
KEYWORDS   GSS: genome survey sequence.
SOURCE     Tetraodon nigroviridis.
ORGANISM   Tetraodon nigroviridis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
            Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
            Holacanthopterygii; Acanthopterygii; Percomorpha;
            Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
            1 (bases 1 to 994)
REFERENCE  1 Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
            Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
            Weissenbach,J.
            Characterization and repeat analysis of the compact genome of the
            freshwater pufferfish Tetraodon nigroviridis
            Unpublished
            2 (bases 1 to 994)
REFERENCE  1 Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
            Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
            Saurin,W. and Weissenbach,J.
            Human gene number estimate provided by genome wide analysis using
            Tetraodon nigroviridis DNA sequence
            Unpublished
            3 (bases 1 to 994)
REFERENCE  1 Genoscope.
            Direct Submission
            Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
            This sequence is a single read and was generated as part of a large
            scale clone-end sequencing project of the Tetraodon nigroviridis
            genome. For more information, please take a look at
            http://www.genoscope.cns.fr/Tetraodon.
            Location/Qualifiers

FEATURES             Location/Qualifiers
     source            1..994
                     /organism="Tetraodon nigroviridis"
                     /db_xref="taxon:99883"
                     /clone="125F09"
                     /clone_lib="G"
                     /note="Genoscope sequence ID : C0BG125C005LP1-end : T7"
BASE COUNT      198 a 295 c 325 g 174 t  2 others
ORIGIN

Query Match      13.6%; Score 37.8; DB 231; Length 994;
Best Local Similarity 51.5%; Pred. No. 5.3;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 14 tgactgtggtcattgtctcaactgctgctggtggtgctgctcccgagccctgtgactc 73
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TGGCTGTGCTCTTCTTCATCGGACAAACAAGCGCTGCTGCCCTCCTTCACGCCGACC 185
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 cctccccaaccctcaaggagctcattgaggagctggtcaacatcaccacccaagaatcaggcat 133
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 TCGGGCAAGTCTTTCAGGAGTCTGTAGAGGACCTTGACACATCTCTCATCTCCAGCTGC 125
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 cctctgtcaacgagcagctggtggtggtcaacctgacccgctgagcctgacat 182
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 TCTGCTGTGATGGCAGCCTTGTCAGATCACCAGCAGCAGAGCCAGGAAT 76
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
BE907816      576 bp      mRNA      EST      20-OCT-2000
LOCUS      601501924F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903965 5',
DEFINITION mRNA sequence.
ACCESSION  BE907816.1 GI:10401759
VERSION    BE907816.1
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 576)
REFERENCE  1 NIH-MGC http://mgi.nci.nih.gov/
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Tel.: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9708 row: 0 column: 06
            High quality sequence stop: 571;
            Location/Qualifiers
     source            1..576
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3903965"
                     /clone_lib="NIH_MGC_70"
                     /tissue_type="epithelioid carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.1 kb. Library constructed by Life
                     Technologies."
BASE COUNT      108 a 174 c 147 g 147 t
ORIGIN

Query Match      13.2%; Score 36.8; DB 141; Length 576;
Best Local Similarity 48.1%; Pred. No. 8.7;
```

```
source

1..994
/organism="Tetraodon nigroviridis"
/db_xref="taxon:99883"
/clone="125F09"
/clone_lib="G"
/note="Genoscope sequence ID : C0BG125C005LP1-end : T7"
BASE COUNT      198 a 295 c 325 g 174 t  2 others
ORIGIN

Query Match      13.6%; Score 37.8; DB 231; Length 994;
Best Local Similarity 51.5%; Pred. No. 5.3;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 14 tgactgtggtcattgtctcaactgctgctggtggtgctgctcccgagccctgtgactc 73
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TGGCTGTGCTCTTCTTCATCGGACAAACAAGCGCTGCTGCCCTCCTTCACGCCGACC 185
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 cctccccaaccctcaaggagctcattgaggagctggtcaacatcaccacccaagaatcaggcat 133
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 TCGGGCAAGTCTTTCAGGAGTCTGTAGAGGACCTTGACACATCTCTCATCTCCAGCTGC 125
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 cctctgtcaacgagcagctggtggtggtcaacctgacccgctgagcctgacat 182
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 TCTGCTGTGATGGCAGCCTTGTCAGATCACCAGCAGCAGAGCCAGGAAT 76
    ||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 4
BE907816      576 bp      mRNA      EST      20-OCT-2000
LOCUS      601501924F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903965 5',
DEFINITION mRNA sequence.
ACCESSION  BE907816.1 GI:10401759
VERSION    BE907816.1
KEYWORDS   EST.
SOURCE     human.
ORGANISM   Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
            1 (bases 1 to 576)
REFERENCE  1 NIH-MGC http://mgi.nci.nih.gov/
AUTHORS   National Institutes of Health, Mammalian Gene Collection (MGC)
TITLE     Unpublished (1999)
JOURNAL    Contact: Robert Strausberg, Ph.D.
            Tel.: (301) 496-1550
            Email: Robert.Strausberg@nih.gov
            Tissue Procurement: ATCC
            CDNA Library Preparation: Life Technologies, Inc.
            CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Incyte Genomics, Inc.
            Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9708 row: 0 column: 06
            High quality sequence stop: 571;
            Location/Qualifiers
     source            1..576
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:3903965"
                     /clone_lib="NIH_MGC_70"
                     /tissue_type="epithelioid carcinoma"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                     Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                     Average insert size 1.1 kb. Library constructed by Life
                     Technologies."
BASE COUNT      108 a 174 c 147 g 147 t
ORIGIN

Query Match      13.2%; Score 36.8; DB 141; Length 576;
Best Local Similarity 48.1%; Pred. No. 8.7;
```


Matches 104; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

[illegible]

RESULT	5	
BF292210	329 bp	mrna
LOCUS	WHE2208_A08_B16	EST
DEFINITION	WHE2208_A08_B16S Aegilops speltoides anther cDNA library Aegilops speltoides cDNA clone WHE2208_A08_B16, mRNA sequence.	
ACCESSION	BF292210	
VERSION	BF292210.1	GI:11223274
KEYWORDS	EST.	
SOURCE	Aegilops speltoides	
ORGANISM	Aegilops speltoides Eukaryota; Viridiplantae; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Aegilops.	
REFERENCE	1 (bases 1 to 329) Akhunov,E., Anderson,O.D., Chao,S., Chin,A., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Kianian,P., Lazo,G.R., Miller,R., Otto,C., Rausch,C.J., Seaton,C.L., Simons,K., Tong,J.C. and Zhang,D.	
AUTHORS	The structure and function of the expressed portion of the wheat genomes - Anther cDNA library from Aegilops speltoides	
TITLE	Unpublished (2000)	
JOURNAL	Contact: Olin Anderson	
COMMENT	US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center 800 Buchanan Street, Albany, CA 94710, USA Tel: 5105595773 Fax: 5105595818 Email: andersn@pw.usda.gov Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 Seq primer: Stratagene SK primer.	

```

seq primer: Stratagene SK primer.
Location/Qualifiers
1. .329
/organism="Aegilops speltoides"
/cultivar="F2 from 2-12-4-8-1-1-1" x PI36909-12-811-(1
)"
/db_xref="taxon:4573"
/clone="WHE2208_A08_B16"
/clone_lib="Aegilops speltoides anther cDNA library"
/tissue_type="Anther"
/dev_stage="Premeiotic anthers"
/lab_host="E. coli SOLR"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRT; Site_2: XhoI; plants were grown in a growth
chamber at the University of California, Davis (Akhunov).
prameiotic anthers were harvested, total RNA and poly(A)
RNA were prepared, from each tissue and then pooled, a
cDNA library was made, and the cDNA clones were in vivo
excised to give pBluescript phagemids in the T3 Close lab
(Akhunov, Chin, Choi, Close, Fenton, Kianian, Otto, Simons
, Zhang) at the University of California, Riverside.
Plasmid DNA preparations and DNA sequencing were performed
in the OD Anderson lab (all other authors)."
61 a 97 c 104 g 67 t

```

BASE COUNT

ORIGIN

Query Match 13.2%; Score 36.6; DB 146; Length 329;
Best Local Similarity 50.9%; Pred. No. 8.7;
Matches 87; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy	20	tggctactgtctcaacctgctcgttgaggcttgcctcccccagaccctgtgaetcccc	79
Db	158	TGCGCATCTCTCTCCCTTTCGTCCAGAAGATCATCGCGAGATTTCGGGACCTACTTCC	217
Qy	80	cacccctcaaggagctcatatgaggagctggttcacaatcacccagaatcaggactccctct	139
Db	218	TCATCTTCGGGGGTGGCGCGGTGACCATCAACAAGACAAGGGGCAGATCACGTTC	277
Qy	140	gaacgycagcatagtgtgtagcgctcaacctgacccgccggcgatctactcgg	190
Db	278	CCGCGCTGGGCATCGTGTGGGGCTCGCCGTGATGTGATGGTGTACTCGG	328

RESULT 6

BE593226	BE593226	277 bp	EST	18-AUG-2000
LOCUS				
DEFINITION	WS1_92_B03.g1_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA, mRNA sequence.			
ACCESSION	BE593226			
VERSION	BE593226.1			
KEYWORDS	EST.			
SOURCE	sorghum.			
ORGANISM	Sorghum bicolor			

REFERENCE
JOURNAL
AUTHORS
COMMENT

1 (bases 1 to 277)
Cordonnier-Pratt,M.-M., Gingler,A., Marsala,C., Sudman,M. and Pratt
L.H.
An EST database from Sorghum: water-stressed plants
Unpublished (2000)
Contact: Cordonnier-Pratt MM

The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude polyA, vector and regions
below phred quality 16. The threshold for highest quality sequence
is 20.

```

43 20.
Seq primer: PolyTMix
High quality sequence start: 5
High quality sequence stop: 246
POLYA=No.

```

FEATURES	Location/Qualifiers
source	1. .277
	/organism="Sorghum bicolor"
	/db_xref="taxon:4558"
	/clone_lib="Water-stressed 1 (WS1)"
	/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
BASE COUNT	47 a 81 c 78 g 71 t

[illegible]

```

Query Match          13.1%; Score 36.4; DB 137; Length 277;
Best Local Similarity 53.5%; Pred. No. 9.4;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

```

Qy 84 ccctcaaggagcctcattgaggagtgtcaacatcacccagaatacaggcatccccctctgcaa 143
|| || || || || || || || || || || || || || || || || || || || || || || || || || ||
Db 22 CCCCATGGAGAGGCTCGGGGASCCCGCGACATCGGCCGGTGTGGGTTCCTCTGCAC 81

Qy	144	cggcagcatggtgtagcgctcaacctgaccgcggcgatgtactgcygcagtcttagaatc	203
Db	82	CGACCCGCCAGTGGGTCAACGGCAGGTCATCCGCACAACGGCGCTACGTGTGATG	141
Qy	204	tctaataatgtctccgactac	225
Db	142	TCTGATCTTTAGCTTCTACAGC	163
RESULT	7		
LOCUS	AQ001086/c	411 bp DNA	GSS 26-JUN-1998
DEFINITION	CIT-HSP-2288N10.TR CIT-HSP Homo sapiens genomic clone 2288N10, DNA sequence.		
ACCESSION	AQ001086		
VERSION	AQ001086		
KEYWORDS	AQ001086.1 GI:3028525		
SOURCE	GSS.		
ORGANISM	human.		
REFERENCE	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H., Simon,M. and Venter,J.C.		
TITLE	Use of a random BAC End Sequence Database for Sequence-Ready Map Building (1998)		
JOURNAL	Contact: Mark Adams		
COMMENT	Department of Eukaryotic Genomics The Institute for Genomic Research 9712 Medical Center Dr., Rockville, MD 20850, USA Tel: 301 838 0200 Fax: 301 838 0208 Email: mdadams@tigr.org Clones are available from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html Seq primer: M13 Reverse Class: BAC ends.		
FEATURES	source Location/Qualifiers		
	1..411 /organism="Homo sapiens"		
	/db_xref="GB:7150045"		
	/db_xref="taxon:9606"		
	/clone="2288N10"		
	/clone_lib="CIT-Hsp"		
	/sex="Male"		
	/cell_type="Sperm"		
	/note="vector: pBelOBAC11; Site_1: HindIII; Site_2: HindIII"		
BASE COUNT	120 a 100 c 101 g 90 t		
ORIGIN			
Query Match	13.18;	Score 36.4;	DB 201; Length 411;
Best Local Similarity	48.5%;	Pred. No.10;	
Matches 100;	Conservative 0;	Mismatches 106;	Indels 0; Gaps 0;
Qy	29	ctctcacctgcctcggtgaggcttcctcccgcgagccctgtgactcccccccccaaccctca	88
Db	287	CCCTCGCCTGCGTCATGCGCAAAAGCCCACCGAGCCCGAGTCCCCCTTGTCACCGCCCTCT	228
Qy	89	aggagctcattgagagctgdgtcaacatcacccagaatcaggcatccctctgcgaacggca	148
Db	227	CCAGACTGGGGTCTGTGTGGGCTGGGGCCACATGGGGTCTCTGAAGGCGAGGGCTG	168
Qy	149	gcattggtgtgagcgtcaacctgcgccggcatgtactgcgcagctctagaatctctga	208
Db	167	GTGCTGAGGGGTCTGTGATGATCATCGTCCCGCCCTCTTCTTTTCTGCTCAGTAATCTCAC	108
Qy	209	tcaatgtctccqactgcagcgccatc	234

ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 1070)
TITLE	N1H+MGC http://mgc.nci.nih.gov/ .
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Tel.: (301) 496-1550 Email: Robert.Strausberg@nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: Incyte Genomics, Inc. DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov Plate: LLAM8424 row: n column: 17 High quality sequence start: 3 High quality sequence stop: 5.

```

/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:3448912"
/clone_lib="NIH_MGC_10"
/cell_line="MGC36"
/lab_host="DH10B"
/notes="Organ: cervix; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT
Average insert size 1.5 kb. Library prepared by Life
Technologies."

```

Db	987	GCCCCACACACTTTCCCCACAAGTAAGCGGCCCCCTTCCACAGGGTCCCACTACTCTGGGCACCTTCAA	928
Qy	168	cc 169	
		—	
Db	927	TC 926	
RESULT	11		
AI909438/c			
LOCUS			
DEFINITION	AI909438	177 bp	EST
	IL-BT208-080499-007	BT208	Homo sapiens cDNA, mRNA sequence.
			30-MAR-2000

REFERENCE
AUTHORS
Mammalia: Eutheria; (b) (cases 1 to 177)
Primates; Catarrhini; Hominoidea; Homo.
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.
Nagai, M.A., da Silva, W. Jr., Zago, M.A., Bordin, S., Costa, F.F.,
Goldman, G.H., Carvalho, A.F., Matsukuma, A., Baia, G.S., Simpson, D.H.
Brunstein, A., de Oliveira, P.S., Bucher, P., Jongeneel, C.V., O'Hare,
M.J., Soares, F., Brentani, R.R., Reis, L.F., de Souza, S.J., and
Simpson, A.J.
Shotgun sequencing of the human transcriptome with ORF expressed
sequence tags
TITLE


```

BASE COUNT      304 a 178 c 184 g 297 t 2 others
ORIGIN          DH10B"

Query Match      12.4%; Score 34.6; DB 217; Length 965;
Best Local Similarity 50.3%; Pred. No. 39;
Matches 85; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 47 gccttgccctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagc 106
   |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 791 GCTTTGGTCTCTAGGGTGCTATGAAAGAAATATGATCTTTGAGGGGCCACACAGGGGAAC 732
   |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY 107 tggtaacatcacccagaaatcaggcatccctctgcaacggcagcatgggtggagcgta 166
   |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 731 CCGTGGTCAACACCCGGTACCAGTACTCGCCACTCAATGGTGGCATGGTTGTCAACCGGCA 672
   |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

QY 167 acctgaccgcggcatgtactgcgcagctctagaaatctctgatcaatgt 215
   |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |
Db 671 ACAGCACGTGNACGTAGAGGGCTCAGATCCTAAAGTACCTCTCAGGGT 523
   |||||  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |  |

```

Search completed: May 13, 2001, 11:39:51
Job time: 16466 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:16:12 ; Search time 9342.78 Seconds
(without alignments):
2055.246 Million cell updates/sec

Title: US-09-451-527-91
Perfect score: 1302
Sequence: 1 ctacgacctgcctgctcttc.....aaaaaaaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues 2566470
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*

- 1: gb_bal.*
- 2: gb_bal.*
- 3: gb_bal.*
- 4: gb_bal.*
- 5: gb_bal.*
- 6: gb_bal.*
- 7: gb_bal.*
- 8: gb_bal.*
- 9: gb_bal.*
- 10: gb_bal.*
- 11: gb_bal.*
- 12: gb_bal.*
- 13: gb_bal.*
- 14: gb_bal.*
- 15: gb_bal.*
- 16: gb_bal.*
- 17: gb_bal.*
- 18: gb_bal.*
- 19: gb_bal.*
- 20: gb_bal.*
- 21: gb_bal.*
- 22: gb_bal.*
- 23: gb_bal.*
- 24: gb_bal.*
- 25: gb_bal.*
- 26: gb_bal.*
- 27: gb_bal.*
- 28: gb_bal.*
- 29: gb_bal.*
- 30: gb_bal.*
- 31: gb_bal.*
- 32: gb_bal.*
- 33: gb_bal.*
- 34: gb_bal.*
- 35: gb_bal.*
- 36: gb_bal.*
- 37: gb_bal.*
- 38: gb_bal.*
- 39: gb_bal.*
- 40: gb_bal.*
- 41: gb_bal.*
- 42: gb_bal.*
- 43: gb_bal.*

- 44: em_ov.*
- 45: em_pat.*
- 46: em_ph.*
- 47: em_pl.*
- 48: em_ro.*
- 49: em_sts.*
- 50: em_sy.*
- 51: em_un.*
- 52: em_vi.*
- 53: gb_sts1.*
- 54: gb_sts2.*
- 55: gb_sts3.*
- 56: gb_sy.*
- 57: gb_un.*
- 58: gb_vil.*
- 59: gb_vil.*
- 60: gb_vil.*
- 61: gb_vil.*
- 62: gb_vil.*
- 63: gb_vil.*
- 64: gb_vil.*
- 65: gb_vil.*
- 66: gb_vil.*
- 67: gb_vil.*
- 68: gb_vil.*
- 69: gb_vil.*
- 70: gb_vil.*
- 71: gb_vil.*
- 72: gb_vil.*
- 73: gb_vil.*
- 74: gb_vil.*
- 75: gb_vil.*
- 76: gb_vil.*
- 77: gb_vil.*
- 78: gb_vil.*
- 79: gb_vil.*
- 80: gb_vil.*
- 81: gb_vil.*
- 82: gb_vil.*
- 83: gb_vil.*
- 84: gb_vil.*
- 85: gb_vil.*
- 86: gb_vil.*
- 87: gb_vil.*
- 88: gb_vil.*
- 89: gb_vil.*
- 90: gb_vil.*
- 91: gb_vil.*
- 92: gb_vil.*
- 93: gb_vil.*
- 94: gb_vil.*
- 95: gb_vil.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	1302	100.0	1302	7	AF244915
2	890	68.4	21343	78	AF276990
3	408.4	31.4	21343	78	AF276990
4	378	29.0	1270	93	HUMIL13A
5	378	29.0	1282	92	HSNC30
6	378	29.0	1290	10	I34548
7	376.4	28.9	1297	9	A29948
8	376.4	28.9	1297	10	I58488
9	251.6	19.3	417	88	AF043334
10	232.2	17.8	3520	7	BTAL32441
11	219.8	16.9	343	7	AF072807


```
Db 901 GCTTTAGAGTCCCTGGGAATAGCACTGTCTGTAAATTCGTACCTCACTGGGATC 960
Qy 961 ctggggccacacaggggacagagagaagggcagagatgctgcttctgctccactca 1020
Db 961 CTGGGGCCACACAGGGGACAGGAGAGAGGGTCAGAGATGCTGCTTCTGCGCACTCA 1020
Qy 1021 gcagctgacctcagccagcagtgatattattgttttcttctgattttaaagttaaagaa 1080
Db 1021 GCAGCTGGCCCTCAGCCAGCAGTAGTAATTATTGTTTTCCTTGTAATTAAAGTTAAGAA 1080
Qy 1081 taaatatgttatcaaaagagtttaataatataatagagagtagcctaaaggctgctattg 1140
Db 1081 TAAATAATGTTATCAACAGTTAATAATATATAGAGAGTAGCCTAAAGAGCTGCATTG 1140
Qy 1141 gtgctgtgcccagccgcccggcggcggcggcggcggcggcggcggcggcggcggcggc 1200
Db 1141 GTGTGTGTGGCCAGCCGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCGGGCTTT 1200
Qy 1201 cactgaccttgcacactggaagccagacgaataaagatggtgacaagagaaaaa 1260
Db 1201 CACTGACTTTGTCAACTGGGAAGCCAGAAATAAAGATGTTGATGACAGAGAAAAA 1260
Qy 1261 aaaaaa 1302
Db 1261 AAAAAA 1302

RESULT 2
AF276990/c
LOCUS AF276990 213343 bp DNA HTG 29-SEP-2000
DEFINITION Canis familiaris chromosome 4 clone RPCI-81 390C13, *** SEQUENCING
IN PROGRESS ***, 25 ordered pieces.
ACCESSION AF276990
VERSION AF276990.1 GI:9964079
KEYWORDS HTG; HTGS_PHASE2.
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
1 (bases 1 to 213343)
Dubchak, I., Brudno, M., Loots, G.G., Pachter, L., Mayor, C., Rubin, E.M.
and Frazer, K.A.
Active conservation of noncoding sequences revealed by three-way
species comparisons
Genome Res. 10 (9), 1304-1306 (2000)
20442524
10984448
2 (bases 1 to 213343)
Blankespoor, C.M., Dean, W.B. and Lewis, K.D.
Direct Submission
Submitted (10-JUN-2000) Genome Sciences Department, Lawrence
Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, CA 94720,
USA
* NOTE: This is a 'working draft' sequence. It currently
* consists of 25 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submitter.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.
1 16269: contig of 16269 bp in length
* 16270 24613: contig of 8344 bp in length
* 24614 28694: contig of 4081 bp in length
* 28695 31694: contig of 3000 bp in length
* 31695 32391: contig of 697 bp in length
* 32392 36538: contig of 4147 bp in length
```

```
* 36539 gap of unknown length
* 39567: contig of 3029 bp in length
* 39568 gap of unknown length
* 41164: contig of 1597 bp in length
* 41165 gap of unknown length
* 56023: contig of 14859 bp in length
* 56024 gap of unknown length
* 69825: contig of 13802 bp in length
* 69826 gap of unknown length
* 71104: contig of 1279 bp in length
* 72258: contig of 1154 bp in length
* 72259 gap of unknown length
* 73132: contig of 874 bp in length
* 73133 gap of unknown length
* 88901: contig of 15769 bp in length
* 88902 gap of unknown length
* 96587: contig of 7686 bp in length
* 96588 gap of unknown length
* 105542: contig of 8955 bp in length
* 105543 gap of unknown length
* 108418: contig of 2876 bp in length
* 108419 gap of unknown length
* 113668: contig of 5250 bp in length
* 113669 gap of unknown length
* 116446: contig of 2778 bp in length
* 116447 gap of unknown length
* 148106: contig of 31660 bp in length
* 148107~ 155037: contig of 6931 bp in length
* 155038 gap of unknown length
* 170050: contig of 15013 bp in length
* 170051 gap of unknown length
* 196830: contig of 26780 bp in length
* 196831 gap of unknown length
* 202835: contig of 6005 bp in length
* 202836 213343: contig of 10508 bp in length.
FEATURES
Location/Qualifiers
Source
1..213343
/organism="Canis familiaris"
/db_xref="taxon:9615"
/clone="RPCI-81 390C13"
/chromosome="4"
BASE COUNT 60084 a 42812 c 44046 g 66392 t 9 others
ORIGIN
Query Match 68.4%; Score 890; DB 78; Length 213343;
Best Local Similarity 99.0%; Pred. No. 1.1e-180;
Matches 907; Conservative 0; Mismatches 5; Indels 4; Gaps 1;
Qy 339 gcagatttcagtgacgcagccagagacacacaaattgaagtgtaccagttggtgaaaaa 398
Db 112104 GCAGATTTCCAGTCACGCGACGCGAGACACCAAATTTGAAGTGATCCAGTTGGTGA 112045
Qy 399 cctgcctcaccatgtgaaggaggatttatcgccatggaaatttcagatgaacatgaaac 458
Db 112044 CTTGCTCACCATGTATGAAGGGAGTTTATCGCCATGGAATTTTCAGATGAAGCA 111985
Qy 459 ttgacatccttatctgtagaccacagacctgaccacttaagtccagatttccttt 518
Db 111984 TTAGCATCCTTATCTGTAGACCCAGACCTGACCACTTAAGTTCCAGATTCATTTCTTT 111925
Qy 519 ccgacgtcacaaatttcttagggagggtgggggggggggagacacatttcctcagctggga 578
Db 111924 CCGACGTCACAAATTTCTTAGGG---GGGGGGGGGGAAGAACCAATTTCTCTCAGCTGGGA 111869
Qy 579 cctcagcctgcacgcgctgctccatgagctgagccagccacccctgccttggtgcat 638
Db 111868 CCTCAGCCTGCACGGCTGCTCCATGAGCTGAGCCAGCCACCCCTGCTTGTGTGCAT 111809
Qy 639 gggggccagccgggtggccctcctcctgtgcaacttcatcaacgctgagggaagcactg 698
```


JOURNAL Patent: EP 0506574-A 21 30-SEP-1992;
ELF SANOFI

FEATURES Location/Qualifiers
source 1..1297
CDS 15...455 /codon_start=1
/transl_table=11
/product="protein with cytokine like activity"
/organism="synthetic construct"
/db_xref="taxon:32630"
15...455 /codon_start=1
/transl_table=11
/product="protein with cytokine like activity"
/protein_id="CAA01982.1"
/db_xref="GI:1249028"
/translation="MPIPLNPLLALGLMALLTTVIALTCLGGFASPGVPVPSTAIR
FLIEELVNITQNGKAPLNCMSWMSINLTADMYCAALESINVSOGSAIEKTORMLSJ
ECPFKHVAGQSSLIHRDFTKEVAQVFQDLLHLKLFRGREN"

BASE COUNT 309 a 341 c 336 g 311 t

ORIGIN

Query Match 28.9%; Score 376.4; DB 9; Length 1297;
Best Local Similarity 66.1%; Pred. No. 8,7e-71;
Matches 779; Conservative 0; Mismatches 291; Indels 108; Gaps 12;

QY 21 cctgcgtcctcctgcaattggctctgggctccataggcgctctggttgactgtgcatgtgc 80
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db CCTCAATCTCTCGTTGGCACGTGGGCCTCATGGCCCTTTGTTGACACGGTCATTGC 85

QY 81 ttcacctgcctcgttggccttgcctcccagacccctgtgactcctccccaaacctcaa 140
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db TCTCATTGCTTGCGGGCTTGGCTCCCCAGGCCCTGTGCCTCCCTCTACAGCCCTCAG 145

QY 141 ggagctcattgagagagctggccaacatcacccagaatc---aggcatcctctctgcaacgg 197
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GGAGCTATTGAGGAGCTGGTCAACATCACCCAGAACCAGAAAGCTCCGGCTCGCAATGG 205

QY 198 cagcatgggtggaagtcacaactgacccggccatgtactgscagctctagaatctct 257
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db CAGCATGGTAGGAGCATCAACCTTGACAGCTGACATGACTGTGCAGCCCTGGAATCCCT 265

QY 258 gatcaatgtctccgactgcagcgccatccaaaaggaccagagatgctgaaagcactgtg 317
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GATCAAGCTGTGAGCTGCGAGTGCATCGAAGACCCAGAGATGCTGACGGGATTCTG 325

QY 318 ctctcaaaagccgcggcaggcagatttccagtgaacgcagccgagacacccaaaaattga 377
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db CCCGCACAAGTCTCAGCTGGSCAGTTTCCAGCTTCATGTCCTCCGAGACACCAATCGA 385

QY 378 agtgatccagttggtaaaacctgctcaactatgtaaggggagtttatgcccatggaaa 437
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GGTGGCCACAGTTTGTAAGGACCTGCTCTTACATTATAAGAAAATTTTTTCGCGAGGACG 445

QY 438 ttccagatgaagcatgaaacttagccttactctatagacca-gacctgacacatta 496
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db GTTCACTGAACATTCGAA----AGCATCATATTTCGAGACAGCAGGACTGACTATTGA 501

QY 497 agttccagattcattttcttccgaogtcacaaaattcttagggaggtgggggg----- 551
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db AGTTGCAGATTCAATTTTCTTCGTGATGTCAAAATGCTTTGGGTAGCGGGAAGGAGGG 561

QY 552 ----gggggagaacatttctcagctgggaacctcagcctgcacccgcctgcctccatggag 608
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db TTAGGGAGGGGTAAATTCCTTAGCTTAGACCTCAGCCTGTGTCGCCGTCTTCAGCCT- 620

QY 609 ctgagccagccaccctgccttgtgtcatgggcccagccgggtgacctcctccctc- 667
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db ----AGCCGACCTCAGGCTTCCCCTTGCCGAGGCTCAGCCTGTGTGGGCTCTCTCTGCC 676

QY 668 -----tgcacttcatacgcgtgagggaaagcactgcattcccatgactgtccccctccctcag 723
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db AGGCCCTTGACCTCGGTGGACCCAGGATGACATGTCCCTACACCCCTCCCTGCCCTAG 736

QY 724 agcaaatgcagcatcatagctggagg-----cagatatgtgtggaggggg----- 769
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy	258	gatacaatgtctccgactgcagcgccatccaaaggagccagagatgctgaaagcactgtg	317
Db	256	GATCAACGTGTCAAGCTGCAGTGCCTCGAGAAGACCCAGAGGATGCTCAGCGGATTCG	325
Qy	318	ctctcaaaagcccgcgagggcagatgttccaagtgaacgagccagagacacaaaaattga	377
Db	326	CCCGCACAAAGGTCTCAGCTGGCGACTTTCCAGCTTGCATGTCCGAGACACCAAAATCGA	385
Qy	378	agtgatccagttggtgaaaaacctgctcacctatgtcaaggggagtttatcgccatggaaa	437
Db	386	GGTGGCCCACTTTGTAAGAGCACTGCTCTTACATTTTAAAGAAACTTTTTCGGCAGGGACG	445
Qy	438	tttcagatgaagcatgaaaacttagcatccttatctgtagacccca-gacctgaccactta	496
Db	446	GTTCAACTGAAACTTCGAA---AGCATCATTTATTGCAGACAGGACCTGACTATTGA	501
Qy	497	agttccagatcattttcttcttcgcagctgcacaaatttcttagggaggtggggggg	551
Db	502	AGTTTGCAGATTCAATTTTCTTCTCATGTCAAAATATGCTTGGCTAGCGGGAAGGAGG	561
Qy	552	---gggggagaacctttccctcagctgggacctaagctcgaaccgctgcctccatggag	608
Db	562	TTAGGGAGGGGTAAATTTCCTTAGCTTAGACCTCAGCCTGTGCTGCCCGTCTTCAGCCCT-	620
Qy	609	ctgagccagcgcaaccctgccttgggtgcatggggccagccgggtggccctcctccgtc-	667
Db	621	----AGCCGACCTCAGCCCTTCCCCCTGGCCAGGGCTCAGCCTGTGTGGGCTCTCTCTGTCC	676
Qy	668	----tgcacttcatacgcgtgagggaaagcaactgcatacccatgactgtcccctccctcag	723
Db	677	AGGGCCCTGAGCTCGGTGGACCCAGGGATGACATGTCCCTACACCCCTCCCTGCCCTAG	736
Qy	724	agcaaaagtgcagcatcacagtggaag-----cagatatgtgtggaggggg----	769
Db	737	AGCACACTGTAGCATTTACAGTGGTGGTGGCCGCCCTTCCAGACATATGTGTGGGACAGGAC	796
Qy	770	-----tcttgctgtacctgggagtgccagacacatgtttctcttcttagcctta	816
Db	797	CACTTTCACACACAGGCNACTGAGGCAGACAGCAGCTCAGGCACACTCTTCTTGTGCTTA	856
Qy	817	tttattatgtgtgtatttaaacaagtgtctttgtgtgctgggacagggagtg---	873
Db	857	TTTTATTATTGTGTATTAAATCAGTCTGTGTGTACCCGTTGGGATTTGGGAAGACT	916
Qy	874	-----gcttgagctgggggccagtgactggggtttaga-----	908
Db	917	GTGGCTGTGGCACTTGGAGCCCAAGGGTTCAGAGACTCAGGCCCCCAGCACATAAGCACT	976
Qy	909	-----gagtcctctgggaataagcactgtgtgtataaattctgctaactcactgggat	959
Db	977	GGACCCCAAGGAGTCCCTGGTAATAAGTACTGTGTACAGAAATTTCTGTACTCCTGGGT	1036
Qy	960	cctggggcc-----gacacaggggacaggaagaggtcagagatgctcttt	1008
Db	1037	CTTGGGGCTCGGAGCCCTCATCCGAGGCAGGGTTCAGGAGGGGGCAGACACCGCTCCT	1096
Qy	1009	gtctgcactcagcagctggccctcagccaaagcagtaatttattgtttttctctgtattt	1068
Db	1097	GTC TGCCAGCCAGCAGCCAGCTCTCAGCCACAGAGTAATTTATTTGTTTTCTCTCTATTT	1156
Qy	1069	aaagttaagaataaataatgtatcaagaagttaata	1106
Db	1157	AA-----ATATTAAATATGTTAGCAAGAGCTTAATA	1187

RESULT	9
AF043334	
LOCUS	AF043334
DEFINITION	Homo sapiens interleukin 13 precursor (IL13), mRNA, complete cds.
ACCESSION	AF043334
VERSION	AF043334.1 GI:2905619
KEYWORDS	

SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS	1 (bases 1 to 417)
TITLE	Jang,J.S. and Kim,B.E.
JOURNAL	Direct Submission
COMMENT	Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea
FEATURES	Nested PCR: 1) first PCR : forward primer (5'-ctcaatctctctctgttgca-3') reverse primer (5'-tagtcaggtctgtctctgc-3') 2) second PCR : forward primer (5'-ctcatggcggtttgttgaccacg-3') reverse primer (5'-gaagtcttcgaatttcagttgaa-3'). Location/Qualifiers 1. .417 /organism="Homo sapiens" /db_xref="taxon:9606" /cell_type="PHA-treated peripheral blood leukocyte" 1. .417 /gene="IL13" 1. .24 /gene="IL13" /note="second PCR" /PCR_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles; Deltacycler II from Ericomp" 4. .402 /gene="IL13" /codon_start=1 /product="interleukin 13 precursor" /protein_id="AAC03535.1" /db_xref="GI:2905620" /translation="MALLITVIALTCIGFASPGVPPTALRELIEELVNTQNK APLNGSMVWSINLTAGMYCAALESINVSCSAIEKTKQRMLGFCFPHKVSAGQFSFL HVRDTKIEVAQFVKDLLLHKLFREGFNF" 4. .63 /gene="IL13" 64. .399 /gene="IL13" /product="interleukin 13" complement(394..417) /note="second PCR"
sig_peptide	91 a 121 c 108 g 97 t
mat_peptide	
primer_bind	
BASE COUNT	
ORIGIN	

	Query Match	19.3%	Score 251.6;	DB 88;	Length 417;
	Best Local Similarity	77.6%;	Pred. No. 4.5e-44;		
	Matches 318;	Conservative 0;	Mismatches 89;	Indels 3;	Gaps 1;
Qy	51	catggcgctctggttgactgtggctaatgtctctcaacctgctctcgctcggttgacctgctccccc	110		
Db	3	CATGGCGCTTTGTTGACACCGCTCATTTGCTCTCACTTTGCCTTGGCGGCTTTGGCTGCC	62		
Qy	111	gagccctgtgactccctcccaaacccctcaaggactcaattgagagctggtgcaacatcac	170		
Db	63	AGGCCCTGTGCTTCCTCTACGAGCCCTCAGGAGCTCATTTGAGAGCTGGTCAACATCAC	122		
Qy	171	ccagaatc---aggcatccctctgcaacggcagcatggtgtggagcgtccaacctgacgcg	227		
Db	123	CCAGAACACAGAGGCTCGGCTCTGCATGGCAGCATGGTTTGGAGCATCAACCTTGACAGC	182		
Qy	228	cggcatgtactgcgcagctctagaatctctctgatcaatgtctccgactgcagcgccatcca	287		
Db	183	TGGCATGTACTGTGCAGGCCCTGGAATCCTCATCAACGTGTCAAGCTGCAGTGCCATCGA	242		
Qy	288	aaggaccacagaggatgctgaaagcactgltgctctcaaaagcccgacggcgagatttc	347		
Db	243	CAAGACCCAGAGGATGCTGGGCGGATTTCTGCCCGCAACAAGGCTCTCAGCTGGGCAAGTTTC	302		

Qy	348	cagtgaacgcgcgcgcgcaccccaaaattgaagtgatccagtttggtgaaaaaacctgctcac	407
Db	303	CAGCTTGTCATGTCGCAGACACACAAATACGAGGTGGCCAGCTTTGTAAAGGACCTGCTCTT	362
Qy	408	ctatgtaaggaggagttatcccatggaatttcagatgaagcatgaaaa	457
Db	363	ACATTTAAAGAAACTTTTTCGCGAGGACGGTTCACCTGAAACTTCGAAA	412
RESULT	10		
BTA132441			
LOCUS	BTA132441	3520 bp	DNA
DEFINITION	Bos taurus il13 gene, exons 1-4.		10-SEP-1999
ACCESSION	AJ132441		
VERSION	AJ132441.1	GI:5420144	
KEYWORDS	il13 gene; interleukin-13.		
SOURCE	Bos taurus.		
ORGANISM	Bos taurus		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.		
REFERENCE	1. (bases 1 to 3520)		
AUTHORS	Buitkamp,J., Jann,O. and Fries,R.		
TITLE	The cattle interleukin-13 gene: genomic organization, chromosomal location, and evolution of the promoter		
JOURNAL	Immunogenetics 49 (10), 872-878 (1999)		
MEDLINE	99367396		
REFERENCE	2 (bases 1 to 3520)		
AUTHORS	Buitkamp,J.		
TITLE	Direct Submision		
JOURNAL	Submitted (19-JAN-1999); Buitkamp J., Tierzucht, TU-Muenchen, Alte		
FEATURES	Submitted 12, 85350 Freising, GERMANY		
source	Location/Qualifiers		
	1..3520		
	/organism="Bos taurus"		
	/db_xref="taxon:9913"		
	/chromosome="4"		
	/dev_stage="adult"		
	/map="4q23-31"		
	/clone="IS165"		
mRNA	join(588..789,1742..1795,2038..2142,2484..2591)		
gene	/gene="il13"		
	588..2591		
exon	/gene="il13"		
	588..789		
	/gene="il13"		
	/number=1		
sig_peptide	657..717		
	/gene="il13"		
CDS	join(658..789,1742..1795,2038..2142,2484..2591)		
	/gene="il13"		
	/codon_start=1		
	/product="interleukin-13"		
	/protein_id="CA846636.1"		
	/db_xref="GI:5420145"		
	/translation="MALLLTAVILICFGLTSPVPSATALKELIELVNTQNK VPLCGSMWVSLNLTSSMYCAULDSLISNCSVIQRTKKMLNLCPHKPSAKVSSSE VYRDTKIEVAQFLKDLIRHSRIYFNRERN"		
mat_peptide	join(718..789,1742..1795,2038..2142,2484..2589)		
	/gene="il13"		
	/product="interleukin-13"		
Intron	790..1741		
	/gene="il13"		
	/number=1		
exon	1742..1795		
	/gene="il13"		
	/number=2		
Intron	1796..2047		
	/gene="il13"		
	/number=2		
exon	2048..2142		
	/gene="il13"		
	/number=3		

[illegible]

ORGANISM
Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 384)
AUTHORS Caput, D., Ferrara, P., Guillemot, J., Kaghad, M., Labit-Le
Boutellier, C., Lepoint, P., Magazin, M., and Minty, A.
TITLE Protein having interleukin-13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 17 29-JUL-1997;
FEATURES Location/Qualifiers
source 1..384
BASE COUNT 97 a 104 c 99 g 84 t
ORIGIN

Query Match 16.1%; Score 209.4; DB 10; Length 384;
Best Local Similarity 76.3%; Pred. No. 5.1e-35;
Matches 271; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

Qy 106 tccccgagccctgtgactccctcccccacacgagcattgagagcgtgtaaac 165
Db 16 TCCCCAGGCCCTGTGCCCTCTACCGCCCTCAGGAGCTCATGAGGAGCTGGTCAAC 75

Qy 166 atcacccaggaac---aggcatccctctgcaacgagcagcatgggtgagcgtaaacctg 222
Db 76 ATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135

Qy 223 accgcccgcgtactgctgagcgtctgagatctctgataatgctccgactgagcgcc 282
Db 136 ACAGCTGCATGTACTGTGAGCCCTGGAATCCCTGATCAACGCTGTCAGGCTGCGTGC 195

Qy 283 atccaaagaccagagagatgctgaaagactgtgctctcaaaagccgagggcag 342
Db 196 ATCGAAGAACCCAGAGAGGCTGCTGAGCGGATCTGCCCGCACAAAGGCTCAGCTGGG 255

Qy 343 atttcagtgaaacgagccagacacacaaattgaagtatccagtggtgtaaaacctg 402
Db 256 TTTTCCAGCTTGATGTCGAGACACCAAAATCGAGGTGCCCTGAGTTGTAAAGGACCTG 315

Qy 403 ctcaacctatgaaggagggtttatcgccatggaatttcagatgaagcagaa 457
Db 316 CTCTTACATTTAAAGAACTTTTTCGGAGGAGCGGTTCAACTGAAACTTCGAAA 370

RESULT 14
AR027065
LOCUS AR027065 425 bp DNA PAT 29-SEP-1999
DEFINITION Sequence 4 from patent US 5856142.
ACCESSION AR027065
VERSION AR027065.1 GI:5937905
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux, R., Maldonado, P. and Salome, M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5856142-A 4 05-JAN-1999;
FEATURES Location/Qualifiers
source 1..425
BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 15.9%; Score 207.6; DB 9; Length 425;
Best Local Similarity 75.7%; Pred. No. 1.3e-34;
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

Qy 103 gctccccgagccctgtgactccctcccccacacccatgagcattgagagcgtgctc 162
Db 55 GCCTTCGCTGGCCCTGTGCCCTCCAGTACTGCCCTCAGGAGCTCATTTGAGAGCTGGTC 114

Qy 163 aacatcacccaggaac---aggcatccctctgcaacgagcagcatgggtgagcgtcaac 219
Db 115 AACATCACCCAGAACACCAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174

Qy 220 ctgaccgcccgcgtactgctgagcgtctgagatctctgataatgctccgactgagc 279
Db 175 CTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCTGATCAACGCTGTCAGGCTCC 234

Qy 280 gccatccaaagaccagagagatgctgaaagcactgtgctctcaaaagcccgagcag 339
Db 235 GCCATCGAAGAACCCAGAGGATGTGAGCGGATTTCTGCCCGCACAAAGGCTCTCAGCTGG 294

Qy 340 cagatttcagtgaaacgagccgagacacacaaattgaaatgagtgatccagttgtaaaaac 399
Db 295 CAGTTTCCAGCTTGATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGAC 354

Qy 400 ctgctcacctatgaaggagggtttatcgccatggaatttcagatgaagcagaa 457
Db 355 CTGCTCTTACATTTAAAGAACTTTTTCGGAGGAGCGGTTCAACTGAAACTTCGAAA 412

RESULT 15
186198
LOCUS 186198 425 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5700665.
ACCESSION 186198
VERSION 186198.1 GI:3205916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
Unclassified.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux, R., Maldonado, P. and Salome, M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5700665-A 4 23-DEC-1997;
FEATURES Location/Qualifiers
source 1..425
BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 15.9%; Score 207.6; DB 10; Length 425;
Best Local Similarity 75.7%; Pred. No. 1.3e-34;
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;

Qy 103 gctccccgagccctgtgactccctcccccacacccatgagcattgagagcgtgctc 162
Db 55 GCCTTCGCTGGCCCTGTGCCCTCCAGTACTGCCCTCAGGAGCTCATTTGAGAGCTGGTC 114

Qy 163 aacatcacccaggaac---aggcatccctctgcaacgagcagcatgggtgagcgtcaac 219
Db 115 AACATCACCCAGAACACCAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174

Qy 220 ctgaccgcccgcgtactgctgagcgtctgagatctctgataatgctccgactgagc 279
Db 175 CTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCTGATCAACGCTGTCAGGCTCC 234

Qy 280 gccatccaaagaccagagagatgctgaaagcactgtgctctcaaaagcccgagcag 339
Db 235 GCCATCGAAGAACCCAGAGGATGTGAGCGGATTTCTGCCCGCACAAAGGCTCTCAGCTGG 294

Qy 340 cagatttcagtgaaacgagccgagacacacaaattgaaatgagtgatccagttgtaaaaac 399
Db 295 CAGTTTCCAGCTTGATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGAC 354

Qy 400 ctgctcacctatgaaggagggtttatcgccatggaatttcagatgaagcagaa 457
Db 355 CTGCTCTTACATTTAAAGAACTTTTTCGGAGGAGCGGTTCAACTGAAACTTCGAAA 412

Search completed: May 13, 2001, 14:20:29
Job time: 19109 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:28:54 ; Search time 472.02 Seconds
(without alignments)
1610.278 Million cell updates/sec

Title: US-09-451-527-91

Perfect score: 1302

Sequence: 1 ctacgcctgcctctcttc.....aaaaaaaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*

1: /cgnl_8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query Match	Score	Length	ID	Description
1	1302	100.0	1302	21	255555 Canine interleukin
2	1302	100.0	1302	21	255556 Canine interleukin
3	1251	96.1	1269	21	255561 Canine interleukin
4	1251	96.1	1269	21	255562 Canine interleukin
5	393	30.2	393	21	255557 Canine interleukin
6	393	30.2	393	21	255558 Canine interleukin
7	378	29.0	1270	21	255558 Human low adenoin
8	378	29.0	1270	21	255558 Human low adenoin
9	378	29.0	1282	21	255558 Human low adenoin
10	378	29.0	1282	21	255558 Human low adenoin
11	378	29.0	1290	15	Q56692 Sequence encoding

12	378	29.0	6952	21	F21333	Human low adenoin
13	378	29.0	6952	21	A35211	Human adenosine re
14	378	29.0	14978	21	F21338	Human low adenoin
15	378	29.0	14978	21	A35216	Human adenosine re
16	377	29.0	390	21	255563	Canine interleukin
17	377	29.0	390	21	255564	Canine interleukin
18	374.8	28.8	1297	13	Q28947	Cytokine NC30. Q
19	333	25.6	333	21	255559	Canine mature inte
20	333	25.6	333	21	255560	Canine mature inte
21	317	24.3	330	21	255565	Canine mature inte
22	317	24.3	330	21	255566	Canine mature inte
23	278	21.4	278	21	255554	Canine interleukin
24	272	20.9	272	21	255553	Canine interleukin
25	207	15.9	1212	15	Q56693	Sequence encoding
26	203.4	15.6	336	13	Q28944	Gly41-Cytokine cod
27	201.8	15.5	336	13	Q28943	Asp41-Cytokine cod
28	169	13.0	5670	21	F21331	Human low adenoin
29	169	13.0	5670	21	F21337	Human low adenoin
30	169	13.0	5670	21	A35209	Human adenosine re
31	169	13.0	5670	21	A35215	Human adenosine re
32	150	11.5	166	21	255552	Canine interleukin
33	72.2	5.5	612	21	C98862	Human secreted pro
34	71.2	5.5	202	21	C98563	Human colon cancer
35	70.2	5.4	2323	19	V59524	Human secreted pro
36	70	5.4	4064	21	A07587	Mouse piwi gene, d
37	69.6	5.3	2604	21	A48576	CDNA encoding whea
38	69.4	5.3	1377	21	C98083	Human colon cancer
39	69.4	5.3	3712	21	F21873	Human breast and o
40	69.2	5.3	1984	20	X52252	Protein PRO271 cDN
41	68.8	5.3	1835	20	X27245	Human CIAR1 coding
42	68.4	5.3	1740	21	Z36914	DNA encoding an ac
43	68.4	5.3	1801	21	Z36893	CDNA encoding an a
44	68.2	5.2	2517	21	C90463	Human uncoupling p
45	68.2	5.2	2549	10	N91467	Sequence of human

ALIGNMENTS

RESULT	1
255555	255555 standard; cDNA; 1302 BP.
ID	255555 standard; cDNA; 1302 BP.
XX	XX
AC	255555;
XX	XX
DT	14-MAR-2000 (first entry)
XX	XX
DE	Canine interleukin-13 (IL-13) clone 80 cDNA.
XX	XX
KW	Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW	Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX	XX
OS	Canis familiaris.
XX	XX
FH	Key Location/Qualifiers
FT	CDS 52..447
FT	/*tag= a
FT	/product= "Canine IL-13 clone 80"
XX	XX
PN	WO9961618-A2.
XX	XX
PD	02-DEC-1999.
XX	XX
PF	28-MAY-1999; 99WO-US11942.
XX	XX
PR	29-MAY-1998; 98US-0087306.
XX	XX
PA	(HESK-) HESKA CORP.
XX	XX
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX	XX
DR	WPI; 2000-072623/06.
DR	P-PSDB; Y58221.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 229-230; 264pp; English.
XX Sequences 25552-25556 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, and their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
XX Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;
SQ

Query Match 100.0%; Score 1302; DB 21; Length 1302;
Best Local Similarity 100.0%; Pred. No. 1.4e-264;
Matches 1302; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ctacgacctgctcttccctgctcctctctgctcattgctctggtcctcatgctcgcgc 60
DB 1 ctacgacctgctcttccctgctcctctctgctcattgctctggtcctcatgctcgcgc 60

QY 61 tggttgaactgtgctcattgctcctcctgctcctgctcctgctcctcctcctgctcctg 120
DB 61 tggttgaactgtgctcattgctcctcctgctcctgctcctgctcctcctcctgctcctg 120

QY 121 actcctcccccacccctcaaggagctcattgagagctggtcctcctcctcctcctcctcctc 180
DB 121 actcctcccccacccctcaaggagctcattgagagctggtcctcctcctcctcctcctcctc 180

QY 181 gcatcctctgcacgcgagcagctggtgagcgtcactgacccgcgcgctgactgctgc 240
DB 181 gcatcctctgcacgcgagcagctggtgagcgtcactgacccgcgcgctgactgctgc 240

QY 241 gcagctcgaatctctgatacattgctcctgactgcgagcgtcccaaaagaccagagg 300
DB 241 gcagctcgaatctctgatacattgctcctgactgcgagcgtcccaaaagaccagagg 300

QY 301 atgctgaagcactgctcctcaaaagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360
DB 301 atgctgaagcactgctcctcaaaagccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 360

QY 361 cgagacacacaaattgaagtgcattggtgaaacacctgctcactcattgtaaggagg 420
DB 361 cgagacacacaaattgaagtgcattggtgaaacacctgctcactcattgtaaggagg 420

QY 421 gttatcgccatggaatttcagatgaagcatgaaactagcatccttattctgtagacc 480
DB 421 gttatcgccatggaatttcagatgaagcatgaaactagcatccttattctgtagacc 480

QY 481 cagacctgaccacttaagtccagattcattttcttctccgacgtcacaaattcttagg 540
DB 481 cagacctgaccacttaagtccagattcattttcttctccgacgtcacaaattcttagg 540

QY 541 gaggtgggggggggagaaaccttctcctcagctggagcctcagctgcaccgcctgct 600
DB 541 gaggtgggggggggagaaaccttctcctcagctggagcctcagctgcaccgcctgct 600

QY 601 coattgagctgagccagccacccctgcttctggtcatggtggcccgagccgggtgcccctc 660
DB 601 coattgagctgagccagccacccctgcttctggtcatggtggcccgagccgggtgcccctc 660

QY 661 ctccgtctgacttcatcaacgctgagggaagcactgcattcccatgactgtccctcct 720
DB 661 ctccgtctgacttcatcaacgctgagggaagcactgcattcccatgactgtccctcct 720

QY 721 cagagcaaaagtgcagcattacagtgaggagcagatatgttgagggggtctgtgtgtac 780
DB 721 cagagcaaaagtgcagcattacagtgaggagcagatatgttgagggggtctgtgtgtac 780

QY 781 ctgggagtgggcagacagatgttctctctagcctattattattgtgtgtatttaaac 840
DB 781 ctgggagtgggcagacagatgttctctctagcctattattattgtgtgtatttaaac 840

QY 841 aagtgtcttctgttctgctgggacagagtggtctgagctggggggccagtgactcg 900
DB 841 aagtgtcttctgttctgctgggacagagtggtctgagctggggggccagtgactcg 900

QY 901 ggttagagagtcctctgggaataagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960
DB 901 ggttagagagtcctctgggaataagcactgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 960

QY 961 ctggggccgacacaggggacagagaaaggggtcagagatgctgctctgtctgccaactca 1020
DB 961 ctggggccgacacaggggacagagaaaggggtcagagatgctgctctgtctgccaactca 1020

QY 1021 gcagctggccctcagccagcagtaattattgttttctctgtattttaaagttaagaaa 1080
DB 1021 gcagctggccctcagccagcagtaattattgttttctctgtattttaaagttaagaaa 1080

QY 1081 taaaatgtttatcaaaaggttaataataatagagtagcctaaaggctgactttg 1140
DB 1081 taaaatgtttatcaaaaggttaataataatagagtagcctaaaggctgactttg 1140

QY 1141 gtgtgtgtgcccagccggggcggtgtgggggggggggtgtgtgtgtgtgtgtgtgtgtgt 1200
DB 1141 gtgtgtgtgcccagccggggcggtgtgggggggggggtgtgtgtgtgtgtgtgtgtgtgt 1200

QY 1201 cactgacttgcacactgggaagccagaaataaagatggtgacagagaaaaaataaaaa 1260
DB 1201 cactgacttgcacactgggaagccagaaataaagatggtgacagagaaaaaataaaaa 1260

QY 1261 aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 1302
DB 1261 aaaaaaataaaaaaataaaaaaataaaaaaataaaaaaataaaaaa 1302

RESULT 2
255556/c
ID 255556 standard; cDNA; 1302 BP.
XX
XX Z55556;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80 cDNA complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
OS Canis familiaris.
FH Key Location/Qualifiers
FT CDS complement (856..1251)
FT /*tag= a
FT /product= "Canine IL-13 clone 80"
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.

Db	1204	TGGTTGACTGTGGTCAATTGCTCTCACTCGCTCGGTGGCTTGGCTTCCCTCCCGAGCCCTGTG	1144
Qy	121	actccctcccaaccctcaagagctcattgaggagctagtcaacatcacccagaatcag	180
Db	1144	ACTCCTCCCCAACCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACCCAGAATCAG	1085
Qy	181	gcatacctctgcaacggcagcatggtgtgagcgtcaacctgaccgcgcgcatgtactgc	240
Db	1084	GCATCCCTCTGCAACGGCAGCATGGTGTGAGCGTCAACCTGACCGCGGCATGTACTGC	1025
Qy	241	gcagctctagaatctctctgatcaatgtctccgactgcagcgccatccaaaggacccagagg	300
Db	1024	GCAGCTCTAGAACTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGAGACCCAGAGG	965
Qy	301	atgctgaagcactgtgctctcaaaagcccgcgagcgcaaatctccagtgaacacgc	360
Db	964	ATGCTGAAGACACTGTGCTCTCAAAAGCCCGCGCAGG--GATTTCCTAGTGAACGCAGC	908
Qy	361	cgagacacccaaattgaagtgcacgttggtgaaacacctgctcacctatgtlaagggga	420
Db	907	CGAGACACCAAAATTGAAGTGATCCAGTTGGTGAAACCTGCTCACTATGTAAAGGGA	848
Qy	421	gtttatcgccatggaatttcagatgaagcatgaaaacttagcatccttatctgtagacc	480
Db	847	GTTTATCGCCATGGAAATTTCAAGATCAAGCATGAACCTTAGCATCTTATCTGTAGACC	788
Qy	481	cagacctgaccacttaagttccagattcattttcttctccgacgtcacaaaattcttagg	540
Db	787	CAGACCTGACCACATTAAGTTCAGATTCATTTTCTTCGAGCTCACAAAATTCCTTAGG	728
Qy	541	gaggtgggggggggagaaacctatctccagctggagacctcagcctgcaccgcctgcct	600
Db	727	GAGGTGGGGGGGGGAGAACCATTTCTCAGCTGGGACCTCAGCCTGCACCGCTGCCT	668
Qy	601	ccatggagctgagcccgagccacctgccttggtgcatgggcccagcggggtggccctc	660
Db	667	CCATGGAGCTGAGCCACAGCACCCCTGCTGGTGATGGGGCCACCGCGGTGGCCCTC	608
Qy	661	ctcgtctgcacttcatacagctgagggaaagcactgcatacccatgactgtcccctcct	720
Db	607	CTCGCTCTGCACCTTCATCAACGCTGAGGGAAGACATGTCATCCCATGACTGTCCCCCTCT	548
Qy	721	cagagcaagtgcagcatctacagtgaggcagatatgtgtggagggggtctctgctgtac	780
Db	547	CAGAGCAAGTGCACATTACAGTGGAGGCAGATATGTGTGGAGGGGGTCTTGTCTGTAC	488
Qy	781	ctggagtgccacagacatgtttcttcttagccttatttattgtgtgttatttaaac	840
Db	487	CTGGAGTGGCACACACATGTTTCTTCTTAGCCTTATTTATTTATTTGTTATTTAAAC	428
Qy	841	aagtgtcttttgttgtgtgggacagggagtggcttgagctggggggccagtgactcg	900
Db	427	AAGTGTCTTTTGTGTGTGGGACAGGGAGTGGCTTGGAGGTGGGGGCCACGTACTCG	368
Qy	901	ggtttagagagtcctctgggaaataagcactgtgtaaaaattctgtacctcactgagatc	960
Db	367	GTTTATGAGATCCCTGGGAATAAGCACHTGTGTGTAAAATTTGTCTACCTTCACTGGGATC	308
Qy	961	ctggggccgacacagggacaggaagaagggtcagagatgtgctctgtctgctgccactca	1020
Db	307	CTGGGGCCGCACACAGGGACAGGAAAGGGTCAGAGATGCTGCTTGTCTGCCACTCA	248
Qy	1021	gcagctggccctcagccaagcagtaatttatgttttctcttgtatttaaagtaagaaa	1080
Db	247	GCAGCTGGCCCTACGCCAAGCAGTAAATTTATTTGTTTTCCTTGTATTTAAAGTTAAGAA	188
Qy	1081	taaatatgttatcaaaagttcaataatatagaaagtagcctaaagagctgcatttg	1140
Db	187	TAAATATGTTATCAAGAGTTAAATATATATAGAAAGTAGCCTAAAAGGCTGCAATTG	128
Qy	1141	gtgtgtgtggccagccggggcggtgtgggggggaggggtgtgtcactgtaatgtgctcttt	1200
Db	127	GTGTGTGTGGCAGGCCGGGGCGGTGGGGGGAGGGTGTGTCTACTGAATGTGTCCTTT	68

QY 1201 cactgactttgtcaaaactggagccagaaataaaagatggtgacaagagaaaaa 1260
 |||||||
 Db 67 CACTGACTTTGTCAAACTGGAGGACGAGAAATTAAGATGCTGACAGAGAAAAA 8
 |||||||
 QY 1261 aaaaaa 1267
 |||||||
 Db 7 AAAAAA 1

RESULT 5
 Z55557
 ID Z55557 standard; cDNA; 393 BP.
 XX
 AC Z55557;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 DR WPI; 2000-072623/06.
 DR P-PSDB; Y58221.
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim 11; Page 232-233; 264pp; English.
 XX
 CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX
 SQ Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Query Match 30.2%; Score 393; DB 21; Length 393;
 Best Local Similarity 100.0%; Pred. No. 8.2e-74;
 Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 52 atggcgctctggtgactgtggtcattgctctcactgctcgtggtgcttgcctccc 111
 |||||||
 Db 1 atggcgctctggtgactgtggtcattgctctcactgctcgtggtgcttgcctccc 60
 |||||||
 QY 112 agccctgtgactccctcccccacccctcaagagagctcattgagagctggtcaacatcac 171
 |||||||
 Db 61 agccctgtgactccctcccccacccctcaagagagctcattgagagctggtcaacatcac 120
 |||||||
 QY 172 cagaatcaggcatccctctgcaacgagcagcatggtgtgagcgtcaacctgaccgcggc 231
 |||||||
 Db 121 cagaatcaggcatccctctgcaacgagcagcatggtgtgagcgtcaacctgaccgcggc 180
 |||||||
 QY 232 atgtactgcgcagctctagaaatctctgatcaatgtctcagactgcagcgcattccaaagg 291
 |||||||
 Db 181 atgtactgcgcagctctagaaatctctgatcaatgtctcagactgcagcgcattccaaagg 240
 |||||||
 QY 292 acccagagagatgctgaaagcactgtctctcaaaagccgcgagggcagattccagt 351
 |||||||
 Db 241 acccagagagatgctgaaagcactgtctctcaaaagccgcgagggcagattccagt 300
 |||||||
 QY 352 gaacgcagcgcagacacccaaattgaagtgtaccagttggtgaaaaacctgtcacctat 411
 |||||||
 Db 301 gaacgcagcgcagacacccaaattgaagtgtaccagttggtgaaaaacctgtcacctat 360
 |||||||
 QY 412 gtaaggggagtttatgcgcattggaatttcaga 444
 |||||||
 Db 361 gtaaggggagtttatgcgcattggaatttcaga 393
 |||||||

RESULT 6
 Z55558/C
 ID Z55558 standard; cDNA; 393 BP.
 XX
 AC Z55558;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 DR WPI; 2000-072623/06.
 DR P-PSDB; Y58221.
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim 11; Page 233; 264pp; English.
 XX
 CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as

QY 141 ggagctcattgagagctggtcaacatcacccagagaac---aggcaccctctctgcaacgg 197
Db 134 ggagctcattgagagctggtcaacatcacccagagaac---aggcaccctctctgcaacgg 193
QY 198 cagcatggtgtgagagctgcaacatcacccagagaac---aggcaccctctctgcaacgg 257
Db 194 cagcatggtgtgagagctgcaacatcacccagagaac---aggcaccctctctgcaacgg 253
QY 258 gatcaatgtctccgactgagcgcacatcaaaaggagccagagatgctgaaagcactgtg 317
Db 254 gatcaatgtctccgactgagcgcacatcaaaaggagccagagatgctgaaagcactgtg 313
QY 318 ctctcaaaagcccgagcagagcagatctccagtgaaacagccagagacacaaatgga 377
Db 314 ccgcacagagctcagctggcagctttccagctggtgcattccgagagacacaaatgga 373
QY 378 agtgcacagctgtgaaacacccctcactcattatagagggaggtttatcgccatgaaa 437
Db 374 ggtgcccagctgtgaaacacccctcactcattatagagggaggtttatcgccatgaaa 433
QY 438 ttccagatgagcagtgaaacacccctcactcattatagagggaggtttatcgccatgaaa 496
Db 434 gttcaactgaaactcga---agcattcattttgagagagcagcagcactgactattga 489
QY 497 agttccagatcattttcttccagctgcacacaaatctttagggaggtggggggg---- 551
Db 490 agttgcagatcattttcttccagctgcacacaaatctttagggaggtggggggg---- 549
QY 552 ---ggggagaaacatttccctcagctggagcctcagcctgcacccgctcctccatggag 608
Db 550 ttagggggggtaaaatctcctgtagagcctcagcctgctgctgcccctcctcagcct- 608
QY 609 ctgagccagcagccctcctgtgtgcatggggccagccgggtggccctcctcctcctc- 667
Db 609 ---agccagcctcagccttcccttcccaggggtcagcctggtgggctcctcctcctc- 664
QY 668 ---tgcacttcaacagctgagggagagcactgacatcccatgactgctccctcctcag 723
Db 665 agggccctgagctggtggagccagggatgacatgctccctacacccctcctcctcctag 724
QY 724 agcaaatgagcagcattcagtgagag-----cagatatgtgtggagggggg---- 769
Db 725 agcactgtgacattacagtggtggcccccctgcccagacatgtgtgggagcagggacc 784
QY 770 -----tctgtgctacacagctgagggagagcactgacatcccatgactgctccctcctcag 816
Db 785 cacttcaacacagcagcactgagggagagcagcagcagcagcagcacttcttctgcttca 844
QY 817 ttattattgtgtgtatttaaaacagtgcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 873
Db 845 ttattattgtgtgtatttaaaacagtgcttctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 904
QY 874 -----gcttgagctggtggggccagctgactgagctggtttttaga----- 908
Db 905 gtgctgctggtgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 964
QY 909 -----gagtcctcctggaataagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 959
Db 965 ggaacccagagcctcctggttaaaagcagctgtgtgtgtgtgtgtgtgtgtgtgtgtgt 1024
QY 960 cctgggggccc-----gacacaggggagcagagagagagagagagagagagagagagag 1008
Db 1025 cctgggggccc-----gacacaggggagcagagagagagagagagagagagagagagag 1084
QY 1009 gctgcacactcagcagctggtccctcagcagcagcagcagcagcagcagcagcagcagc 1068
Db 1085 gctgcacactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 1144
QY 1069 aaagttaagaataaaatatttatcaagaagatttaata 1106
Db 1145 aa-----attataaatgttagcaagaagatttaata 1175

RESULT 9
F21332 ID F21332 standard; DNA; 1282 BP.
XX
F21332; AC
XX
DT 14-MAR-2001 (first entry)
XX
Human low adenosine antisense oligonucleotide related sequence #2899.
DE Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
KW human; airway disorder; bronchoconstriction; lung inflammation;
KW surfactant depletion; respiratory; bronchodilator; antiinflammatory;
KW immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
KW respiratory obstruction; pulmonary obstruction; impeded respiration;
KW surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
KW respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
KW pulmonary hypertension; emphysema; pulmonary transplantation rejection;
KW chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
KW cancer; ss.
XX
OS Homo sapiens.
XX
PN WO200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
XX 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
XX
XX (NYCE/) NYCE J W.
PI Nyce JW;
XX
XX WPI; 2000-679539/66.
XX
XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for treating
PT cancers and respiratory obstructions -
XX
PS Disclosure: Page 1333-1334; 1592pp; English.
XX
CC The present invention describes low adenosine (A) content antisense
CC oligonucleotides and compositions (I) comprising them. In the antisense
CC oligonucleotides the A is replaced by a 'Universal' or alternative base.
CC (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
CC The antisense oligonucleotides and (I) can be used to down-regulate the
CC expression and or activity of target polypeptides associated with
CC lung/respiratory disorders and malignancies, such as stimulating and
CC activating peptide factors and transmitters, transcription factors,
CC immunoglobulins and antibodies, antibody receptors, cytokines and
CC chemokines, endogenously produced specific and non-specific enzymes,
CC binding proteins, adhesion molecules and their receptors, cytokine and
CC chemokine receptors, adenosine receptors, bradykinin receptors, central
CC nervous system (CNS) and peripheral nervous and non-nervous system
CC receptors, CNS and peripheral nervous and non-nervous system peptide
CC transmitters, defensins, growth factors, vasoactive peptides and
CC receptors, binding proteins and malignancy associated proteins. The
CC antisense oligonucleotides may be used in this way to treat disorders
CC including respiratory obstruction (especially pulmonary obstruction
CC and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
CC and/or surfactant hypoproduction which are associated with a disease or
CC condition selected from pulmonary vasoconstriction, inflammation,
CC allergies, asthma, impeded respiration, respiratory distress syndrome
CC (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
CC hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
CC pulmonary transplantation rejection, pulmonary infections, bronchitis,
CC and/or cancer. F18434 to F21543 represent human polynucleotide fragments
CC and antisense oligonucleotides used in the exemplification of the

```

CC present invention.
XX
SQ - Sequence 1282 BP: 293 A; 341 C; 337 G; 311 T; 0 other;

Query Match      29.0%; Score 378; DB 21; Length 1282;
Best Local Similarity 66.2%; Pred. No. 1.6e-70;
Matches 780; Conservative 0; Mismatches 250; Indels 108; Gaps 12;

QY 21 cctgcgtcctcgtgcatggctggtgggtccatggcgtctggttgactgtggtcattgc 80
   ||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 26 cctcaatcctcctctgtggcactgggctcatggcgtctttgttgaccacggtcattgc 85

QY 81 tctcacctgcctgggtggccttgctctcccagacccgtgactgactcctcccacccctcaa 140
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 86 tctcaattgcttggcgcttggctctcccagccctgctcctcctctacagcctcag 145

QY 141 ggaagtcaattgagagctgggtcaacatcacccagaatc---aggcatcctcttgcacgg 197
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 146 ggaagtcaattgagagctgggtcaacatcacccagaacccagaggctcgtctgcaatgg 205

QY 198 cagcatgggttggagcgtcaacctgacccggcgatgtactgctgcagctctagaatctct 257
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 206 cagcatgggttggagcgtcaacctgacagctggcatgtactgtgcagccctggaaacctc 265

QY 258 gatcaatgtctcgcactgcagcggccatccaaaggacccagaggtatgctgaagcaactgtg 317
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 266 gatcaacgtgtcagcgtgcagtcgcctcagagaacccagaggtatgctgacggattctg 325

QY 318 ctctcaaaagcccgcgagcgaggtcttcagtgaaacgcgcgcgagacacccaaaattga 377
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 326 ccgcacaaggtctcagctggcgaggttttcagagttgcattcgcagacacccaaaatcga 385

QY 378 agtgatccagttgttgaaaaacctgctcacctatgtaaagggagtttatgccatggaaa 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 ggtggccagttgtaaaggagcctgctcttaccatttaagaacatcttttcgcgaggagc 445

QY 438 ttccagatgaagcatgaaacctagcatccttattctgtagacca-gacctgaccactta 496
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 446 gtcaactgaaactcga---agcatcatatttcgagacagcaggacctgactattga 501

QY 497 agttccagattcatcttcttcgcagtcgcaaatctcttagggaggtggggg----- 551
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 502 agttgcagattcatcttcttcgatgtcaaaaatgtcttggtaggcgggaaggaggg 561

QY 552 ---gggggaacacatttctcagctgggaacctcagcgtgcacgcctgcctccatggag 608
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 562 ttagggggggtgaaattctcttagcttagacactcagcctgtgtgcccgttctctgtccc 620

QY 609 ctgagccagccacccctgccttggctgagtgggcccgagcgggtggccctccctccgtcc- 667
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 621 ---agcgcactcagccttccccttggccagggctcagcctgtggtggccttctctgtccc 676

QY 668 ---tgcactttcaacgctgagggaagcactgcatcccatgactgtcccctcctcag 723
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 677 agggccctgagctcgttggacccagggtgacatgtccctacacccctcccctgacctag 736

QY 724 agcaaatgcagcattacagtggagg-----cagatatgtgtggaggggg----- 769
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 737 agcaactgtagcattacagtgggtgcccccttgcagacatgtgtgtggacagggacc 796

QY 770 -----cttgcgttacctggggagtgacagacatgtttctcttagcctta 816
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 797 caactcaacacagggcaacttgaggacagacagctcaggcacacttctcttggctcta 856

QY 817 ttattattgtgtattttaaacaggtcttcttgtttgtgtgtgggacagaggagtg--- 873
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 857 ttattattgtgtattttaaaagtagtgtgttctgtcaccgttgggagtggaagact 916

QY 874 -----gcttggagctgggggcccagtgactcgggtttaga----- 908
   |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| |||| ||||
Db 917 gttgctgtggcacttggagccagggttccagagcactcagggcccccagcactaaagcgt 976

```


CC was radioactively labelled and hybridised with filter lifts prep
CC from a cDNA library made from a clone of an A10 T cell line. One
CC clone, designated PA 10.66, was subcloned into M13 and sequenced.
CC This sequence encodes human IL-13.

Sequence 1290 BP; 308 A; 335 C; 336 G; 311 T; 0 other;

Query Match 29.0%; Score 378; DB 15; Length 1290;
Best Local Similarity 66.2%; Pred. NO. 1.6e-70;
Matches 780; Conservative 0; Mismatches 290; Indels 108

12;

[illegible]

905	gtggctgtcgtgcaacttggagcccaaggttcagagactcagggccccagcactaaagcagt	964
909	-----gagtcctctgggaataagcactgtgtgtaaaattctgtacctcactcgggat	959
965	ggaccccgagggtccctcgttaataagctcgtgtcacgaattctgtacctcactcgggt	1024
960	ctctggggccc-----gacacaggggacagagaaaggggtcagagatgctctctt	1008
1025	ctctggggcctcggagcctcatccggagccaggttcaggagagggggcagaaacgcgtcct	1084
1009	gtctgcactcagcagctggccctcagccaaagcagtaattattgttttctctgtatatt	1068
1085	gtctgcagccagcagccagcgtctcagccaaagcagtaattattgttttctctgtatt	1144
1069	aaagttaagaataaaataatgtttatcaagagatttaata	1106
1145	aa-----atatataatgtttagcaaaagatttaata	1175

RESULT 12

RECEIVED 12
F21333
ID F21333 standard: DNA: 6952 BP.

AA F21333;
AC

DT 14-MAR-2001 (first entry)

Human low adenosine antisense oligonucleotide related sequence #2900.

Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

OS Homo sapiens.

PN WO200062736-A2.

XX
PD 26-OCT-2000.

24-MAR-2000: 2000WO-US08020.

06-APR-1999; 99US-0127958.

XX PA (UYEC-) UNIV EAST CAROLINA.

XX
PA (NICE/)XX
XX
NYce JW;

XX Low adenosine (A) content antisense oligonucleotides which do not
PT trigger adenosine receptors during metabolism, useful e.g. for tr
PT cancers and respiratory obstructions -
PT

XX
PS Disclosure: Page 1334-1335: 159200: English

The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base, (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, immunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the expression and/or activity of target polypeptides associated with lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors.

KW phosphothioate; impaired respiration; inflammation; allergy;
 KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
 KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
 KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
 KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
 KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
 KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
 XX
 OS Homo sapiens.
 XX
 PN WO200009525-A2.
 XX
 PD 24-FEB-2000.
 XX
 PF 03-AUG-1999; 99WO-US17712.
 XX
 PR 03-AUG-1998; 98US-0095212.
 XX
 PA (UYEC-) UNIV EAST CAROLINA.
 XX
 PI Nyce JW;
 XX
 DR WPI; 2000-205971/18.
 XX
 PT New antisense oligonucleotides useful for treating e.g. pulmonary
 PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
 PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
 PT cancers -
 XX
 PS Disclosure; Page 1255-1259; 1343pp; English.
 XX
 CC The present invention describes a new composition comprising an antisense
 CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
 CC nucleic acids involved in bronchoconstriction, allergies, and/or
 CC inflammation. The ON can have antiinflammatory, antiallergic,
 CC antiasthmatic, cytostatic and analgesic activities. The compositions are
 CC useful for the treatment of diseases associated with inflammation,
 CC impaired airways, including lung disease and diseases whose secondary
 CC effects afflict the lungs of a subject. They can be used for treating
 CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
 CC impaired respiration, respiratory distress syndrome, pain, cystic
 CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
 CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
 CC carcinomas, and cancers which may metastasize to the lungs, including
 CC breast and prostate cancer. The reduction of the adenosine content of
 CC ONs reduces side effects. The A-containing ONs break down with the
 CC release of deoxyadenosine which activates adenosine receptors causing
 CC bronchoconstriction and inflammation. A3213 to A3512 represent the
 CC nucleotide sequences given in the sequence listing from the present
 CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
 CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
 CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
 CC to A33992) are specifically claimed ONs from the present invention.
 CC N.B. Sequences given in the disclosure of the present invention do not
 CC match up with their corresponding SEQ ID NO: sequences given in the
 CC sequence listing.
 XX
 SQ Sequence 14978 BP; 3793 A; 3676 C; 3696 G; 3813 T; 0 other;

Query Match 29.0%; Score 378; DB 21; Length 14978;
 Best Local Similarity 66.2%; Pred. No. 3.3e-70;
 Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

Qy 21 cctcgctcctcgtcattgctctggctccatggcgcctctggttgactgtgctatgc 80
 Db 14 cctcaatcctcctctgttggcactgggcccctcattggcctttgtgaccacggctatgc 73
 Qy 81 tctcactgcctcgttggtgcttgcctcccgagccctgtgactcctcccaaccctcaa 140
 Db 74 tctcactgcctcgttggtgcttgcctcccgagccctgtgactcctccctacagccctcag 133
 Qy 141 ggaagctattgagagctggtcaacatcaccacagaate---aggcatcctctgcaacgg 197

Db 134 ggaagctattgagagctggtcaacatcaccacagaacaggctccgctctgcaatgg 193
 Qy 198 cagcatggtgtgagcgtcacaacctgaccgcgcgcgtactgctgcagctctagaatctct 257
 Db 194 cagcatggtgtgagcgtcacaacctgaccgcgcgcgtactgctgcagccttgaatccct 253
 Qy 258 gatcaatgctcgcagctgcagcgcctcacaaggaccacagagatgctgaaagcactgtg 317
 Db 254 gatcaatgctcgcagctgcagcgcctcacaaggaccacagagatgctgagcggattctg 313
 Qy 318 ctctcaaaagcccgcgagggcagatctccagtgaaagcagcagcagacacaaatga 377
 Db 314 ccgcacaaaggtctcagctgggagctttccagcttgcatgtccgagacacaaatga 373
 Qy 378 agtgatccagttggtgaaacacctgctcaccatgtaaagggaggtttatcgccatggaaa 437
 Db 374 ggtggcccgagttgtaaaggacctgctctacatttaagaaaccttttcgcgagggacg 433
 Qy 438 ttccagatgaagcagtgaacaccttagcactctctatctgtagacca--gacctgaccactta 496
 Db 434 gttcaactgaacttcgaa---agcatcatatttgcagagacagagacctgactattga 489
 Qy 497 agttccagattcaattttcttccagctcacacagtcacaaatttcttagggaggtggggg 551
 Db 490 agttcagattcaattttcttctctctgatgcaaaaatgtctctgggtaggcggaaagggg 549
 Qy 552 ---gggggagaaccatttctcagctgggacctcagctgcacgcctgcctccctcctcag 608
 Db 550 ttaggggaggggtaaattccttagcttagacctgagcctgctgctccgctcttcagcct- 608
 Qy 609 ctgagccagcagcccccctgcttggatggggcccgagggcccggtggccctcctcctc- 667
 Db 609 ---agcgacctcagctctcccttgcacagggctcagcctggtgggctcctctgtcc 664
 Qy 668 ---tgacctcacaacgctgaggaagaaacactgcatccatcactgactgctccctcctcag 723
 Db 665 agggccctgagctcgtggaccagggatgacatgtccctacacccctccctcctgacctag 724
 Qy 724 agcaagtgcagcattacagtgagg--------cagatatgtgtggaggggg--- 769
 Db 725 agcacactgtagcattacagtgagggtgcccctctgccagacatgtggtggacagggacc 784
 Qy 770 ---tctgtgtacctggagtgagtgccagacacatgtttcttcttagcctta 816
 Db 785 cacttcacacagcagcagcagggcagacagcagcagcagcagcactctcttctgctta 844
 Qy 817 ttattattgtgtatttaaacagtgctttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 873
 Db 845 ttattattgtgtatttaaacagtgctttgtgtgtgtgtgtgtgtgtgtgtgtgtgtgtgt 904
 Qy 874 ---gcttgagctggggcccgctgactcgggtttaga----- 908
 Db 905 gtggctgtgacactggagccaaaggttccagagactcagggcccccagcactaaagcagt 964
 Qy 909 ---gagtcctcgggaataagcactgtgtataaatctctgactcactcactgggat 959
 Db 965 ggaacccagagctcctcgttaataagtagtactgtgtacagaattctgactcactcactgggt 1024
 Qy 960 cctggggcc-----gacacaggggacagagagaaaggggtcagagatgctgctctt 1008
 Db 1025 cctgggctcggagcctcctcagcagggaggggtcagagaggggagagagagagagagagagag 1084
 Qy 1009 gtcgccaactcagcagctggcctcagcagcagcagcagcagcagcagcagcagcagcagcag 1068
 Db 1085 gtcgccaactcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcag 1144
 Qy 1069 aaagttaagaaataaatatgttatcaagagatttaata 1106
 Db 1145 aa-----atattaaatgttagcaagagatttaata 1175

Search completed: May 13, 2001, 14:29:52
Job time: 18307 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:52 ; Search time 226.02 Seconds
(without alignments)
1005.808 Million cell updates/sec

Title: US-09-451-527-91
Perfect score: 1302
Sequence: 1 ctacgacctgcctgctcttc.....aaaaaaaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq:*
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq:*
3: /cgnl_7/ptodata/1/ina/6A_COMB.seq:*
4: /cgnl_7/ptodata/1/ina/6B_COMB.seq:*
5: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgnl_7/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	378	29.0	1290	1	US-08-012-543-1
2	378	29.0	1290	5	PCT-US93-07645A-1
3	378	29.0	1290	5	PCT-US93-07645-1
4	376.4	28.9	1297	1	US-08-371-121-15
5	209.4	16.1	384	1	US-08-371-121-17
6	207.6	15.9	425	1	US-08-594-469-4
7	207.6	15.9	425	2	US-08-906-957-4
8	207.6	15.9	4410	1	US-08-594-469-1
9	207.6	15.9	4410	2	US-08-906-957-1
10	207	15.9	1212	1	US-08-012-543-3
11	207	15.9	1212	5	PCT-US93-07645A-3
12	207	15.9	1212	5	PCT-US93-07645-3
13	203.4	15.6	336	1	US-08-371-121-24
14	201.8	15.5	336	1	US-08-371-121-2
15	176	13.5	447	1	US-08-371-121-26
16	68.2	5.2	2550	6	5258287-23
17	68	5.2	1023	1	US-08-252-966B-16
18	67.8	5.2	1882	4	US-09-370-253-1
19	67.2	5.2	2447	2	US-09-014-969-14
20	67.2	5.2	7218	1	US-08-232-463-14
21	67	5.1	1817	1	US-08-473-981A-5
22	67	5.1	1817	2	US-08-474-087-5
23	66.4	5.1	903	5	PCT-US95-06406A-21
24	66	5.1	1512	2	US-08-909-965C-8
25	65.8	5.1	1066	1	US-08-157-101A-4
26	65.2	5.0	260	2	US-08-520-678A-29
27	65	5.0	2010	1	US-07-864-475A-4

28	65	5.0	2010	2	US-08-468-249A-4
29	64.8	5.0	2671	6	5168051-9
30	64.4	4.9	227	2	US-08-520-678A-28
31	64.4	4.9	1558	1	US-08-467-607-2
32	64.4	4.9	1558	2	US-08-469-362-2
33	64.4	4.9	1558	2	US-08-850-392-2
34	64.2	4.9	1733	3	US-09-073-569-1
35	64	4.9	1582	3	US-08-545-196B-10
36	64	4.9	1582	3	US-08-545-196B-12
37	63.8	4.9	1307	2	US-08-960-022-17
38	63.8	4.9	2233	1	US-08-496-631-1
39	63.4	4.9	144	1	US-08-702-344-26
40	63.4	4.9	270	2	US-08-520-678A-30
41	63.4	4.9	1098	3	US-09-248-335-35
42	63.4	4.9	1134	3	US-09-248-335-29
43	63.4	4.9	6671	1	US-08-280-443-1
44	63.4	4.9	6671	1	US-08-457-459-1
45	63.4	4.9	6671	1	US-08-555-678-1

ALIGNMENTS

RESULT 1
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Bancheureau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA

Sequence 4, Appli
Patent No. 5168051
Sequence 28, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 2, Appli
Sequence 1, Appli
Sequence 10, Appli
Sequence 12, Appli
Sequence 17, Appli
Sequence 1, Appli
Sequence 26, Appli
Sequence 30, Appli
Sequence 35, Appli
Sequence 29, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli

```

; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
US-08-012-543-1

```

Query Match 29.0%; Score 378; DB 1; Length 1290;
Best Local Similarity 66.2%; Pred. NO. 4.3e-86;
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

Qy	21	cctcgcctccctcgacattgacctgtggcttgagctatgaggcgtctgatgactgtggtcatatgc	80
Db	14	CCTCAATTTTCCTCCTGTTGGACATGGGCCTCATATGAGCGCTTTTGTTCACCACGCTCATATGC	73
Qy	81	tctcaactgcctcggtagccttgaacctcccgaagccctgtgactccctccccaacctcaaa	140
Db	74	TCTCACTTGCCCTTGGGGCGCTTGCCCTCCGACGCCCTGTGCCCTCTACAGCCCTCAG	133
Qy	141	ggagctcattgagagagctggtaacaatcacccagaatac---aggaatccctctctgcaacgg	197
Db	134	GGAGCTCATTTAGGAGCTGGTCAACATCACCCAGAACCAGMAGGCTCCGCTCTGCAATGG	193
Qy	198	cagcatggtgtgagcgtcaaacctgaccgcccggaatgtactgcgcagtctctagaatctct	257
Db	194	CAGCATGGTATGAGCATCAAACTGACAGCTGGCATGTACTGTGTCAGCCCTGGAATCCCT	253
Qy	258	gatcaatgctccagctgcagcgcccatcaaaggacccagagatgctgaaagcactgtg	317
Db	254	GATCACGCTGACGCTGCACTAGTGCCTATCGAAGAACCCAGAGATGCTGAGCGGATTCTG	313
Qy	318	ctctcaaaagccgcgagcgggcagattctccagtgaacycagccgagagacaccaaatga	377
Db	314	CCCGCACAAGGTCTAGCTGGGCAGTTTTCCAGCTTGATGTCCGAGACACCAAATCGA	373
Qy	378	agtgtatccagtgtggtgaaaaaacctctcaactatgtaaagggagtttatcgccaatggaaa	437
Db	374	GGTGGCCCCAGTTTTGTAAAGACCTGCTCTTACATTTTAAAGAAACTTTTTTCGGGAGGAGC	433
Qy	438	tctcagatgaagcatgaaacttagcatcttatctgtagacca-gacctgaacacttta	496
Db	434	GTTCACTGNAACTTCGA---AGCATCATTTATTCGAGACAGAGCCTGACTATTGA	489
Qy	497	agttccagatatcttcttcctccagctgcaaaaattctcttagggaggtgggggg-----	551
Db	490	AGTTGCAGATTCTATTTTCTTCTGATGTCAAAAATGTCTTGGTAGGCGGNAGGAGG	549
Qy	552	----ggggggagaaacattctcctcagctgggacatcagcctgcaaccgctgcctccatggag	608
Db	550	TTAGGGAGGGGTAAAAATTTTCTTACCTTAGACCTACAGCTGTGTCGCCCTCTCTACGCTT	608
Qy	609	ctgagcccagcacccctgccttggtagcatggggccacagcgggtgagccctcctccgtc-	667
Db	609	----AGCCGACCTACGCTTCCCTTTGCCAGGGCTCAGCCTGTGTGGGCTCTCTGTGCC	664
Qy	668	----tgcaacttcatcaacgctgaggaaagcactgcattcccactgactgtcccctcctcag	723
Db	665	AGGGCCCTGAGCTCGGTGGACCCAGGGATGACATGTCCCTACACCCCTCCCTGCCCTAG	724
Qy	724	agcaaatgcagcattacagtggag------cagatatgtgtggaggggg-----	769
Db	725	AGCACACTGACATTTACAGTGGGTGCCCTCCCTTTGCCAGACATGTGTGTGGACAGGGACC	784
Qy	770	-----tcttgctgtacctggagtggaacagacatgtttctctaagccttta	816
Db	785	CACCTTCACACAGGCACTGAGGCAGACAGACNGCTCAGGCACACTTCTCTTGTGCTTA	844
Qy	817	ttttatttgtgttatttaaacsagttctttgtttgtctggggacagggagtg----	873
Db	845	TTTATTATTGTGTATTATAATGAGTGTGTTGTACCGTTGGGATTGGGGAAGACT	904
Qy	874	-----gcttggagctg9ggggccagtgactcgggtttaga-----	908
Db	905	GTGGCTGCTGGCACTTTGAGCCAAGGGTTTCAGAGACTCAGGGCCCCAGACACTTAAAGCAGT	964

Qy	909	-----gagtcctcgggaaataacacactgtgtgtataaattctgtcaactcaactgggat	959
Db	965	GGACCCACGAGGAGTCCCTGGTAAATAGTACTGTGTACAGAAATCTGCTACCTCACTGGGGT	1024
Qy	960	cctgggggc-----gacacaggggacagagagaaagggtcagagatcgtcgtctt	1008
Db	1025	CTGTGGGGCCTCGAGGCTCATCCGAGGCGAGGTCAGGAGAGGGGACAGAACCGCGCTCCT	1084
Qy	1009	gtctggcactcagcagctggccctcagcacaagcagtaattattgttttctcctgtattt	1068
Db	1085	GTCTGCCACCCACGCCAGCTCTCAGCCACACGAGTAATTTATTTGTTTTTCTCGTATTT	1144
Qy	1069	aaggttaagaaataaataatgttatcaaaagagtttaata	1106
Db	1145	AA-----ATATTAAATATGTTAGCAAAAGAGTTAATA	1175

```

RESULT      2
PCT-US93-07645A-1
; sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; FILING DATE: US 08/012543
; PRIOR APPLICATION DATA:
; FILING DATE: 01-FEB-1993
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

```

Query Match 29.0%; Score 378; DB 5; Length 1290;
Best Local Similarity 66.2%; Pred. No. 4.3e-86;
Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

QY	21	cctcgctcctctgcattgagctctgggctccatgagcgctgtggttgactgtggctattgc	80
Db	14	CTCAATCCCTCTCCTGTGTCATGGGCGTCATGGGCGCTTTTGTGACACGGGTCAATGC	73
QY	81	tctcaactgcctcggctggccttgctctcccgagcgccctgtgactccctccccaaacctcaa	140
Db	74	TCCTCACTTGCTTTGGGGCGCTTGCTTCCCGAGGCCGTGTCCTCCCTACAGCCCTCAG	133
QY	141	ggagctcattgaggaactggtgaacatcacccagaatc---aggcatccctctgcaacgg	197
Db	134	GGACCTCATTTGAGGAGCTGGTCAACATCACCCAGAACAGAGGCTCCCGCTCTGCAATGG	193
QY	198	cagcatgggttgagcgctcaacctgacccggcgatgctactgcgcagctctagaatctct	257
Db	194	CAGCATGGTATGGAGCATCAACCTGACAGCTGGCATGTACTGTGCAGCCCTGGAAATCCCT	253
QY	258	gatcaatgtctccgactgcagcgccctccaaaggaccagagagatgctgaaagcactgtg	317

```
Db 254 GATCAACGTGTCAGGCTGCAGTGCCATCGAGAAGACCCAGAGATGCTGAGCGGATTCTG 313
Qy 318 ctctcaaaagcccgaggcagagatttccagtgaaacagccagagacacaaattga 377
Db 314 CCCGACAAAGTCTCAGCTGGGCGATTTTCCAGCTTGATGTCGAGACACCAAAATCGA 373
Qy 378 agtgatccagtggtgtaaaacctctcaccctatgaagggagttatcgccatgaaa 437
Db 374 GGTGGCCAGTTGTAAGGACCTGCTTACATTTAAAGAAACTTTTCCGGAGGGAGG 433
Qy 438 ttccagatgaagcagcaaaacttagcctcttctgtagaccca-gacctgaccactta 496
Db 434 GTTCAACTGAACATCGAA---AGCATCATTTTTCGAGACAGGACCTGACTATTGA 489
Qy 497 agttccagatccatttctcttccagctgcacaaatttcttagggaggtggyggg---- 551
Db 490 AGTTCCAGATTCAATTTCTTCTGATGTAAGAAATGCTCTGGGTAGGCGGAAGGAGG 549
Qy 552 ---gggggagaacatttccctcagctgggacccagcctgcacccgctgcctccatggag 608
Db 550 TTAGGGAGGGTAAATTCCTTAGCTTAGACCTCAGCCCTGCTGCTGCCCTCTTACGCC- 608
Qy 609 ctgagccagccacccctgccttggtgcatggggcccgagcgggtggccctcctccg- 667
Db 609 ---AGCCGACCTCAGCCTTCCCTTGGCCAGGGCTCAGCCCTGCTGCTGCTCTGTC 664
Qy 668 ---tgacctcaacagctgagggaaagcactgcacccatgactgcccctcctcag 723
Db 665 AGGCGCCTGAGCTCGGTGGACCCAGGGATGACATGTCCTACACCCCTTCCCTGCCC- 724
Qy 724 agcaaaagtgcagcatcacagtgaggg-----cagatatgtgtggaagggg---- 769
Db 725 AGCACACTGTAGCATACAGTGGTGGCGCCCTTCCACAGACATGTGGTGGGACAGGACC 784
Qy 770 -----tctgctgtacctggagtggtggcccttgcacagacatgtttctttagcctta 816
Db 785 CACTTCACACAGCACTGAGGAGAGACAGCAGCTCAGGCACACTTCTCTTGGTCTTA 844
Qy 817 ttattattgtgtatttaaaagtgcttcttgggtggtgggagcagggagtg--- 873
Db 845 TTTATTATTGTGTGTTATTTAAATCAGTGTGTTTCTCACCCTTGGGATTTGGGAAGACT 904
Qy 874 -----gcttgagctggggcccagtgactcgggtttaga----- 908
Db 905 GTGGCTGTGTCACATTGGAGCCAGGGTTACAGACTCAGGGCCCCCAGCAGCTAAAGCAGT 964
Qy 909 -----gagtccttggaataagcactgtgtgtataaattctgctactcactgggat 959
Db 965 GGACCCAGGAGTCCCTGGTAAATAGTACTGTGTACAGAAATCTGCTACTCTCCTGGGT 1024
Qy 960 cctggggcc-----gacacaggggacagagagaaaggtcagagatgctgctctt 1008
Db 1025 CCTGGGCTCGGACCCNATCCGAGGAGGCTCAGGAGAGGGCAGACAGCCGCTCCT 1084
Qy 1009 gctgcacctcagcagctggccctcagcagaagcaaatatttggtttttctgtattt 1068
Db 1085 GTCTGCCAGCCAGCAGCAGCTCTCAGCCACGAGTAATTTATTTGTTTCTCTGTAATT 1144
Qy 1069 aaagttaagaaataaataatgttatcaagagtttaata 1106
Db 1145 AA-----ATATTAAATATGTTAGCAAGAGTTAATA 1175
```

RESULT 3

PCT-US93-07645-1

; Sequence 1, Application PC/TUS9307645

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Human Interleukin-13

; NUMBER OF SEQUENCES: 6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

```
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; PCT-US93-07645-1
```

Query Match 29.0%; Score 378; DB 5; Length 1290;

Best Local Similarity 66.2%; Pred. No. 4.3e-86;

Matches 780; Conservative 0; Mismatches 290; Indels 108; Gaps 12;

Qy 21 cctcgctccctcgctgcttggctccatggcctctggtgactggtggtcattgc 80

Db 14 CCTCAATCTCTCTGTTGGCACTGGGCGCTCATGGCGCTTTGTTGACACGGTCAATTGC 73

Qy 81 tctcactgctcgtggccttgcctcccgagccctgtgactcctcccaacccctcaa 140

Db 74 TCTCACTTGCTTGGCGCTTTCCTCCCGAGGCGCTTGCTCCCTCTACAGCCCTCAG 133

Qy 141 gggagtcattgaggagctggtcaacatcaaccagaatc---aggacatccctctgcaacgg 197

Db 134 GGAGCTCATTTAGGAGCTGCTGTCAACATCACCCAGAACGAGCTCGCTCTGCAATGG 193

Qy 198 cagatggtgtgagcgtcaacctgaccgcgcatctactgacgctctagatctct 257

Db 194 CAGCATGGTATGGAGCATCAACTGACAGCTGGCATGTACTGTGCGCCCTGGGAATCCCT 253

Qy 258 gatcaatgtctcagctgcagcgcattccagtgaaacgagccgagacacacaaattga 377

Db 254 GATCAACGTGTCAGGCTGCAGTGCCATCGAAGACCCAGAGATGCTGACGGATTTCTG 313

Qy 318 ctctcaaaagcccgaggcagagatttccagtgaaacgagccgagacacacaaattga 377

Db 314 CCCGACAAAGTCTCAGCTGGGCGATTTTCCAGCTTGCATGTCGAGACACCAAAATCGA 373

Qy 378 agtgatccagttggtgaaaaacctgctcactatgtgaagggagtttatcgccatggaaa 437

Db 374 GGTGGCCCGCTTTGTAAGGACCTGCTTACATTTAAAGAAACTTTTTCGCGAGGAGC 433

Qy 438 ttccagatgaagcatgaaaccttagccttactgtagaccca-gacctgaccactta 496

Db 434 GTTCACTGAACATTCGAA---AGCATCATTTATTTCGAGAGACGAGGACCTGACTATTGA 489

Qy 497 agttccagatctatttcttcttcgcagctcacaaattcttagggaggtgggggg---- 551

Db 490 AGTTGAGGATTCATTTTCTTCTGTGATGTCANAAATGCTCTGGGTAGCGGAGGAGGG 549

Qy 552 ---gggggagaacatttctcctcagctggagccctcagcctgcacccgctgcctccatggag 608

Db 550 TTAGGGAGGGGTAATAATTCCTTAGCTTAGACCTCAGCCTGCTGCTGCCCTCTTTCAGCCT- 608

Qy 609 ctgagccagccacccctgcttgggtcatggggcccgagcgggtggccctcctccgctc- 667

Db 609 ---AGCCGACCTCAGCCTTCCCTTGGCCAGGGCTCAGCCTGGTGGGCTCTCTGTCC 664

Qy 668 ---tgaccttcatcaacgctgaggggaagcactgcatcccatgactgctccctccctcag 723

Qy	609	ctgagccacagccacccctgccttggctgcaagggccagcgcagggtggccctctccgtc-	667
Db	621	---AGCCGACCTCAGCCTTCCTCCCTTGGCCAGGGTCAGCCTGGTGGGCTCCTCTGTCC	676
Qy	668	---tgacttcatacaacgctgagggaaagcaactgcatcccaatgactgtccctctctcag	723
Db	677	AGGGCCCTTGAGCTCGGTGGACCCAGGGATGACATGCCCTACACCCCTCCCTGCCCTAG	736
Qy	724	agcaaatgacgattacagtgagag-----caqatatgttgagggggg-----	769
Db	737	AGCACACTGTAGCATTTACAGTGGGTGCCCCCTTGGCAGACATGTGGTGGGACAGGACC	796
Qy	770	-----tcttgctgtacctggagtggcacagacatgttcttcttagcctta	816
Db	797	CAC TTCACACAGCACA CTGAGGCAGACAGCAGCTCAGGCACACTCTCTTGGTCTTTA	856
Qy	817	tttattatgtgtgtattttaacaagtcttttggctggggacagggagtg---	873
Db	857	TTTATTATTGTGTATTAAATCAGTGTGTTGTACCGTTGGGATTGGGGAAGACT	916
Qy	874	-----gcttgagctggggccagtgactgactgggttaga-----	908
Db	917	GTGGCTGTGCACCTTGGAGCCAAAGGGTTCAGAGACTCAGGGCCCAAGCAGT	976
Qy	909	-----gagtccttgggaataagcactgtgtgtataaaatctctctaactcactgggat	959
Db	977	GGACCCCAAGAGTCCCTGGTATAAAGTACTGTGTACAGAAATTCGTACTCTACTCGGGT	1036
Qy	960	cctggggcc-----gacacaggggacaggaagaaggtcagagatgcgtcctt	1008
Db	1037	CCTGGGCCCTCGGAGCCTCATCCGAGGCAGGGTTCAGGAGAGGGGCAGACAGCCGCTCCT	1096
Qy	1009	gtctgccactcagcagctggccctcagccaagcagtaattattgttttccctgtattt	1068
Db	1097	GTCTGCCAGGCAGCAGCCAGCTCTCAGCCACAGGATTAATTTATTGTTTTCTCTGATT	1156
Qy	1069	aaagttaagaataaaaaatgtatttcaagaagttaata	1106
Db	1157	AA-----ATATTAAATATTGTTAGCAAGAGCTTAATA	1187

RESULT

```

US-08-371-121-17
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-DE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:

```

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match	16.1%	Score 209.4;	DB 1;	Length 384;
Best Local Similarity	76.3%	Pred. No. 6.8e-44;		

Query Match 16.1%; Score 209.4; DB 1; Length 384;
Best Local Similarity 76.3%; Pred. NO. 6.8e-44;
Matches 271; Conservative 0; Mismatches 81; Indels 3; Gaps 1;

Qy	106	tccccgagccctgtgactccctcccccacacccctcagagagctcattgagagctggtgcaac	165
Db	16	TCCCGAGCGCCTGTGCCTCCTTACGGCCCTCAGGAGGCTCATTGGAGAGCTGGTCAAC	75
Qy	166	atcaccagaatc---aggcatccctctgaaacggcagcagcatggtgtggagcgtcaacctg	222
Db	76	ATCACCAGAACCAAGAGGCTCCGCTCTGCAATGGAGCAGCATGTATGGAGCATCAACCTG	135
Qy	223	accgcggcgtgtactgcgcagctctagaatctcctaataatgtctccagctcagcgc	282
Db	136	ACAGCTGACATGTACTGTGCAGCCCTGGAATCCCTGATCAACCTGTCAAGCTGCATGTGC	195
Qy	283	atccaaaggaccagaggaatgctgaaagcactgtgctctcaaaagcccgcgagcgag	342
Db	196	ATCAGAGAGACCCAGAGATGCTGAGCGGATTTCTGCCGCACANGTCTCAGCTGGGCAG	255
Qy	343	attccagtgaaacgagcccgagacaccaaattgaaagtatccagttggtgaaacacctg	402
Db	256	TTTTCCAGCTTGCATGTCCGAGACACCAAAATCAGSGTGGCCCGATTGTAAAGGACCTG	315
Qy	403	ctcaccctatgaaggggagtttatcgccatggaaatttcagatgaagcatgaaaa	457
Db	316	CTCTTACATTTAAAGAACCTTTTTCGGAGGAGCGGTTTCAACTGAACCTTCGAAA	370

RESULT

RESOL 0
US-08-594-469-4
Sequence 4, Application US/08594469
Patent No. 5700665
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for
TITLE OF INVENTION: periplasmic
TITLE OF INVENTION: presence of
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:

AFFILIANI: SALOME, malC
 :
 : TITLE OF INVENTION: Method for the extraction of
 :
 : TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
 :
 : TITLE OF INVENTION: presence of arginine
 :
 : NUMBER OF SEQUENCES: 9
 :
 : CORRESPONDENCE ADDRESS:
 :

ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/594,469
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-1080
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-594-469-4

Query Match 15.9%; Score 207.6; DB 1; Length 425;
Best Local Similarity 75.7%; Pred. No. 2e-43;
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;
QY 103 gcctcccccagccctgtgactccctcccccacccctcaaggagctcattgagagctggtc 162
DB 55 GCCTTCGCTGGCCCTGTGCTCCCTCCAGTACTGCTCCCTCAGGAGCTCATTGAGGAGCTGGTC 114
QY 163 aacatcacccagcaatc---aggcatccctctgcaacgagcagctggtgtgagcgtaaac 219
DB 115 AACATCACCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174
QY 220 ctgaccgcgcgcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 279
DB 175 CTGACAGCTGGCATGTACTGTGAGCCCTGGAATCCCTGATCAACGCTGTCAGGCTGCAGT 234
QY 280 gccatccaaaggagcagagatgctgaagcactgtgctctcaaaagccgcgcgcaggg 339
DB 235 GCATCGAGAGACCCAGAGATGCTGAGCGGATTCGCCCGCACAGGCTCAGCTGGG 294
QY 340 cagattccagtgaaagcagccgagacacacaaattgaagtgtatccagttggtgaaagac 399
DB 295 CAGTTTCCAGCTTGATGTGTCGAGACACCAAAATCGAGGTGGCCCAAGTTGTGAAGGAC 354
QY 400 ctgctcacctatgaagggaggtttatcgccatggaatttcagatgaagcatgaaa 457
DB 355 CTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGAGCGGTTCACACTGAAATTCGAAA 412

RESULT 7
US-08-906-957-4
; Sequence 4, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of

TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,957
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 08/594,469
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 425 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-906-957-4

Query Match 15.9%; Score 207.6; DB 2; Length 425;
Best Local Similarity 75.7%; Pred. No. 2e-43;
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;
QY 103 gcctcccccagccctgtgactccctcccccacccctcaaggagctcattgagagctggtc 162
DB 55 GCCTTCGCTGGCCCTGTGCTCCCTCCAGTACTGCTCCCTCAGGAGCTCATTGAGGAGCTGGTC 114
QY 163 aacatcacccagcaatc---aggcatccctctgcaacgagcagctggtgtgagcgtaaac 219
DB 115 AACATCACCAGAACAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174
QY 220 ctgaccgcgcgcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagc 279
DB 175 CTGACAGCTGGCATGTACTGTGAGCCCTGGAATCCCTGATCAACGCTGTCAGGCTGCAGT 234
QY 280 gccatccaaaggagcagagatgctgaagcactgtgctctcaaaagccgcgcgcaggg 339
DB 235 GCATCGAGAGACCCAGAGATGCTGAGCGGATTCGCCCGCACAGGCTCAGCTGGG 294
QY 340 cagattccagtgaaagcagccgagacacacaaattgaagtgtatccagttggtgaaagac 399
DB 295 CAGTTTCCAGCTTGATGTGTCGAGACACCAAAATCGAGGTGGCCCAAGTTGTGAAGGAC 354
QY 400 ctgctcacctatgaagggaggtttatcgccatggaatttcagatgaagcatgaaa 457
DB 355 CTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGAGCGGTTCACACTGAAATTCGAAA 412
RESULT 8
US-08-594-469-1
; Sequence 1, Application US/08594469

Patent No. 5700665
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-594-469-1

Query Match 15.9%; Score 207.6; DB 1; Length 4410;
Best Local Similarity 75.7%; Pred. No. 6.1e-43;
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;
Qy 103 gctctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtc 162
Db 392 GCCTTCGCTGGCCCTGTGCCTCCAGTACTGCCCTCAGGAGCTCATTGAGGAGCTGGTC 451
Qy 163 aacatcaccagaatc---aggcatccctctgcaacgagcagctatgtgtgagcgtcaac 219
Db 452 AACATCACCAGAACCCAGAGGCTCGGCTCTGCAATGGCAGCATGTGATGGAGCATCAAC 511
Qy 220 ctgacgcgcgcgcgtactgacgcagctctagaatctctgaatctcctcagactcagc 279
Db 512 CTGACAGCTGGCATGTACTGTGAGCCCTTGGAAATCCCTGATCAACGTGTGAGGCTGCAGT 571
Qy 280 gccatccaaagaccagagagtgctgaaagcactgtgctctcaaaagccgcgcgcaggg 339
Db 572 GCCATCGAGAACACCCAGAGGATGCTGAGCGGATTTGCCCCGACACAGGCTCAGCTGGG 631
Qy 340 cagattccagtgaaagcgcgcgcagacacacaaattgaagtgtatccagttggtgaaaac 399
Db 632 CAGTTTTCAGGCTGCATGCTCGGAGACACAAATCCAGGTGGCCCGAGTTTGTAAAGGAC 691
Qy 400 ctgctcacctatgtaagggagtttatcccatggaatttcagatgaagcatgaaaa 457
Db 692 CTGCTCTTACATTAAAGAAACTTTTTCGAGGGGACGGTTTCAACTGAAACTTCGAAA 749

RESULT 9
US-08-906-957-1
Sequence 1, Application us/08906957
Patent No. 5856142
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,957
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,469
FILING DATE:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4410 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-906-957-1
Query Match 15.9%; Score 207.6; DB 2; Length 4410;
Best Local Similarity 75.7%; Pred. No. 6.1e-43;
Matches 271; Conservative 0; Mismatches 84; Indels 3; Gaps 1;
Qy 103 gctctcccgagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtc 162
Db 392 GCCTTCGCTGGCCCTGTGCCTCCAGTACTGCCCTCAGGAGCTCATTGAGGAGCTGGTC 451
Qy 163 aacatcaccagaatc---aggcatccctctgcaacgagcagctatgtgtgagcgtcaac 219
Db 452 AACATCACCAGAACCCAGAGGCTCGGCTCTGCAATGGCAGCATGTGATGGAGCATCAAC 511
Qy 220 ctgacgcgcgcgcgtactgacgcagctctagaatctctgaatctcctcagactcagc 279
Db 512 CTGACAGCTGGCATGTACTGTGAGCCCTTGGAAATCCCTGATCAACGTGTGAGGCTGCAGT 571
Qy 280 gccatccaaagaccagagagtgctgaaagcactgtgctctcaaaagccgcgcgcaggg 339
Db 572 GCCATCGAGAACACCCAGAGGATGCTGAGCGGATTTGCCCCGACACAGGCTCAGCTGGG 631
Qy 340 cagattccagtgaaagcgcgcgcagacacacaaattgaagtgtatccagttggtgaaaac 399
Db 692 CTGCTCTTACATTAAAGAAACTTTTTCGAGGGGACGGTTTCAACTGAAACTTCGAAA 749

```

Db      532  CAGTTTTCAGCTTGCATGTCCGAGACACCAAAATCGAGGTGCCCCAGTTTGTAAAGGAC 691
Qy      400  ctgctcacctatgaaggaggagtttatcgccatggaaatttcagatgaagcatgaaaa 457
          |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||  |||||
Db      692  CTGCTCTTACATTAAAGAAACTTTTTCGGGAGGACGGTTCAACTGAAACTTCGAAA 749

RESULT 10
US-08-012-543-3
: Sequence 3, Application US/08012543
: Patent No. 5596072
: GENERAL INFORMATION:
: APPLICANT: Culpepper, Janice
: APPLICANT: McKenzie, Andrew
: APPLICANT: Dang, Warren
: APPLICANT: de Waal Malefyt, Rene
: APPLICANT: Heath, Andrew
: APPLICANT: Aversa, Gregorio
: APPLICANT: Briere, Francine
: APPLICANT: Banchereau, Jacques
: APPLICANT: de Vries, Jan
: APPLICANT: Zurawski, Gerard
: TITLE OF INVENTION: Human Interleukin-13
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/012,543
: FILING DATE: 01-FEB-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/933,416
: FILING DATE: 21-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Egwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0302K1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-852-9196
: TELEFAX: 415-496-1200
: INFORMATION FOR SEQ ID NO: 3:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1212 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: CDNA
: FEATURE:
: NAME/KEY: CDS
: LOCATION: 70..465
: US-08-012-543-3

Query Match 15.9%; Score 207; DB 1; Length 1212;
Best Local Similarity 56.8%; Pred. No. 4.7e-43;
Matches 715; Conservative 0; Mismatches 415; Indels 129; Gaps

Qy      30  tctctgactggcttgaggctcccatggcgctctggttgactgtggttcattgctctcacctg 89
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||
Db      48  TCCTCACTGGCTCTGGGCTTCATGGCGCTCTGGGTGACTGTCAGTCTGGCTCTGGCTCTGCTTG 107
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

Qy      90  cctcgttggccttgctcccccgcg-----agcccttgactccctccccaccct 137
          ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||  ||

```


APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match 15.6%; Score 203.4; DB 1; Length 336;
Best Local Similarity 77.8%; Pred. No. 2.1e-42;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;
QY 113 gccctgtgactccctcccaacccctcaaggagctcattgaggagctggtaacatcaccc 172
Db 2 GCCCTGTGCCCTCCCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61
QY 173 agaatc---aggatccctctgcaacgagcagcatggtgagcgtcaacccgtgacgcgcg 229
Db 62 AGACCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121
QY 230 gcatgtactgcgagctctagatctctgataatgctctccgactgcagcgccatccaaa 289
Db 122 GCATGTACTGTGCAGCCCTCGGAATCCCTGATCAACGCTGCAGGCTGCAGTGCCATCGA 181
QY 290 ggaccagagatgctgaaagcactgtgctctcaaaagcccgagcgagatttcca 349
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGCTCAGCTGGCGAGTTTTC 241
QY 350 gtgaacgcagcgagacacaaaattgaagtatccagtgtgtgaaacacccgtcacct 409
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTGTAAAGGACCTGCTCTTAC 301
QY 410 atgtaagggggtttatcgccatggaaattcca 442
Db 302 ATTTAAAGAAACTTTTCGCGAGGACGGTTTCA 334

RESULT 14
US-08-371-121-2
Sequence 2, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTEILLER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: Transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match 15.5%; Score 201.8; DB 1; Length 336;
Best Local Similarity 77.5%; Pred. No. 5.3e-42;
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;
QY 113 gccctgtgactccctcccaacccctcaaggagctcattgaggagctggtaacatcaccc 172
Db 2 GCCCTGTGCCCTCCCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61
QY 173 agaatc---aggatccctctgcaacgagcagcatggtgagcgtcaacccgtgacgcgcg 229
Db 62 AGACCAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121
QY 230 gcatgtactgcgagctctagatctctgataatgctctccgactgcagcgccatccaaa 289
Db 122 ACATGTACTGTGCAGCCCTCGGAATCCCTGATCAACGCTGCAGGCTGCAGTCCATCGA 181
QY 290 ggaccagagatgctgaaagcactgtgctctcaaaagcccgagcgagatttcca 349
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGCTCAGCTGGCGAGTTTTC 241
QY 350 gtgaacgcagcgagacacaaaattgaagtatccagtgtgtgaaacacccgtcacct 409
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTGTAAAGGACCTGCTCTTAC 301
QY 410 atgtaagggggtttatcgccatggaaattcca 442
Db 302 ATTTAAAGAAACTTTTCGCGAGGACGGTTTCA 334

RESULT 15
US-08-371-121-26
Sequence 26, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:39:51 ; Search time 5997.24 Seconds
(without alignments)
1896.606 Million cell updates/sec

Title: US-09-451-527-91
Perfect score: 1302
Sequence: 1 ctacgacctgcctgccttc.....aaaaaaaaaaaaaaaaaa 1302

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST.*

- 1: gb_est1.*
- 2: gb_est2.*
- 3: gb_est3.*
- 4: gb_est4.*
- 5: gb_est5.*
- 6: gb_est6.*
- 7: gb_est7.*
- 8: gb_est8.*
- 9: gb_est9.*
- 10: gb_est10.*
- 11: gb_est11.*
- 12: gb_est12.*
- 13: gb_est13.*
- 14: gb_est14.*
- 15: gb_est15.*
- 16: gb_est16.*
- 17: gb_est17.*
- 18: gb_est18.*
- 19: gb_est19.*
- 20: gb_est20.*
- 21: gb_est21.*
- 22: gb_est22.*
- 23: gb_est23.*
- 24: gb_est24.*
- 25: gb_est25.*
- 26: gb_est26.*
- 27: gb_est27.*
- 28: gb_est28.*
- 29: gb_est29.*
- 30: gb_est30.*
- 31: gb_est31.*
- 32: gb_est32.*
- 33: gb_est33.*
- 34: gb_est34.*
- 35: gb_est35.*
- 36: gb_est36.*
- 37: gb_est37.*
- 38: gb_est38.*
- 39: gb_est39.*
- 40: gb_est40.*
- 41: gb_est41.*
- 42: gb_est42.*
- 43: gb_est43.*
- 44: gb_est44.*
- 45: gb_est45.*
- 46: gb_est46.*
- 47: gb_est47.*

- 44: em_esthum10.*
- 45: em_esthum11.*
- 46: em_esthum12.*
- 47: em_esthum13.*
- 48: em_esthum14.*
- 49: em_esthum15.*
- 50: em_esthum16.*
- 51: em_esthum17.*
- 52: em_esthum18.*
- 53: em_esthum19.*
- 54: em_esthum20.*
- 55: em_esthum21.*
- 56: em_esthum22.*
- 57: em_esthum23.*
- 58: em_esthum24.*
- 59: em_esthum25.*
- 60: em_esthum26.*
- 61: em_esthum27.*
- 62: em_esthum28.*
- 63: em_estin1.*
- 64: em_estin2.*
- 65: em_estin3.*
- 66: em_estin4.*
- 67: em_estin5.*
- 68: em_estom1.*
- 69: em_estom2.*
- 70: em_estov1.*
- 71: em_estov2.*
- 72: em_estpl1.*
- 73: em_estpl2.*
- 74: em_estpl3.*
- 75: em_estpl4.*
- 76: em_estpl5.*
- 77: em_estpl6.*
- 78: em_estpl7.*
- 79: em_estpl8.*
- 80: em_estpl9.*
- 81: em_estpl10.*
- 82: em_estro1.*
- 83: em_estro2.*
- 84: em_estro3.*
- 85: em_estro4.*
- 86: em_estro5.*
- 87: em_estro6.*
- 88: em_estro7.*
- 89: em_estro8.*
- 90: em_estro9.*
- 91: em_estro10.*
- 92: em_estro11.*
- 93: em_estro12.*
- 94: em_estro13.*
- 95: em_estro14.*
- 96: em_estro15.*
- 97: em_estro16.*
- 98: em_estro17.*
- 99: em_estro18.*
- 100: em_estro19.*
- 101: em_estro20.*
- 102: gb_est25.*
- 103: gb_est26.*
- 104: gb_est27.*
- 105: gb_est28.*
- 106: gb_est29.*
- 107: gb_est30.*
- 108: gb_est31.*
- 109: gb_est32.*
- 110: gb_est33.*
- 111: gb_est34.*
- 112: gb_est35.*
- 113: gb_est36.*
- 114: gb_est37.*
- 115: gb_est38.*
- 116: gb_est39.*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
C	1	101	7.8	534	17	AI208823	AI208823 qg38e05.x
C	2	96.4	7.4	517	13	AA905851	AA905851 OJ87e03.s
C	3	96.2	7.4	430	10	AA646049	AA646049 vs34d01.f
C	4	81.2	6.2	431	105	AL513947	AL513947 AL513947
C	5	81	6.2	300	105	AL513837	AL513837 AL513837
C	6	80	6.1	596	111	AW129722	AW129722 xg23b07.x
C	7	79.8	6.1	407	103	AI921379	AI921379 wc24b03.x
C	8	78.6	6.0	967	229	CNS00JUP	AL077063 Drosophll
C	9	78.4	6.0	248	17	AI224992	AI224992 qw95a10.x
C	10	78.2	6.0	319	104	AI950892	AI950892 wx56f05.x
C	11	78.2	6.0	351	110	AW089036	AW089036 xc79a04.x
C	12	78.2	6.0	1290	105	AL514843	AL514843 AL514843
C	13	77.8	6.0	339	22	AI609594	AI609594 tw28d06.x
C	14	77.6	6.0	506	105	AL514437	AL514437 AL514437
C	15	77.2	5.9	733	110	AW074172	AW074172 xD08q08.x
C	16	77.2	5.9	968	225	AZ682070	AZ682070 ENTG002R
C	17	77	5.9	297	103	AI871697	AI871697 vm51c05.x
C	18	77	5.9	903	174	BG178352	BG178352 602330117


```
source 1. .517
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:1505308"
/clone_lib="Soares_NFL_T_GBC_S1"
/lab_host="DH10B"
/notes="Organ: pooled; Vector: pYT3D-Pac (pharmacia) with
a modified polylinker; Site_1: Not I; Site_2: Eco RI;
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung NBHL19W, testis NHT, and B-cell
NCICGAP GCBI) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 125 a 131 c 120 g 141 t
ORIGIN

Query Match 7.4%; Score 96.4; DB 13; Length 517;
Best Local Similarity 74.5%; Pred. No. 2.1e-11;
Matches 155; Conservative 0; Mismatches 36; Indels 17; Gaps 2;

QY 909 gagtcctcggaataaagcactgtgtgtataaattctgtacctcactcgtggatcctggggcc 968
Db 294 GAGTCCCTGGTAATAGTACTGTGTACAGAAATTCGTACTCTACTGGGGTCTGGGGCC 235

QY 969 ga-----cacaggggacagagaaaggtcagagatgctgtcttctgtccact 1018
Db 234 TCGGACCTCATCCAGGCGAGGTCAGGAGAGGGCAGAACAGCGCGCTCTCTGCCAGC 175

QY 1019 cagcagctggccctcagccagcagtaattattgttttcttctgtatttaaagtaaga 1078
Db 174 CAGCAGCCAGCTCTCAGCCACGAGTAATTTATTTTCTCTGTATTTAA-----A 122

QY 1079 aataaataattatcaagaagttaata 1106
Db 121 TATTAATATGTTAGCAAGAGTTAATA 94

RESULT 3
AA646049 430 bp mRNA EST 28-OCT-1997
LOCUS vs14301.r1 Stratagene mouse Tcell 937311 Mus musculus cDNA clone
DEFINITION IMAGE:1140097 5' similar to gb:M23504 Mus musculus t cell secreted
protein (MOUSE);, mRNA sequence.
ACCESSION AA646049
VERSION AA646049.1 GI:2572478
KEYWORDS EST.
SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
AUTHORS 1 (bases 1 to 430)
Marra M., Hallier L., Allen M., Bowles M., Dietrich N., Dubuque T.,
Geisel S., Kucaba T., Lacy M., Le M., Martin J., Morris M.,
Schellenberg K., Steptoe M., Tan F., Underwood K., Moore B.,
Theising B., Wylie T., Lennon G., Soares B., Willson R. and
Waterston R.
TITLE The WashU-HMI Mouse EST Project
JOURNAL Unpublished (1996)
COMMENT Contact: Marra M/Mouse EST Project
WashU-HMI Mouse EST Project
Washington University School
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
Tel: 314 286 1800
Fax: 314 286 1810
Email: mousees@watson.wustl.edu
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.

MGI:621369
Seq primer: -28ml3 rev1 ET from Amersham
High quality sequence stop: 409.
FEATURES
Location/Qualifiers
1. .430
/organism="Mus musculus"
/db_xref="taxon:10090"
/clone="IMAGE:1140097"
/clone_lib="Stratagene mouse Tcell 937311"
/tissue_type="Tcell"
/dev_stage="M30 CD4+ cells"
/lab_host="SOLR (kanamycin resistant)"
/notes="Organ: blood; Vector: pBluescript SK-; Site_1:
EcoRI; Site_2: XhoI; Cloned unidirectionally. Primer:
Oligo dt. M30 CD4+ cells. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGCACGAG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTTT 3'."
BASE COUNT 126 a 83 c 112 g 109 t
ORIGIN

Query Match 7.4%; Score 96.2; DB 10; Length 430;
Best Local Similarity 64.7%; Pred. No. 2.3e-11;
Matches 231; Conservative 0; Mismatches 103; Indels 23; Gaps 5;

QY 909 gagtccctcggaataaagcactgtgtgtataaattctgtacctcactcgtggatcctgggg-- 966
Db 91 GGGGTCCCTGGCAATATTACTGTATACATAATTCTGCTACCTCAGCTGCAGCTCCAGGTC 150

QY 967 ----ccgacacaggggacaggaagggtcagagatgctgtctgtgtgcactcagc 1022
Db 151 TCACCCCGCAGCAGGAGATGGGAGGGAGGCCAGAGCAAC-ACTCCYGTCTGCCACGGAGC 209

QY 1023 agctgacctcagcaagcagtaattattgttttcttctgtatttaaagtaagaata 1082
Db 210 AACCCAGCCCTCAGCCATGAATAACTTATTGTT-----TTGTTCTTATATTAAAGTATT 264

QY 1083 aaatgttatcaagagttaataataataagaagtagctcctaaaggctgcatttgg 1142
Db 265 AAATAGCTTAGCAAGAGTTATATATATATGAGAGAGTGCCTGTTTACACTCAAGGTGAT 324

QY 1143 gtgtgtgcccagggccgggggggtggtgggggggggtgtgtgtcactgaatgtgtcttca 1202
Db 325 GTGTAGTGAATG-----GGGGGAGGGTGGTGGTGTGTCTACTCAACAAATTTT--- 373

QY 1203 ctgactttgtcaactggaagccagcaaaaataagaatgtgtgacagaagaaaaa 1259
Db 374 CATTGACTGTCAAACTAGAAACCCGGAATAAAGATGGTGCAGATATAAAAAA 430

RESULT 4
AL513947/c 431 bp mRNA EST 13-FEB-2001
LOCUS AL513947 LTI_NFL006_PL2 Homo sapiens cDNA clone CL0BA0102G04 3
DEFINITION prime, mRNA sequence.
ACCESSION AL513947
VERSION AL513947.1 GI:12777441
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
AUTHORS 1 (bases 1 to 431)
Li W.B., Gruber C., Jessee J., and Polayes D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
1. .431
/organism="Homo sapiens"
```



```

Db 155 CCCCCCGGGGGCGGGGGGGTCTTTTCCAAAAATTTTTTTTTTTTTTTT 196
Qy 1211 gtcaactggaagcagaataaagatggtgacagagaaaaa 1270
Db 95 TTTTAAAAA 36
Qy 1271 aaaaaa 1302
Db 35 AAAAAA 4

RESULT 7
AI921379/c
LOCUS
DEFINITION
  wo24b03.x1 NCI_CGAP_Pan1 Homo sapiens cDNA clone IMAGE:2456237 3'
  similar to contains element TAR1 repetitive element ;, mRNA
  sequence.
ACCESSION
  AI921379
VERSION
  AI921379.1 GI:5657343
KEYWORDS
  EST.
SOURCE
  human.
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
  1 (bases 1 to 407)
  NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
  Tumor Gene Index
  Unpublished (1997)
  Contact: Robert Strausberg, Ph.D.
  Tel: (301) 496-1550
  Email: Robert.Strausberg@nih.gov
  Life Technologies catalog #: 11548-013
  DNA Sequencing by: Washington University Genome Sequencing Center
  Clone distribution: NCI-CGAP clone distribution information can be
  found through the I.M.A.G.E. Consortium/LENL at:
  www-bio.lnl.gov/bbrp/image/image.html
  Insert Length: 1337 Std Error: 0.00
  Seq primer: -400P from Gibco
  High quality sequence stop: 391.
  Location/Qualifiers
    1..407
      /organism="Homo sapiens"
      /db_xref="taxon:9606"
      /clone="IMAGE:2456237"
      /clone_lib="NCI_CGAP_Pan1"
      /tissue_type="adenocarcinoma"
      /lab_host="DH10B"
      /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: SalI;
      Site_2: NotI; Cloned unidirectionally. Primer: Oligo dT.
      Average insert size 1.72 kb. Life Technologies catalog #:
      11548-013"
BASE COUNT 82 a 74 c 110 g 141 t
ORIGIN

Query Match 6.1%; Score 79.8; DB 103; Length 407;
Best Local Similarity 66.7%; Pred. No. 1.1e-07;
Matches 114; Conservative 0; Mismatches 57; Indels 0; Gaps 0;

Qy 1132 ctgcattggtgtgtggtggccggcggtgggtggggagggtgtgtcactgaat 1191
Db 220 CGGGTTTTTTTTTTTTTGGGGGGGGGGGGGGGGGGGGGGGGCCCTCCCTTTT 161
Qy 1192 gtgctcttcactgacttgcacactggagccagagataaagatggtgacagagaaa 1251
Db 160 TTTTTCCTCCCAAAATTTTTCCTTTTAAAAA 101

Qy 1252 aaaaaa 1302
Db 100 AAAAAA 50

us-09-451-527-91.rst

```

```

RESULT 8
CNS00JUP
LOCUS
DEFINITION
  CNS00JUP 967 bp DNA GSS 03-JUN-1999
  Drosophila melanogaster genome survey sequence TET3 end of BAC:
  BACR39K04 of RPCI-98 library from Drosophila melanogaster (fruit
  fly), genomic survey sequence.
ACCESSION
  AL077063
VERSION
  AL077063.1 GI:4956338
KEYWORDS
  GSS.
SOURCE
  fruit fly.
ORGANISM
  Drosophila melanogaster
  Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
  Pterygota; Metazoa; Endopterygota; Diptera; Brachycera;
  Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
REFERENCE
  1 (bases 1 to 967)
  Genoscope.
  Direct Submission
  Submitted (02-JUN-1999) Genoscope - Centre National de Sequencage :
  BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
  - Web : www.genoscope.cns.fr)
  Determination of this BAC-end sequence was carried out as part of a
  collaboration with the Berkeley Drosophila Genome Project (BDGP).
  The BDGP is constructing a physical map of the Drosophila
  melanogaster genome using these BACs. For further information
  please see http://www.fruitfly.org The BDGP Drosophila
  melanogaster BAC library was prepared by Kazutoyo Osoegawa and
  Aaron Mammoser in Pieter de Jong's laboratory in the Department of
  Cancer Genetics at the Roswell Park Cancer Institute in Buffalo,
  NY. The library is named RPCI-98 and was constructed by partial
  EcoRI digestion of Drosophila DNA provided by the BDGP from the
  isogenic strain y2; cn bw sp, the same strain used for the BDGP's
  P1 and EST libraries. A more detailed description of the library
  and how to order individual BAC clones, the entire library, or
  filters for hybridization from the BACPAC Resource Center can be
  found at http://bacpac.med.buffalo.edu/drosophila_bac.htm.
  Location/Qualifiers
    1..967
      /organism="Drosophila melanogaster"
      /db_xref="taxon:7227"
      /clone_lib="RPCI-98"
      /clone="BACR39K04"
      /note="end : TET3"
BASE COUNT 392 a 25 c 93 g 86 t 371 others
ORIGIN

Query Match 6.0%; Score 78.6; DB 229; Length 967;
Best Local Similarity 52.8%; Pred. No. 2.2e-07;
Matches 123; Conservative 0; Mismatches 110; Indels 0; Gaps 0;

Qy 1059 aaagttaagaaataaataatgttatcaagagtttaataataataagagtagctaaa 1128
Db 194 AAAAAA 253

Qy 1129 aggtcattggtgtgtgtggtggccaggcggtggggggagggtgtgtcactg 1188
Db 254 AAATCAACAGCGNANGGGGAAAGAGAGGNGGCGGNNAGNNGNAGNNTNAGG 313
Qy 1189 aatgtgctcttcactgacttgcacactggaagcagagataaagatggtgacaagag 1248
Db 314 AAGANGANNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN 373
Qy 1249 aaaaaa 1301
Db 374 AAAAAA 426

RESULT 9
AI224992/c
LOCUS
DEFINITION
  AI224992 248 bp mRNA EST
  qw95a10.x1 NCI_CGAP_Gas4 Homo sapiens cDNA clone IMAGE:1998810 3'
  similar to TR:Q04154 Q04154 SALIVARY PROLINE-RICH PROTEIN RP15

```


Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.lnl.gov/bbrp/image/image.html
Seq primer: -40UP from Gibco
High quality sequence stop: 342.

FEATURES
source

```

location/vcudallileis
I..351
source
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="IMAGE:2590446"
/clone_lib="NCI_CGAP_Brn35"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DHI0B"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: SalI;
Site_2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Average insert size 1.33 kb. Tumor types include:
meningioma, oligodendroglioma, astrocytoma (grade II),
medulloblastoma, astrocytoma (grade IV). Life technologies
catalog #: 11544-012"
BASE COUNT      54 a    119 c     76 g    102 t
ORIGIN
Query Match          6.0%; Score 78.2; DB 110; Length 351;
Best Local Similarity 67.5%; Pred. No. 2.4e-07;
Matches 110; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1140 gggtgtgtgccagccggcggggctgtggggggagggtgtgttcactgaatgtgccttt 1199
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 166 GGGGGGGGGGGGGGGGGGGGGGGGAAGGGGGGGGATTTGGGTTCAGGGGTTTGGCCC 107
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1200 tcactgactttgtcaaaccttgaaagccagaataaagatggtgacaagagaaaaaaa 1259
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 106 CCTTTGCTTTTGCAACTTCAGGTTCAAAAACCCAGGGGGTTTTAAAAAATAAAAA 47
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1260 aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa 1302
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 46 AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA 4
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

```

RESULT	12
AL514843/c	
LOCUS	1290 bp mRNA
DEFINITION	EST
	AL514843 LRI_NFL006.PL2 Homo sapiens cDNA clone CLOBB0142F09 3
	prime, mRNA sequence.
ACCESION	AL514843
VERSION	AL514843.1 GI:12778336
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE	1 (bases 1 to 1290)
AUTHORS	Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
TITLE	Full-length cDNA libraries and normalization
JOURNAL	Unpublished (2001)
COMMENT	Contact: Genoscope

FEATURES

```

FEATURES
    source
        1. 1290
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /clone="CLOB014ZF09"
            /clone_lib="LTI_NFL006_PL2"
            /tissue_type="placenta"
            /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
            was primed with a NotI-oligo(dT) primer. Five prime end
            enriched, double-stranded cDNA was digested with Not I and
            cloned into the Not I and Eco RV sites of the pCMVSPORT 6
            vector. Library was normalized. Library was constructed by
            Life Technologies. Contact : Feng Liang Life Technologies,

```

a division of Invitrogen 9800 Medical Center Drive
Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
Email : flange@lifetech.com URL :
<http://fulllength.invitrogen.com>"

BASE COUNT	381 a	293 c	310 g	225 t	81 others
ORIGIN					

Query Match	6.0%	Score 78.2;	DB 105;	Length 1290;	
Best Local Similarity	64.8%	Pred. No. 2.8e-07;			
Matches 107;	Conservative 4;	Mismatches 54;	Indels 0;	Gaps 0;	
Qy 1138	ttggtgtgtgtggtccagcgccggcggtgggggggaggtgtgtgtcactgaatgtgtctc	1197			
Db 194	TTTGTGTGTCNCAGAGACNCTGTGTGTGTGTGTGTGTGTCTCTCTCTGTGTCTC	135			
Qy 1198	tttcaactgactttgtcaaaatggaagccagaataaaagatggtgcaagagaaaaa	1257			
Db 134	TCTCTCTGTGTGTGAGAGWGCACASAGAGAGAGAGACATAAAAA	75			
Qy 1258	aaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaaa	1302			
Db 74	AAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAAA	30			
RESULT 13					
AI609594/C					
LOCUS	AI609594	339 bp	mrna	EST	14-MAY-1999
DEFINITION	tw28606.x1 NCI-CGAP_Ov35 Homo sapiens cdna clone IMAGE:2261003 3', mRNA sequence.				
ACCESSION	AI609594				
VERSION	AI609594.1	GI:4618761			

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 339)
 AUTHORS NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Tel: (301) 496-1550
 Email: Robert.Strausberg@nih.gov
 Tissue Procurement: Christophor A. Moskaluk, M.D., Ph.D., Michael
 R. Emmert-Buck, M.D., Ph.D.
 CDNA Library preparation: Life Technologies, Inc.
 CDNA Library Arrayed by: Greg Lennon, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center
 Clone distribution: NCI-CGAP clone distribution Information can be
 found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
 Insert Length: 949 Std Error: 0.00
 Seq primer: -40UP from Gibco
 High quality sequence stop: 337
 POLYA=NO

```

FEATURES
source
Location/Qualifiers
1. .339
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2261003"
/clone_lib="NCI_CGAP_Ov35"
/tissue_type="tumor, 5 pooled (see description)"
/lab_host="DH10B"
/notes="Organ: ovary; Vector: pCMV-SPORT6; Site_1: Sali;
Site_2: NotI; This library represents the normalized
version of NCI_CGAP_Ov23. Cloned unidirectionally.
Primer: Oligo dT. Average insert size 0.86 kb. Tumor
types include: mixed Mullerian tumor, papillary serous,
clear cell, spindle cell. All are primary tumors,
metastasis positive. Constructed by Life Technologies."
75 a 66 c 79 q 118 t 1 others
BASE COUNT

```


Search completed: May 13, 2001, 11:40:07
Job time: 16482 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:29 ; Search time 9342.78 Seconds
(without alignments)
620.362 Million cell updates/sec

Title: US-09-451-527-94

Perfect score: 393

Sequence: 1 atggcgctctgtgtgactgt.....atggccatggaatttcaga 393

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_om.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
14: gb_pl3.*
15: gb_pl4.*
16: em_ba1.*
17: em_ba2.*
18: em_fun.*
19: em_hcgo_hum.*
20: em_hcgo_inv.*
21: em_hcgo_rod.*
22: em_hcgo_hum1.*
23: em_hcgo_hum2.*
24: em_hcgo_hum3.*
25: em_hcgo_hum4.*
26: em_hcgo_hum5.*
27: em_hcgo_hum6.*
28: em_hcgo_hum7.*
29: em_hcgo_hum8.*
30: em_hcgo_inv1.*
31: em_hcgo_inv2.*
32: em_hcgo_other.*
33: em_hum1.*
34: em_hum2.*
35: em_hum3.*
36: em_hum4.*
37: em_hum5.*
38: em_hum6.*
39: em_hum7.*
40: em_hum8.*
41: em_in.*
42: em_om.*
43: em_or.*

44: em_ov.*
45: em_pat.*
46: em_ph.*
47: em_pl.*
48: em_rod.*
49: em_sts.*
50: em_sy.*
51: em_un.*
52: em_vi.*
53: gb_sts1.*
54: gb_sts2.*
55: gb_sts3.*
56: gb_sy.*
57: gb_un.*
58: gb_vil.*
59: gb_vil2.*
60: gb_vil3.*
61: gb_vil4.*
62: gb_vil5.*
63: gb_vil6.*
64: gb_vil7.*
65: gb_vil8.*
66: gb_vil9.*
67: gb_vil10.*
68: gb_vil11.*
69: gb_vil12.*
70: gb_vil13.*
71: gb_vil14.*
72: gb_vil15.*
73: gb_vil16.*
74: gb_vil17.*
75: gb_vil18.*
76: gb_vil19.*
77: gb_vil20.*
78: gb_vil21.*
79: gb_vil22.*
80: gb_vil23.*
81: gb_vil24.*
82: gb_vil25.*
83: gb_vil26.*
84: gb_vil27.*
85: gb_vil28.*
86: gb_vil29.*
87: gb_vil30.*
88: gb_vil31.*
89: gb_vil32.*
90: gb_vil33.*
91: gb_vil34.*
92: gb_vil35.*
93: gb_vil36.*
94: gb_vil37.*
95: gb_vil38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	393	100.0	1302	7	AF244915	AF244915 Canis fam
2	246.8	62.8	1270	93	HUMIL13A	L06801 Homo sapien
3	246.8	62.8	1282	92	HSNC30	X69079 H. sapiens i
4	246.8	62.8	1290	10	I34548	I34548 Sequence 1
5	245.2	62.4	417	88	AF043334	AF043334 Homo sapi
6	245.2	62.4	1297	9	A29948	A29948 Coding sequ
7	245.2	62.4	1297	10	I58488	I58488 Sequence 15
8	219.8	55.9	343	7	AF072807	AF072807 Bos tauri
9	204	51.9	384	9	A29950	A29950 Nucleic aci
10	204	51.9	384	10	I58489	I58489 Sequence 17
11	203.4	51.8	336	9	A29931	A29931 Sequence co

```

12 203.4 51.8 336 10 I58494
13 202.2 51.5 425 9 AR027065
14 202.2 51.5 425 10 I86198
15 202.2 51.5 4410 9 A52326
16 202.2 51.5 4410 9 AR027062
17 202.2 51.5 4410 10 I86195
18 201.8 51.3 336 9 A29930
19 201.8 51.3 336 10 I58481
20 159.2 40.5 447 10 I58495
21 159.2 40.5 1207 94 MUSSTCPE
22 159.2 40.5 1212 10 I34549
23 153.8 39.3 213343 94 RATIL13A
24 130.8 33.3 3714 93 HUM11DC99Z
25 101.8 25.9 3714 93 HUM11DC99Z
26 101.8 25.9 4600 93 HSU10307
27 101.8 25.9 4740 93 HSU10307
28 101.8 25.9 5670 93 HSU10307
29 101.8 25.9 50282 85 AC004039
30 101.8 25.9 78469 75 AC074127
31 101.8 25.9 78469 75 AC074127
32 92.2 23.5 3520 7 BTA132441
33 70.6 18.0 3395 93 HUM11DC98Z
34 61.6 15.7 4376 94 MUSL113A
35 61.6 15.7 142732 88 AC084392
36 61.6 15.7 159500 94 AC005742
37 61.6 15.7 237823 66 AC020886
38 44.6 11.3 60 9 A29941
39 44.6 11.3 60 10 I58485
40 44.6 11.3 102 9 A29939
41 44.6 11.3 102 10 I58483
42 40.8 10.4 1008 94 RATNACHRR5
43 40.8 10.4 2461 95 RATNACHRR5
44 40.8 10.4 38390 3 SC2H12
45 39.6 10.1 54 9 A29940

```

ALIGNMENTS

```

RESULT 1
LOCUS AF244915 1302 bp mRNA MAM 16-OCT-2000
DEFINITION Canis familiaris Interleukin-13 mRNA, complete cds.
ACCESSION AF244915
VERSION AF244915.1 GI:7528273
KEYWORDS dog.
SOURCE Canis familiaris
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 1302)
AUTHORS Yang,S., Borroughs,K.L. and McDermott,M.J.
TITLE Canine Interleukin-13: molecular cloning of full-length cDNA and expression of biologically active recombinant protein
JOURNAL J. Interferon Cytokine Res. 20 (9), 779-785 (2000)
MEDLINE 20485146
PUBMED 11032397
REFERENCE 2 (bases 1 to 1302)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation, 1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES
source Location/Qualifiers
1..1302
/db_xref="taxon:9615"
52..447
/codon_start=1
/product="interleukin-13"
/protein_id="AAF63204.1"
/db_xref="GI:7528274"
/translation="MALWLTIVIALTCGLGLASPSVTPSPSTLKELIEELVNITQNOA

```

```

SLCNGSMVSVNLTAGMYCAALESINVSDCSAIQRTORMLKALCSQKPAAGQISSR
SRDIKIEVIQLVKNLLITVRGVYRHGFR"
448..1302
337 a 318 c 340 g 307 t
BASE COUNT
ORIGIN
Query Match 100.0%; Score 393; DB 7; Length 1302;
Best Local Similarity 100.0%; Pred. No. 3.9e-91;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggcgctctgtgactgtggtcattgctcaccctgctcgtggtggtgcttgcctccccc 60
Db 52 ATGGCGCTCTGTTGACTGTGTTGCTCATCTGCTCAACCTGCTCGGTGCTTGCCTCCCC 111
QY 61 agcctgtgactcctcccccaccctcaaggagctcattgagaggtggtgagagctcacc 120
Db 112 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGTTCAACATCACC 171
QY 121 cgaatcaggcctcctctgcaacgagcagcagcagcagcagcagcagcagcagcagcagc 180
Db 172 CAGATCAGGCATCCCTCTGCAACGCGCAGCAGTGGTGTGAGCGTCAACCTGACCGCGGC 231
QY 181 atgtactgcgcagctctagaatctctgtatcattcctcagctgcagcagcagcagcagc 240
Db 232 ATGTACTGCGGAGCTCTAGAAATCTGTATCAATGTCTCGACTGCGAGCCATCCAAAGG 291
QY 241 acccagagatctgaaagcagcagcagcagcagcagcagcagcagcagcagcagcagc 300
Db 292 ACCCAGAGATGCTGAAAGCAGTGTGCTCTCAAAAGCCCGCGGAGGAGGAGATTTCAGT 351
QY 301 gaacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 360
Db 352 GAACGAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAGCAG 411
QY 361 gtaagggaagttatcccatggaatttcaga 393
Db 412 GTAAGGGAGTTATCGCCATGGAATTTTCA 444
RESULT 2
LOCUS HUMIL13A 1270 bp mRNA PRI 22-JUL-1993
DEFINITION Homo sapiens Interleukin 13 mRNA, complete cds.
ACCESSION L06801
VERSION L06801.1 GI:186275
KEYWORDS cytokine; growth factor; Interleukin 13; regulatory protein.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1270)
AUTHORS McKenzie,A.N.J., Cuipepper,J.A., de Waal Malefyt,R., Briere,F., Ponnunen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de Vries,J.E., Banchereau,J. and Zurawski,G.R.
TITLE Interleukin-13, a T cell-derived cytokine that regulates human monocyte and B cell function
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)
MEDLINE 93234572
FEATURES
source Location/Qualifiers
1..1270
/organism="Homo sapiens"
/db_xref="taxon:9606"
45..443
/codon_start=1
/product="interleukin 13"
/protein_id="AAA36107.1"
/db_xref="GI:186276"
/translation="MALWLTIVIALTCGLGFASPGVPPSTALRELIELVNITQNK
APLNGSMVSVNLTAGMYCAALESINVSDCSAIEKTMRLSGCPHKVSAQGFSSL
HVRDKIEVAQFVKDLLLLLKLKLFREGFN"
polyA_site 288 a 335 c 336 g 311 t
BASE COUNT

```

ORIGIN

Query Match 62.8%; Score 246.8; DB 93; Length 1270;
Best Local Similarity 78.4%; Pred. No. 2e-53;
Matches 309; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

Qy 1 atggcgctgtggtgactgtgctcctcactgctcgtggtgcttgcctcccg 60
Db 45 ATGGCGCTTTGTTGACACGGTCATGCTCTCACTTGGCTTGGCGCTTGCCTCCCCA 104
Qy 61 agcctgtgactccctcccccacccctcaaggagctcattgagagctggtcaacatcac 120
Db 105 GGCCCTGTGCTCCTCTACAGCCCTCAGGAGCTCATTGAGAGCTGCTCAACATCAC 164
Qy 121 cagaatc---aggatccctctgcaacggcagcagtgtgtgagcgtcaacctgaccgc 177
Db 165 CAGAACCAAGAGGCTCCGCTCTGCAATGCGACAGCTGTTGAGGATCAACCTGACAGCT 224
Qy 178 ggcattgactgcagctcagaatctctgataatgctcctcagactgagcgccatccaa 237
Db 225 GCATGTGATGTCGACGCTCGAATCCCTGTCAACGCTCAGGCTGCAGTGCCTCGAG 284
Qy 238 aggaccagagatgctgaaacactgtgctctcaaaagccgcgagcgagcagattcc 297
Db 285 AAGACCCAGAGATGCTGAGCGGATCTGCCCGCACAGGCTCTCAGCTGGCAGTTTCC 344
Qy 298 agtgaacgagccgagacacccaaattgaagtgtatccagttgtgaaacacctgtccac 357
Db 345 AGCTTGATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTA 404
Qy 358 tatgtaagggagtttatcgccatggaattcca 391
Db 405 CATTTAAAGAAACTTTTTCGCGAGGACGGTTTCA 438

RESULT 3

HSNC30 HSN30 1282 bp mRNA PRI 17-FEB-1997
LOCUS H.sapiens interleukin-13 mRNA.
DEFINITION X69079
ACCESSION X69079
VERSION X69079.1 GI:297787
KEYWORDS lymphokine.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 1282)
AUTHORS Minty,A.J.
TITLE Direct Submission
JOURNAL Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches,
Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
REFERENCE 2 (bases 1 to 1282)
AUTHORS Minty,A.J., Chalon,P., Derocq,J.M., Dumont,X., Guillemot,J.C.,
Keghad,M., Labit,C., Lepiatcois,P., Liauzun,P., Miloux,B., Minty,C.,
Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and
Ceput,D.
TITLE Interleukin-13 is a new human lymphokine regulating inflammatory
and immune responses
JOURNAL Nature 362 (6417), 248-250 (1993)
MEDLINE 93211479
FEATURES Location/Qualifiers
1..1282
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="5q 23-31"
/cell_type="peripheral blood lymphocytes"
15..455
/gene="NC30"
15..116
/gene="NC30"
/product="NC30; alternative"
15..455

gene

sig_peptide

CDS

/gene="NC30"
/note="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1
/evidence=experimental
/protein_id="CAA48823.1"
/db_xref="GI:580330"
/db_xref="SWISS-PROT:P35225"
/translation="MHPLNPLLLALGLMALLLTVTYIALTCLGFGFASGPGVPVPPSTALR
ELIEELVNITQKQKAPLCNGSMVMSINLTAGMYCAALESINVTGSCSAIEKTRMLSGFCPHKVSAGOFSS
LHVRDTRKIEVAQFVKDILLHLKLFREGRFN"
57..455
/gene="NC30"
/note="alternative; ATG at 15 is an alternative start
codon"
/codon_start=1
/evidence=experimental
/protein_id="CAA48824.1"
/db_xref="GI:673420"
/db_xref="SWISS-PROT:P35225"
/translation="MALLLTVTYIALTCLGFGFASGPGVPVPPSTALRELIEELVNITQKQ
KAPLCNGSMVMSINLTAGMYCAALESINVTGSCSAIEKTRMLSGFCPHKVSAGOFSS
LHVRDTRKIEVAQFVKDILLHLKLFREGRFN"
57..116
/gene="NC30"
/product="NC30; alternative"
117..452
/gene="NC30"
/evidence=experimental
238
/gene="NC30"
/replace="a"
856..860
/note="ATTTA motif"
873..877
/note="ATTTA motif"
1134..1138
/note="ATTTA motif"
1153..1157
/note="ATTTA motif"
1264..1269
polyA_signal 293 a 341 c 337 g 311 t
BASE COUNT
ORIGIN
Query Match 62.8%; Score 246.8; DB 92; Length 1282;
Best Local Similarity 78.4%; Pred. No. 1.9e-53;
Matches 309; Conservative 0; Mismatches 82; Indels 3; Gaps 1;
Qy 1 atggcgctgtggtgactgtgctcctcactgctcgtggtgcttgcctcccg 60
Db 57 ATGGCGCTTTGTTGACACGGTCATGCTCTCACTTGCCTTGGCGGCTTGCCTCCCCA 116
Qy 61 agcctgtgactccctcccccacccctcaaggagctcattgagagctggtcaacatcac 120
Db 117 GGCCCTGTGCTCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCAC 176
Qy 121 cagaatc---aggatccctctgcaacggcagcagtgtgtgagcgtcaacctgaccgc 177
Db 177 CAGAACCAAGAGGCTCCGCTCTGCAATGCGACAGCTGTTGAGGATCAACCTGACAGCT 236
Qy 178 ggcattgactgcagctcagaatctctgataatgctcctcagactgagcgccatccaa 237
Db 237 GCATGTGATGTCGAGCCCTGGAATCCCTGATCAACGCTGTCAGGCTGCATGCTCAG 296
Qy 238 aggaccagagatgctgaaagcactgtgctctcaaaagccgcgagcgagcagattcc 297
Db 297 AAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGTCTCAGCTGGCAGTTTCC 356
Qy 298 agtgaacgagccgagacacccaaattgaagtgtatccagttgtgaaacacctgtccac 357
Db 357 AGCTTGATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTA 416

JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea

COMMENT Nested PCR:
1) first PCR : forward primer (5'-ctcaatcctctcctgttgga-3') reverse primer (5'-tagtcaggtcctgctctgc-3')
2) second PCR : forward primer (5'-ctcatggcgcttttggaccacg-3') reverse primer (5'-gatgcttcgaagtccagttgaa-3').

FEATURES Location/Qualifiers
source 1..417
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /cell_type="PHA-treated peripheral blood leukocyte"
gene 1..417
 /gene="IL13"
primer_bind 1..24
 /note="second PCR"
PCR_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles; DeltaCycler II from Ericomp"
CDS 4..402
 /gene="IL13"
 /codon_start=1
 /product="interleukin 13 precursor"
 /protein_id="AAC03535.1"
 /db_xref="GI:2905620"
translation="MALLTVIALCLGFGFASPGVPSTALRELIELVNTQNSA
APLCGSMVMWSINLTAGMYCAALESINVSQSAIEKRTQMLGGPCPHKVSAQSFS
HVDRTKIEVAQFVKDILLHLKLFRBGRN"
sig_peptide 4..63
mat_peptide 64..399
primer_bind complement(394..417)
 /note="second PCR"
BASE COUNT 91 a 121 c 108 g 97 t
ORIGIN

Query Match 62.4%; Score 245.2; DB 88; Length 417;
Best Local Similarity 78.4%; Pred. No. 5.5e-53;
Matches 308; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

Qy 1 atggcgctctgttgactgtggttcattgctcaccctgctgctggtgacctgctgccccc 60
Db 4 ATGGCGCTTTTGTTCACCCAGCGCTCATTCCTCATTGCTGCCTTGCGGCGCTTGCTCCCCA 63

Qy 61 agccctgtgactcctcccccaaccctcaaggagctcattgaggagctggtcaacatcac 120
Db 64 GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGGTCAACATCAC 123

Qy 121 cagaatc---aggcatcctctgcaacggcagcatggtgtggagcggtcaacctgacgc 177
Db 124 CAGAACACAGAGGCTCCGCTCTGCANTGGCAGCATGTTTGGAGCATCACCTGACAGCT 183

Qy 178 ggcatgtactgcagctctagaaatctctgatcaatctctccgactcagcgccatccaa 237
Db 184 GCATGTACTTGCAGCCCTGGAATCCCTGATCAACGTGTCCAGCTGCAGTGCATCGAG 243

Qy 238 aggaccagagagatgctgaaagacactgtgctctcaaaaagcccgagggcagattcc 297
Db 244 AAGACCAGAGAGTGTGGCGGATTTCTGCCCGCACAAAGGTCTCAGTGGGCGAGTTTTTC 303

Qy 298 agtgaacgcagcgagacaccaaattgaagtgatccagtgtgtgaaaaaacctgctcac 357
Db 304 AGCTTGATGTCCGAGACACCAAATCGAGGTGGCCAGCTTTTAAGGACCTGCTCTTA 363

Qy 358 tatgtaagggaggttatcgccatggaattcca 391
Db 364 CATTTAAGAACAATTTTTCGCGAGGACGGTTCA 397

RESULT 4
LOCUS T34548 1290 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5596072.
ACCESSION T34548
VERSION T34548.1 GI:1825339
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refoolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
FEATURES Location/Qualifiers
source 1..1290
 /organism="unknown"
BASE COUNT 308 a 335 c 336 g 311 t
ORIGIN

Query Match 62.8%; Score 246.8; DB 10; Length 1290;
Best Local Similarity 78.4%; Pred. No. 1.9e-53;
Matches 309; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

Qy 1 atggcgctctgttgactgtggttcattgctcaccctgctgctggtgacctgctgccccc 60
Db 45 ATGGCGCTTTTGTTCACCCAGCGCTCATTCCTCATTGCTGCCTTGCGGCGCTTGCTCCCCA 104

Qy 61 agccctgtgactcctcccccaaccctcaaggagctcattgagagctggtcaacatcac 120
Db 105 GGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTCAGGAGCTGGTCAACATCAC 164

Qy 121 cagaatc---aggcatcctctgcaacggcagcatggtgtgaggctcaacctgacgc 177
Db 165 CAGAACACAGAGGCTCCGCTCTCATGTCGAGCATGTTGAGGAGCATCAACCTGACAGCT 224

Qy 178 ggcatgtactgcagctctagaaatctctgatcaatgtctccgactcagcgccatccaa 237
Db 225 GGCATGTACTGTGAGCCCTGGAACTCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAG 284

Qy 238 aggaccagagagatgctgaaagacactgtgctctcaaaaagcccgagggcagattcc 297
Db 285 AAGACCAGAGAGTGTGGCGGATTTCTGCCCGCACAAAGGTCTCAGTGGGCGAGTTTTTC 344

Qy 298 agtgaacgcagcgagacaccaaattgaagtgatccagtgtgtgaaaaaacctgctcac 357
Db 345 AGCTTGATGTCCGAGACACCAAATCGAGGTGGCCAGCTTTTAAGGACCTGCTCTTA 404

Qy 358 tatgtaagggaggttatcgccatggaattcca 391
Db 405 CATTTAAGAACAATTTTTCGCGAGGACGGTTCA 438

RESULT 5
LOCUS AF043334
DEFINITION Homo sapiens Interleukin 13 precursor (IL13) mRNA, complete cds.
ACCESSION AF043334
VERSION AF043334.1 GI:2905619
KEYWORDS human.
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 417)
AUTHORS Jang,J.S. and Kim,B.E.
TITLE Direct Submission

<hr/>					
ACCESSION	I58488				
VERSION	138488.1	GI:2477726			
KEYWORDS					
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 1297)				
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.				
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms				
JOURNAL	Patent: US 5652123-A 15 JAN-1997;				
FEATURES	Location/Qualifiers 1..1297				
source	/organism="unknown"				
BASE COUNT	309 a 341 c 336 g	311 t			
ORIGIN					
<hr/>					
Query Match	62.4%	Score 245.2;	DB 10;	Length 1297;	
Best Local Similarity	78.2%;	Pred. No. 5e-53;			
Matches	308; Conservative	0; Mismatches	83; Indels	3; Gaps	1;
<hr/>					
Qy	1 atgcgctgtgttgactggtagtcattgcctcaccgcctcgttggccttgccctcccgcg	60			
Db					
Db	57 ATGCGCGCTTTTGTGGACCAAGTGTCATTTGCTCTCATTGCCTTGGCGGCTTTGGCTCCGCCA	116			
Qy	61 agccctatgatccctcccccaacacctcaaggagctcattgaaggagctgggtcaaacatacc	120			
Db					
Db	117 GGCCCTGTGGCTCCCTCTACAGCCCTCAGGAGGCTCATTTAGGAGCTGGTCAACATCAC	176			
Qy	121 cagaatc---aggcatccctctgcaacggcagcagtgtgtgagcgtcaacctgaccgcc	177			
Db					
Db	177 CAGAACCAGAAAGGCTCCGCTCTGCAATGGCAGCATGTFATGGAGCATCAACTGACAGCT	236			
Qy	178 ggcatgtactgcgcagctctagaaatctctgatatcaatgtctccgactcagcggccatccaa	237			
Db					
Db	237 GACATGTACTGTGCAGCGCTTGAATCCCTCATCAACCTGTTCAGGCTGCAGTGCCTCGAG	296			
Qy	238 aggaccagaggatgctgaagacactgctctcaaaagccgcgcgaggaagatctcc	297			
Db					
Db	297 AAGACCCAGAGGATGCTTGAGCGGATCTTCGCCGCCACAAGGCTCAGCTGGGACGTTTTTC	356			
Qy	298 agtgaacgcgcgcgcagacacccaattgaagtatcagtttgtgaaaacacctgtctcac	357			
Db					
Db	357 AGCTTGATGTCGCAGACACCAANAATCAGGTGGCCAGCTTTGTAAAGGACCTGCTCTTA	416			
Qy	358 tatgtaggggagtttatccocatggaaattcca	391			
Db					
Db	417 CATTTAAAGAAACCTTTTCGCGAGGACGGTTCA	450			
<hr/>					
RESULT	8				
AF072807	LOCUS	343 bp	mRNA	MAM	21-JAN-2000
DEFINITION	Bos taurus interleukin-13 precursor (IL-13) mRNA, partial cds.				
ACCESSION	AF072807				
VERSION	AF072807.1	GI:4558813			
KEYWORDS					
SOURCE	cov.				
ORGANISM	Bos taurus				
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
AUTHORS	Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;				
TITLE	1 (bases 1 to 343)				
JOURNAL	Trigona,W.L., Brown,W.C. and Estes,D.M.				
MEDLINE	Functional implications for signaling via the IL4R/TL13R complex on bovine cells				
PUBMED	Vet. Immunol. Immunopathol. 72 (1-2), 73-79 (1999)				
REFERENCE	20080132				
AUTHORS	10614495				
TITLE	2 (bases 1 to 343)				
JOURNAL	Trigona,W.T., Hirano,A. and Estes,D.M.				
MEDLINE					
PUBMED					
REFERENCE					


```

Db 55 GCCTTCGCTGGCCCTGTGCTCCAGTACTCCCTCAGGAGCTCATTTGAGAGCTGGTC 114
Qy 112 aacatcaccagaaac---aggcatccctctgcaacgcagcagcagcagcagcagc 168
Db 115 AACATCACCAGAACAGAGGCTCCGCTCTGCAATGCGCAGCATGTTGAGGATCAAC 174
Qy 169 ctgaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 228
Db 175 CTGACAGCTGGCATGTACTGTGCGAGCCCTGGAATCCCTCAACGCTGTCAGGCTG 234
Qy 229 gcatcacaaggaccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgc 288
Db 235 GCATCAGAGAACCCAGAGATGCTGAGCGGATCTGCCCGCACAGGCTCTCAGCTGG 294
Qy 289 cagattccagtgaaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 348
Db 295 CAGTTTCCAGCTTGATGTGCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAG 354
Qy 349 ctgctcacctatgtaaggaggtttatcgccatggaatttca 391
Db 355 CTGCTCTTACATTTAAAGAACTTTTTCGCGAGGACGGTTCA 397

RESULT 14
LOCUS 186198 425 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5700665.
ACCESSION 186198
VERSION 186198.1 GI:3205916
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 425)
AUTHORS Legoux,R., Maldonado,P. and Salome,M.
TITLE Method for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: US 5700665-A 4 23-DEC-1997;
FEATURES
Location/Qualifiers
source 1..425
BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 51.5%; Score 202.2; DB 10; Length 425;
Best Local Similarity 76.4%; Pred. No. 6.7e-42;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy 52 gcctcccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 111
Db 55 GCCTTCGCTGGCCCTGTGCTCCAGTACTCCCTCAGGAGCTCATTTGAGAGCTGGTC 114
Qy 112 aacatcaccagaaac---aggcatccctctgcaacgcagcagcagcagcagcagc 168
Db 115 AACATCACCAGAACAGAGGCTCCGCTCTGCAATGCGCAGCATGTTGAGGATCAAC 174
Qy 169 ctgaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 228
Db 175 CTGACAGCTGGCATGTACTGTGCGAGCCCTGGAATCCCTCAACGCTGTCAGGCTG 234
Qy 229 gcatcacaaggaccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgc 288
Db 235 GCATCAGAGAACCCAGAGATGCTGAGCGGATCTGCCCGCACAGGCTCTCAGCTGG 294
Qy 289 cagattccagtgaaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 348
Db 295 CAGTTTCCAGCTTGATGTGCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAG 354
Qy 349 ctgctcacctatgtaaggaggtttatcgccatggaatttca 391
Db 355 CTGCTCTTACATTTAAAGAACTTTTTCGCGAGGACGGTTCA 397
```

```

RESULT 15
LOCUS A52326 4410 bp DNA PAT 12-DEC-1997
DEFINITION Sequence 1 from Patent EP0725140.
ACCESSION A52326
VERSION A52326.1 GI:2851987
KEYWORDS unidentified.
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE 1 (bases 1 to 4410)
AUTHORS Legoux,R., Maldonado,P. and Salome,M.
TITLE Process of extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
JOURNAL Patent: EP 0725140-A 1 07-AUG-1996;
COMMENT SANOFI SA (FR)
Other publication SK 10696 960904
Other publication CZ 9600290 960814
Other publication JP 8242879 960924
Other publication FI 960427 960801
Other publication PL 312543 960805
Other publication NO 960396 960801
Other publication FR 2729972 960802
Other publication CA 2168382 960801
Other publication AU 4224496 960808.
FEATURES
Location/Qualifiers
source 1..4410
/organism="unidentified"
/promoter 5'UTR 283..337
/mb_xref="taxon:32644"
misc_RNA 338..762
terminator /note="SEQUENCE DE LA REGION 5' NON TRADUITE DU MESSAGE"
terminator /note="SEQUENCE CODANT POUR LE PRECURSEUR DE L'IL-13"
terminator 813..1012
terminator /note="TERMINATEUR DU GENE 10 DU PHAGE T7"
misc_RNA 1013..1253
misc_RNA /note="TERMINATEUR DU PHAGE FD"
misc_RNA 1254..2505
misc_RNA /note="GENE CODANT POUR LE REPRESSEUR DE L'OPERON LACTOSE"
misc_RNA 2506..4410
BASE COUNT 1078 a 1142 c 1096 g 1094 t
ORIGIN

Query Match 51.5%; Score 202.2; DB 9; Length 4410;
Best Local Similarity 76.4%; Pred. No. 5.6e-42;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy 52 gcctcccccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 111
Db 392 GCCTTCGCTGGCCCTGTGCTCCAGTACTCCCTCAGGAGCTCATTTGAGGAGCTGGTC 451
Qy 112 aacatcaccagaaac---aggcatccctctgcaacgcagcagcagcagcagcagc 168
Db 452 AACATCACCAGAACAGAGGCTCCGCTCTGCAATGCGCAGCATGTTGAGGATCAAC 511
Qy 169 ctgaccgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 228
Db 512 CTGACAGCTGGCATGTACTGTGCGAGCCCTGGGAATCCCTGATCAACGCTGTCAG 571
Qy 229 gccatccaaaggaccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgc 288
Db 572 GCCATCGAGAGAACCCAGAGGATGTCGCGGATTTCTGCCCGCACAGGCTCTCAGCTGG 631
Qy 289 cagattccagtgaaacgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 348
Db 632 CAGTTTCCAGCTTGATGTGCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAG 691
```

Qy 349 ctgctcacctatgttaaggagggtttatcgccatggaaatttca 391
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 CTGCTTACATTTAAGAAACTTTTTTCGGAGGGACGGTTCA 734

Search completed: May 13, 2001, 14:20:33
Job time: 19113 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:29:52 ; Search time 472.02 Seconds
(without alignments)
486.052 Million cell updates/sec

Title: US-09-451-527-94
Perfect score: 393
Sequence: 1 atggcgctctgttgactgt.....atcgccatggaaatttcaga 393

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_0401.*
1: /cgnl_8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	393	100.0	393	21	Canine interleukin
2	393	100.0	393	21	Canine interleukin
3	393	100.0	1302	21	Canine interleukin
4	393	100.0	1302	21	Canine interleukin
5	377	95.9	390	21	Canine interleukin
6	377	95.9	390	21	Canine interleukin
7	377	95.9	1269	21	Canine interleukin
8	377	95.9	1269	21	Canine interleukin
9	333	84.7	333	21	Canine mature inte
10	333	84.7	333	21	Canine mature inte
11	317	80.7	330	21	Canine mature inte

C	12	317	80.7	330	21	255566	Canine mature inte
	13	278	70.7	278	21	255554	Canine interleukin
	14	272	69.2	272	21	255553	Canine interleukin
	15	246.8	62.8	1270	21	F21334	Human low adenosin
	16	246.8	62.8	1270	21	A35212	Human adenosine re
	17	246.8	62.8	1282	21	F21332	Human low adenosin
	18	246.8	62.8	1282	21	A35210	Human adenosine re
	19	246.8	62.8	1290	15	Q56692	Sequence encoding
	20	246.8	62.8	6952	21	F21333	Human low adenosin
	21	246.8	62.8	6952	21	A35211	Human adenosine re
	22	246.8	62.8	14978	21	F21338	Human low adenosin
	23	246.8	62.8	14978	21	A35216	Human adenosine re
	24	245.2	62.4	1297	13	Q28947	Cytokine NC30. Q
	25	203.4	51.8	336	13	Q28944	Gly41-Cytokine cod
	26	201.8	51.3	336	13	Q28943	Asp41-Cytokine cod
	27	159.2	40.5	1212	15	Q56693	Sequence encoding
	28	101.8	25.9	5670	21	F21331	Human low adenosin
	29	101.8	25.9	5670	21	F21337	Human low adenosin
	30	101.8	25.9	5670	21	A35209	Human adenosine re
	31	101.8	25.9	5670	21	A35215	Human adenosine re
	32	99	25.2	166	21	255552	Canine interleukin
	33	44.6	11.3	60	13	Q28942	Cytokine signal se
	34	44.6	11.3	102	13	Q28941	Cytokine signal se
	35	40.8	10.4	2460	11	Q06086	Plasmid p2PC13 enc
	36	37.2	9.5	66	20	232227	Human interleukin
	37	35.8	9.1	2249	18	T74283	Cellulose binding
	38	35.8	9.1	2300	18	T74282	Cellulose binding
	39	35.8	9.1	3187	17	T10922	Laccase gene. Myc
	40	35.8	9.1	3192	18	T72106	Myceliophthora the
	41	35.8	9.1	3192	18	T63318	Myceliophthora the
	42	35.8	9.1	3192	21	224236	M. thermophilla lac
	43	34.4	8.8	772	19	V48405	Dominant-negative
	44	34.4	8.8	1521	12	Q14388	Human neuronal nic
	45	34.4	8.8	2448	15	V12201	Human neuronal nic

ALIGNMENTS

RESULT 1
255557
ID 255557 standard; cDNA; 393 BP.
XX 255557;
XX
XX 14-MAR-2000 (first entry)
XX Canine interleukin-13 (IL-13) clone 80 cDNA coding region.
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
XX P-PSDB; Y58221.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 232-233; 264pp; English.

CC Sequences Z5552-Z5560 and Z55561-Z55566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80-
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD134 (CD40ligand), canine IL-5, canine IL-13, feline

CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
XX Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;

Query Match 100.0%; Score 393; DB 21; Length 1302;
Best Local Similarity 100.0%; Pred. No. 4.9e-103;
Matches 393; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 atggcgctgtgtgactgtggtcattgctctcaccctgctcgtggtgcttgcctcccg 60
DB 1251 ATGGCGCTGTGTTGACTGTGTTGCTATTGCTCTCACTGCCCTGCGTGGCTTGCCTCCCG 1192
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgaaggagctggtcaacatcacc 120
DB 1191 AGCCCTGTGACTCCCTCCCAACCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 1132
QY 121 cagaatcaggcaccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcgcgc 180
DB 1131 CAGAAATCAGGATCCCTCTGCAACGGCAGCATGTGTGGAGCGTCAACCTGACCGCGGC 1072
QY 181 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
DB 1071 ATGTACTGCGGAGCTCTAGAAATCTCTGATCAATCTCTCCGACTGCAGCGCCATCCAAAGG 1012
QY 241 acccagagagctgaaagcactgtgctctcaaaagccgcgcgcagggcagatttccagt 300
DB 1011 ACCCAGAGGATGTCGAAAGCACTGTCTCTCAAAAGCCCGCGGAGGCGAGATTTCCAGT 952
QY 301 gaacgcagcgagacacacaaatgaagtgtatccagttggtgaaacacctgtcacctat 360
DB 951 GAGCGAGCGGAGACACCAAAATGAAGTGTATCCAGTTGGTGAACCTCTCACCTAT 892
QY 361 gtaaggaggatttatcgccatggaatttcaga 393
DB 891 GTAAGGGGAGTTTATCGCCATGGAAATTTTCAGA 859

RESULT 5
Z55563
ID Z55563 standard; cDNA; 390 BP.
XX
XX Z55563;
AC
XX
XX 14-MAR-2000 (first entry)
DT
XX
XX Canine interleukin-13 (IL-13) clone 78 cDNA coding region.
DE
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
KW
XX
XX Canis familiaris.
OS
XX
XX WO961618-A2.
PN
XX
XX 02-DEC-1999.
PD
XX
XX 28-MAY-1999; 99WO-US11942.
PF
XX
XX

PR 29-MAY-1998; 98US-0087306.
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR P-PSDB:Y58223.
DR
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
PS Claim 1i; Page 238-239; 264pp; English.
XX
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
XX Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match 95.9%; Score 377; DB 21; Length 390;
Best Local Similarity 99.2%; Pred. No. 1.2e-98;
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 atggcgctgtgtgactgtggtcattgctctcaccctgctcgtggtgcttgcctcccg 60
DB 1 atggcgctgtgtgactgtggtcattgctctcaccctgctcgtggtgcttgcctcccg 60
QY 61 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 120
DB 61 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 120
QY 121 cagaatcaggcaccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcgcgc 180
DB 121 cagaatcaggcaccctctgcaacggcagcatggtgtggagcgtcaacctgaccgcgcgc 180
QY 181 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
DB 181 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaagg 240
QY 241 acccagagagctgaaagcactgtgctctcaaaagccgcgcgcagggcagatttccagt 300
DB 241 acccagagagctgaaagcactgtgctctcaaaagccgcgcgcagggcagatttccagt 297
QY 301 gaacgcagcgagacacacaaatgaagtgtatccagttggtgaaacacctgtcacctat 360
DB 298 gaacgcagcgagacacacaaatgaagtgtatccagttggtgaaacacctgtcacctat 357
QY 361 gtaaggaggatttatcgccatggaatttcaga 393
DB 358 gtaaggaggatttatcgccatggaatttcaga 390
RESULT 6
Z55564/c

ID 255564 standard; cDNA; 390 BP.
 XX 255564;
 XX 14-MAR-2000 (first entry)
 DT Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.
 DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 OS Canis familiaris.
 XX WO9961618-A2.
 XX 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US11942.
 XX 29-MAY-1998; 98US-0087306.
 XX (HESK-) HESKA CORP.
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 PI WPI: 2000-072623/06.
 DR P-PSDB; Y58223.
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX Claim 1i; Page 239; 264pp; English.
 XX Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 95.9%; Score 377; DB 21; Length 390;
 Best Local Similarity 99.2%; Pred. No. 1.2e-98;
 Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 Qy 1 atggcgctgtgactgtgctcattgtctcactcgtcgtggtgctgctccccc 60
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||
 390 ATGGCGCTGTGACTGTGCTCATTGTCTCACCCTGCTCGTGGCTGCTCCCG 331
 Qy 61 accctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatacc 120
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||
 330 ACCCTGTGACTCCCTCCCAACCCCTCAAGAGCTCATTGAGAGCTGTCACATCACC 271
 Qy 121 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 180
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||
 270 CAGATCAGGCATCCCTCTGCAACGGCAGCATGCTGTGGAGCGTCAACCTGACCGCGGC 211

Qy 181 atgtactgcgagctctagaaatctctgatcaatgtctccgactcagcgccatccaaagg 240
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||
 210 ATGTACTGCGGAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCGGCCATCCAAAGG 151
 Qy 241 acccagagatgctgaaagcactgtctctcaaaagccgcgagggcagagatttccagt 300
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||
 150 ACCCAGAGGATGCTCAAGACACTGTGCTCTCAAAAGCCCGCGGCAGG---GATTTCCACT 94
 Qy 301 gaacgcagcagcagacacacaaatgaagtgcattgagttggtagaaacctgctacccat 360
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||
 93 GAACGCAGCCGAGACACCAAAATGAAGTATCCAGTTGGTGAAAGACCTGCTCCTAT 34
 Qy 361 gtaaggaggatttatcgccatgaaatttcaga 393
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||
 33 GTAAGGGGAGTTTATGCCCATGGAAATTTTCAGA 1
 RESULT 7
 Z55561
 ID 255561 standard; cDNA; 1269 BP.
 XX 255561;
 XX 14-MAR-2000 (first entry)
 DT Canine interleukin-13 (IL-13) clone 78 cDNA.
 DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX Canis familiaris.
 XX Key Location/Qualifiers
 FH CDS 57..449
 FT /*tag= a
 FT /product= "Canine IL-13 clone 78"
 XX WO9961618-A2.
 XX 02-DEC-1999.
 XX 28-MAY-1999; 99WO-US11942.
 XX 29-MAY-1998; 98US-0087306.
 XX (HESK-) HESKA CORP.
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WPI: 2000-072623/06.
 DR P-PSDB; Y58223.
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX Claim 1i; Page 235-236; 264pp; English.
 XX Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

QY 121 cagaatcaggcatcctctcaagcagcagcatggtgtggagcgtcaacctgaccgcccgc 180
 Db 273 CAGAATCAGGCATCCCTCTCAACGCGCAGCATGCTGTGGAGCGTCAACCTGACCGCCGGC 214
 QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacatccaaagg 240
 Db 213 ATGTACTGCCACTCTAGAAATCTCTGATCAATGTCTCCGACTGCACGCGCATCCAAAGG 154
 QY 241 accagagagatgctgaagcactgtgctctcaaaagcccgccgagcgcagatttccagt 300
 Db 153 ACCAGAGGATGCTGAAAGCACGTGCTCTCAAAAGCCGCGCAGGCAGATTTCCAGT 94
 QY 301 gaacgagcgcagacacccaaatgaagtatccagtgtgtgaaaaacctgctcacctat 360
 Db 93 GAACGCGCCGAGACACCAAAATGAAGTATCCAGTTGGTGTGAAAAACCTGCTCACCTAT 34
 QY 361 gtaaggaggagttatgccatgaaatttcaga 393
 Db 33 GTAAGGGAGATTATCCCATGGAATTTTCAGA 1
 RESULT 11
 ID 255565 standard; cDNA; 330 BP.
 AC 255565;
 XX
 DT 14-MAR-2000 (first entry)
 DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 DR WPI; 2000-072623/06.
 DR P-PSDB; Y58224.
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PS Claim 11; Page 239-240; 264pp; English.
 XX
 CC Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte-macrophage
 CC colony-stimulating factor (CM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;
 Query Match 80.7%; Score 317; DB 21; Length 330;
 Best Local Similarity 99.1%; Pred. No. 1.7e-81;
 Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 QY 61 agccctgtgactccctcccccaccctcaaggagctcattgagagctggtcaacatcac 120
 Db 1 agccctgtgactccctcccccaccctcaaggagctcattgagagctggtcaacatcac 60
 QY 121 cagaatcaggcatcctctcaagcagcagcatggtgtggagcgtcaacctgaccgcccgc 180
 Db 61 cagaatcaggcatcctctcaagcagcagcatggtgtggagcgtcaacctgaccgcccgc 120
 QY 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacatccaaagg 240
 Db 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacatccaaagg 180
 QY 241 accagagagatgctgaagcactgtgctctcaaaagcccgccgagcgcagatttccagt 300
 Db 181 accagagagatgctgaagcactgtgctctcaaaagcccgccgagcgcagatttccagt 237
 QY 301 gaacgagcgcagacacccaaatgaagtatccagtgtgtgaaaaacctgctcacctat 360
 Db 238 gaacgagcgcagacacccaaatgaagtatccagtgtgtgaaaaacctgctcacctat 297
 QY 361 gtaaggaggagttatgccatgaaatttcaga 393
 Db 298 gtaaggaggagttatgccatgaaatttcaga 330
 RESULT 12
 ID 255566/C
 ID 255566 standard; cDNA; 330 BP.
 AC 255566;
 XX
 DT 14-MAR-2000 (first entry)
 DE Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 DR WPI; 2000-072623/06.
 DR P-PSDB; Y58224.
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PS Claim 11; Page 241; 264pp; English.
 XX
 CC Sequences 255552-255560 and 255561-255566 represent cDNA

immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

Canis familiaris.

WO9961618-A2.

28-DEC-1999.

28-MAY-1999; 99WO-US11942.

29-MAY-1998; 98US-0087306.

(HESK-) HESKA CORP.

Sim G, Yang S, Drelitz MJ, Wonderling RS;

WPI; 2000-072623/06.

Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease -

Claim 11; Page 228; 264pp; English.

Sequences 25552-25560 and 25561-25566 represent cDNA sequences encoding canine interleukin-13 (IL-13) clones 80 and 78 respectively. The invention relates to canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline interferon-alpha (IFN-alpha) and feline granulocyte macrophage colony-stimulating factor (GM-CSF), and nucleotides which encode these immunoregulatory proteins. The proteins, their associated nucleic acids, specific antibodies and inhibitors may be used as vaccines for therapeutic or prophylactic regulation of an immune response in animals (particularly cats, dogs, horses and humans). They may be used to treat autoimmune or infectious diseases including allergies, tumours, inflammation and graft rejection, and to increase the response from a co-administered antigen. The nucleotide sequences can also be used for the recombinant production of a protein, while nucleotide fragments are useful as probes, as amplification primers and as sources of inhibitory therapeutics (e.g., antisense oligonucleotides). The proteins may be used to raise antibodies and to screen for modulators of activity, while the antibodies may be used in detection, and in drug targeting.

Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;

Query Match 69.2%; Score 272; DB 21; Length 272;
 Best Local Similarity 100.0%; Pred. No. 1.2e-68;
 Matches 272; Conservative 0; Mismatches 0; Indels 0; Gaps 0

45 tggccttgctcccgagccgtgtgactccctccccaacccctcaaggagctcattgagga 104
 Db 1 tggccttgctcccgagccgtgtgactccctccccaacccctcaaggagctcattgagga 60

105 gctggtcaacatcaccagaatcagatccctctgcaacgcagcatggtgtgagcgt 164
 Db 61 gctggtcaacatcaccagaatcaggaaccctctgcaacgcagcatggtgtgagcgt 120

165 caacctgaccgcgcgatgtactgcgcagctctagaaatctgataatgtctccgactg 224
 Db 121 caacctgaccgcgcgatgtactgcgcagctctagaaatctgataatgtctccgactg 180

225 cagcgccatcgaagaccagaggatgctgaaagcactgtgctcctcaaaagccgcggc 284
 Db 181 cagcgccatcgaagaccagaggatgctgaaagcactgtgctcctcaaaagccgcggc 240

285 agggcagatttcagtgaaacgacgcgcgagaca 316
 Db 241 agggcagatttcagtgaaacgacgcgcgagaca 272

RESULT 15

SQ Sequence 1270 BP; 288 A; 335 C; 336 G; 311 T; 0 other;

Query Match 62.8%; Score 246.8; DB 21; Length 1270;
 Best Local Similarity 78.4%; Pred. No. 3.2e-61;
 Matches 309; Conservative 0; Mismatches 82; Indels 3; Gaps 1;

Qy	1	atggcgctctggtgactggtgctctcactcctcggtggtgcttgcctcccg	60
Db	45	atggcgcttctggtgaccacggtcctcactcctccttggcgcttgcctccca	104
Qy	61	agccctgtgactccctcccccacccctcaaggagctcattgagagctggtcaacatcacc	120
Db	105	ggccctgtgctccctctacagccctcagggagctcattgagagctggtcaacatcacc	164
Qy	121	cagaatc---aggaatccctctgcaacggcagcatggtgagcggtcaacctgaccgcc	177
Db	165	cagaaccgagaggtccgctcctgcaatggcagcatggtatggagcatcaacctgacagct	224
Qy	178	ggcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa	237
Db	225	ggcatgtactgtgcagccctggaatccctgatcaacgtgtcaggtgcagtgccatcgag	284
Qy	238	aggaccagaggtgctgaaagcactgtgctctcaaaagcccgccgagggcagatttcc	297
Db	285	aagaccagaggtgctgagcggtattctgcccgcacaaaggtctcagctgggcagtttcc	344
Qy	298	agtgaacgcagccgagacacccaaattgaagtgatccagtgtgtaaaaaacctgctcacc	357
Db	345	agcttgcatgtccgagacacccaaatcgaggtggcccagtttgttaaaaggacctgctctta	404
Qy	358	tatgtaaggaggtttatcgccatggaatttca	391
Db	405	catttaagaaacttttcgcgaggagcggttca	438

Search completed: May 13, 2001, 14:29:54
 Job time: 18309 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:14 ; Search time 226.02 Seconds
(without alignments)
303.596 Million cell updates/sec

Title: US-09-451-527-94

Perfect score: 393
Sequence: 1 atggcgctgtgtgactgt.....atgccatgggaatttcaga 393

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq.*
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq.*
3: /cgnl_7/ptodata/1/ina/6A_COMB.seq.*
4: /cgnl_7/ptodata/1/ina/6B_COMB.seq.*
5: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	246.8	62.8	1290	1	US-08-012-543-1
2	246.8	62.8	1290	5	PCT-US93-07645A-1
3	246.8	62.8	1290	5	PCT-US93-07645-1
4	245.2	62.4	1297	1	US-08-371-121-15
5	204	51.9	384	1	US-08-371-121-17
6	203.4	51.8	336	1	US-08-371-121-17
7	202.2	51.5	425	1	US-08-594-469-4
8	202.2	51.5	425	2	US-08-906-957-4
9	202.2	51.5	4410	1	US-08-594-469-1
10	202.2	51.5	4410	2	US-08-906-957-1
11	201.8	51.3	336	1	US-08-371-121-2
12	159.2	40.5	447	1	US-08-371-121-26
13	159.2	40.5	1212	1	US-08-012-543-3
14	159.2	40.5	1212	5	PCT-US93-07645A-3
15	159.2	40.5	1212	5	PCT-US93-07645-3
16	144.6	11.3	60	1	US-08-371-121-12
17	144.6	11.3	102	1	US-08-371-121-10
18	39.6	10.1	54	1	US-08-371-121-11
19	39.6	10.1	96	1	US-08-371-121-9
20	35.8	9.1	2249	3	US-08-814-052-19
21	35.8	9.1	2300	3	US-08-814-052-18
22	35.8	9.1	3183	2	US-08-939-218A-1
23	35.8	9.1	3187	5	PCT-US95-06815-1
24	35.8	9.1	3192	1	US-08-706-037-26
25	35.8	9.1	3192	1	US-08-940-661A-1
26	35.8	9.1	3192	2	US-09-083-485-1
27	35.8	9.1	3192	2	US-09-003-397-26

28 34.4 8.8 1322 4 US-09-128-450-27
29 34.4 8.8 1521 1 US-08-496-855A-3
30 34.4 8.8 1521 2 US-07-938-154-9
31 34.4 8.8 1521 5 PCT-US91-02311-9
32 34.4 8.8 2450 2 US-08-466-589-9
33 34.4 8.8 2450 2 US-08-700-636-9
34 34.4 8.8 2450 3 US-08-467-574-9
35 33.2 8.4 2712 3 US-09-025-691-4
36 32.4 8.2 720 4 US-09-094-359-3
37 32.4 8.2 720 4 US-09-094-359-7
38 32.4 8.2 720 4 US-09-172-063-11
39 32.4 8.2 720 4 US-09-172-063-13
40 32.4 8.2 762 1 US-08-532-390-40
41 32.4 8.2 762 4 US-08-717-294-40
42 32.4 8.2 768 4 US-09-094-359-11
43 32.4 8.2 850 4 US-09-062-102-2
44 32.4 8.2 972 4 US-09-172-063-27
45 32.4 8.2 972 4 US-09-172-063-29

ALIGNMENTS

RESULT 1
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Bancheureau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: Human Interleukin-13
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,543
FILING DATE: 01-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933,416
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0302K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA

QY 61 agcctgtgaatccctcccaacccctcaagagctcattgaggagctggtcaacatcacc 120
Db 105 GGCCTGTGCTCCCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACC 164
QY 121 cagaatc---aggatccctctgaacggcagcattggtgagcggtcaacccgaccgcc 177
Db 165 CAGAACAGAAAGGCTCCCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224
QY 178 ggcgtgactgcagctctgaatctctgatcaatgtctccgactcagcgccatccaa 237
Db 225 GGCATGTACTGTGAGCCCTGGAATCCCTGATCAACGTGTACGGCTGAGTCCCATCGAG 284
QY 238 aggaccagagagtgctgaagacactgtctctcaaaagccgcggcagggcagatttcc 297
Db 285 AAGACCAGAGAGATGCTGAGCGGATTTGCCCGCACAGGTCTCAGCTGGGAGTTTCC 344
QY 298 agtgaacgagcagcagacacacaaattgaagtgtatccagttggtgaaacacgtctcacc 357
Db 345 AGCTTGATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTA 404
QY 358 tatataagggagtttatcgccatggaatttca 391
Db 405 CATTTAAGAAACTTTTTCGGGAGGACGGTTCA 438

RESULT 4

US-08-371-121-15
; Sequence 15, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136

INFORMATION FOR SEQ ID NO: 15:

SEQUENCE CHARACTERISTICS:

LENGTH: 1297 base pairs

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: cDNA

FEATURE:

NAME/KEY: CDS

LOCATION: 15..452

FEATURE: mat_peptide

LOCATION: 117..452

US-08-371-121-15

Query Match 62.4%; Score 245.2; DB 1; Length 1297;
Best Local Similarity 78.2%; Pred. No. 3.7e-66;
Matches 308; Conservative 0; Mismatches 83; Indels 3; Gaps 1;

QY 1 atggcgctctgtgactgtgtcattgtctcaccctgcctcggtggcctgctcccg 60
Db 57 ATGGCGCTTTGTGACCAACGGTCAATGCTCTCACTTGGCTTGGCGCTTGGCCTCCCA 116
QY 61 agcctgtgactccctcccaacccctcaagagctcattgaggagctggtcaacatcacc 120
Db 117 GGCCTGTGCTCCCTACAGCCCTCAGGGAGCTCATTGAGGAGCTGGTCAACATCACC 176
QY 121 cagaatc---aggatccctctgaacggcagcattggtgagcggtcaacccgaccgcc 177
Db 177 CAGAACAGAAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 236
QY 178 ggcgtgactgcagctctgataatctctgataatctctcagactcagcgccatccaa 237
Db 237 GACATGTACTGTGACGCCCTGGAATCCCTGATCAACGTGTCAAGCTCAGTGGCATCGAG 296
QY 238 aggaccagagagctgtaaacacactgtctcctcaaaagccgcggcagcgagatttcc 297
Db 297 AAGACCCAGAGGATGCTGACGGATTTCTGCCCGCACAAAGGTCTCAGCTGGCAGTTTCC 356
QY 298 agtgaacgagcagcagacacacaaattgaagtgtatccagttggtgaaacacgtctcacc 357
Db 357 AGCTTGATGTCCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTA 416
QY 358 tatgtaagggagtttatcgccatggaatttca 391
Db 417 CATTTAAGAAACTTTTTCGGGAGGACGGTTCA 450

RESULT 5

US-08-371-121-17
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500

CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE: 27-MAR-1992
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
APPLICATION DATA: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match 51.9%; Score 204; DB 1; Length 384;
Best Local Similarity 77.1%; Pred. No. 1e-53;
Matches 262; Conservative 0; Mismatches 75; Indels 3; Gaps 1;
QY 55 tccccaagccctgtgactccctcccaaccctcaaggagctcattgaggagctggtcaac 114
Db 16 TCCCCAGGCCCTGTGCTCCCTCTACGGCCCTCAGGGAGCTCATTTAGGAGCTGGTCAAC 75
QY 115 ataccacagaatc---aggcatccctctgcaacggcagcatggtgtgagcgtaacctg 171
Db 76 ATACCAGAACAGAGGCTCGCTCTGCAATGGCAGCATGTTATGGAGCATCAACCTG 135
QY 172 accgcggcgtactgctgcagctctagaaatctctgtatcaatgtctccgactgcagcgcc 231
Db 136 ACAGCTGACATGTACTGTGCAGCCCTGGAATCCTGTATCAAGCTGTGAGCTGCAGTGC 195
QY 232 atccaaagaccagagagatgctgaaagcactgtctctcaaaagcccgaggagcag 291
Db 196 ATCCAGAAAGACCCAGAGGATGCTGAGCGGATTTCTGCCCGACAAAGTCTCAGCTGGCAG 255
QY 292 atttcagtgaaagcagcagcagacacaaatgaaagtgtaccagttggtgaaaaactg 351
Db 256 TTTTCCAGCTTGATGTCGAGACACCAAAATCGAGTGGCCCAAGTTGTAAGGACCTG 315
QY 352 ctcaacctgtgaaggaggtttatccgcatggaaattca 391
Db 316 CTCTTACATTTAAAGAAACTTTTTCGGAGGAGCGGTCA 355

RESULT 6

US-08-371-121-24

; Sequence 24, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLIER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; NUMBER OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-371-121-24

Query Match 51.8%; Score 203.4; DB 1; Length 336;
Best Local Similarity 77.8%; Pred. No. 1.5e-53;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;
QY 62 gccctgtgactccctcccaaccctcaaggagctcaattgaggagctggtcaacatcaacc 121
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCATTTAGGAGCTGGTCAACATCACCC 61
QY 122 agaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgacgcgcg 178
Db 62 AGAACAGAGGCTCCGCTCTGCAATGCGAGCATGGTATGGTATGGTATGGTATGGTATGG 121
QY 179 gcatgtactgcgcagctctctagaatctctgatcaatgtctccgactgcagcgccatccaa 238

Db 122 GCATGTACTGTGAGCCCTGGAATCCTGATCAACGTGTGAGGCTGCAGTGCATCGACA 181
Qy 239 gaccagaggtgctgaagcactgtgtctcaaaagccggcaggcagatttcca 298
Db 182 AGACCCAGAGGAGTGTGAGCGGATTCTGCCCGCAACAAGTCTCAGCTGGCGAGTTTCCA 241
Qy 299 gfgaacgagccgagacacacacaaattgaagtgtatccagtgtgtgaaaaacccctgcacct 358
Db 242 GCTTCATGTCGAGACACACAAATCGAGTGGCCAGTTGTAAAGGACCTGCTCTTAC 301
Qy 359 atgaagggagtttatccatccatggaatttcca 391
Db 302 ATTTAAGAAACTTTTTCGAGGGAGCGGTCA 334
RESULT 7
US-08-594-469-4
; Sequence 4, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-4

Query Match 51.5%; Score 202.2; DB 1; Length 425;
Best Local Similarity 76.4%; Pred. No. 3.9e-53;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

Qy 52 gctcccgagccctgtgactccctcccaaccccaagagctcattgaggagctggctc 111
Db 55 GCCTTCGCTGGCCCTGTGCTCCCACTACTGCTCAGGAGGCTCATTTGAGGAGCTGGTC 114
Qy 112 aacatcacccagaatc---aggatccctctgtcaacggcagcatggtgtggagcgtcaac 168

Db 115 AACATCCCCAGAACCCAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGGAGCATCAAC 174
Qy 169 ctgaccgccgactgtactgtcgagctctagaatctctgataatgtctccgactgcagc 228
Db 175 CTGACAGTGCATGTACTGTGCGAGCCCTGGAATCCCTGTATCAAGCTGTTCAGGCTGCAGT 234
Qy 229 gccatcaaaagccagagatgataaagcactgtctctcaaaagcccgaggcaggg 288
Db 235 GCCATCCAGAAAGCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGG 294
Qy 289 cagattccagtgaaagcagcgagacacacaaattgaagtgtatccagtgtgtgaaaaac 348
Db 295 CAGTTTTCCAGCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGAC 354
Qy 349 ctgctcacctatgtaaggggagtttatccatccatggaatttcca 391
Db 355 CTGCTCTTACATTTAAAGAAACTTTTTCGCGAGGGAGCGGTCA 397
RESULT 8
US-08-906-957-4
; Sequence 4, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-4

Query Match 51.5%; Score 202.2; DB 2; Length 425;
Best Local Similarity 76.4%; Pred. No. 3.9e-53;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 52 gctcccccagagccctgtgactccctcccccacccctcaaggagctcattgagagctgctc 111
Db 55 GCCTTCGCTGGCCCTGTGCTCCAGTACTCCCTCAGGGAGCTCAATTGAGAGCTGGTC 114
QY 112 aacatccaccagaaatc---aggcaccctctgcaacgcagacatggtgtgagagctcaac 168
Db 115 AACATCACCCAGAACAGAGAGCTCCCGCTCTGCAATGCGACATGGTATGAGAGCATCAAC 174
QY 169 ctgaccgccggcatgtactgcgcagctctagaatctctgtatcaatgtctccgactgcagc 228
Db 175 CTGACAGCTGGCATGTACTGTGACAGCCCTGGAATCCCTGATCAACGTCTCAGCTGCACT 234
QY 229 gccatccaaaggacccagagatgctgaaagcactgtgctctcaaaagccgcgcaggg 288
Db 235 GCCATCGAGAAGACCCAGAGATGCTGAGCGGATTTGCCCGCACAAAGGTCTCAGCTGGG 294
QY 289 cagattccagtgaaacgcagccagacacacaaattgaagtgtccagttgtaaaaaac 348
Db 295 CAGTTTTTCCAGCTTGCAATGCTCGAGACACCAAAATCGAGGTGGCCCAAGTTGTAAAGGAC 354
QY 349 ctgctccacctatgaaggagggtttatcgccatggaatttca 391
Db 355 CTGCTCTTACATTTAAAGAAACTTTTTCGGCGAGGACGGTTCA 397

RESULT 9

US-08-594-469-1
; Sequence 1, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-1080
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-1

Query Match 51.5%; Score 202.2; DB 1; Length 4410;
Best Local Similarity 76.4%; Pred. No. 9.1e-53;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;
QY 52 gctcccccagagccctgtgactccctcccccacccctcaaggagctcattgagagctgctc 111
Db 392 GCCTTCGCTGGCCCTGTGCTCCAGTACTCCCTCAGGGAGCTCAATTGAGAGCTGGTC 451
QY 112 aacatccaccagaaatc---aggcaccctctgcaacgcagacatggtgtgagagctcaac 168
Db 452 AACATCACCCAGAACAGAGAGCTCCCGCTCTGCAATGCGACATGGTATGAGAGCATCAAC 511
QY 169 ctgaccgccggcatgtactgcgcagctctagaatctctgtatcaatgtctccgactgcagc 228
Db 512 CTGACAGCTGGCATGTACTGTGACAGCCCTGGAATCCCTGATCAACGTCTCAGCTGCACT 571
QY 229 gccatccaaaggacccagagatgctgaaagcactgtgctctcaaaagccgcgcaggg 288
Db 572 GCCATCGAGAAGACCCAGAGATGCTGAGCGGATTTGCCCGCACAAAGGTCTCAGCTGGG 631
QY 289 cagattccagtgaaacgcagccagacacacaaattgaagtgtccagttgtaaaaaac 348
Db 632 CAGTTTTTCCAGCTTGCAATGCTCGAGACACCAAAATCGAGGTGGCCCAAGTTGTAAAGGAC 691
QY 349 ctgctccacctatgaaggagggtttatcgccatggaatttca 391
Db 692 CTGCTCTTACATTTAAAGAAACTTTTTCGGCGAGGACGGTTCA 734

RESULT 10

US-08-906-957-1
; Sequence 1, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs

```

; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-1

Query Match          51.5%; Score 202.2; DB 2; Length 4410;
Best Local Similarity 76.4%; Pred. No. 9.1e-53;
Matches 262; Conservative 0; Mismatches 78; Indels 3; Gaps 1;

QY 52 gctcccgagccgtgactccctcccaaccctcaaggagctcattgagagctgggtc 111
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 392 GCCTTCGCTGGCCCTGCTGCCAGTACTGCCCTCAGGAGCTCATTTGAGGAGCTGGTC 451

QY 112 aacatccccagaatc---aggcatccctctgcaacgagcagcatggtgagcgtcaac 168
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 452 AACATCACCAGACAGCAAGGCTCGCTCTGCAATGGCAGCATGTTATGAGGAGCATCAAC 511

QY 169 ctgaccgcggcatgtactgcagctctagatctctgataatgtctccgactcagc 228
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 512 CTGACGCTGGCATGTACTGTGTCGCCCTCGAATCCCTGATCAACGTGTGACGGCTGCAGT 571

QY 229 gccatccaaagaccagaggtgtgaaagcactgtctctcaaaagccgcgcaggg 288
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 572 GCCATCGAAGACACCAGAGGATGTGACGGATTTCTGCCCGCACAAAGTCTCAGCTGGG 631

QY 289 cagattccagtgaaagcgcagcagacacacacaaattgaagtgtatccagttggtgaaaac 348
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 632 CAGTTTTCAGCTTGCATGTCCGAGACACCAAAATCGAGTGCCCGCAGTTGTGTAAGGAC 691

QY 349 ctgctcaactatgtgaagggagtttatgcctatggaatttca 391
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 CTGCTCTTACATTAAAGAAACTTTTTCGCGAGGGACGGTTCA 734

RESULT 11
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
```

```

; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match          51.3%; Score 201.8; DB 1; Length 336;
Best Local Similarity 77.5%; Pred. No. 4.7e-53;
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 62 gcctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcaacc 121
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGGAGCTCAITTGAGGAGTGGTCAACATCACCC 61

QY 122 agaatc---aggcatccctctgcaacgagcagcatggtgagcgtcaacctgacgcgcg 178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 62 AGAACAGAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGAGAGCATCAACCTGACAGTG 121

QY 179 gcattgactgcgcagctctagaatctctgataatgtctccgactgcagcgccatccaaa 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 122 ACATGTACTGTGAGCCCTGGAATCCCTGTATCAAGGTGTGAGGTGTCAGTGCATCGAGA 181

QY 239 ggaccagagagatgctgaaagcactgtgtctctcaaaagccgcgcagggagattcca 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 182 AGACCCAGAGAGTGTGAGCGGATTTCTCCCGCACAAAGTCTCAGCTGGGCAAGTTTCCA 241

QY 299 gtgaacgcagccgagacacacaaattgaagtgtatccagttgtagaaacctgctcacct 358
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCCGCTTTGTAAGAGGACCTGCTTAC 301

QY 359 atgaaggaggagtttatcgccatggaatttca 391
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 302 ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA 334

RESULT 12
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
```

```

; REFERENCE/DOCKREI NUMBER:   DA0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; FAX: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 70..465
; US-08-012-543-3
;
; Query Match          40.5%; Score 159.2; DB 1; Length 1212;
; Best Local Similarity 66.7%; Pred. No. 9e-40;
; Matches 268; Conservative 0; Mismatches 113; Indels 21; Gaps
;
; Qy 1 atgcgcctctgttgactgtggtcattgctctcaccctgcctcggtagcctgcctccccg 60
;   |||||
; Db 70 ATGGCGCTCTGGGTGACTGTCAGTCTGCTGCTTGGCTTGGTGGTCTCGCGCCCA 129
;
; Qy 61 agcc-----ctgtgactccctcccaaccctcaaggactcattgagagactg 108
;   |
; Db 130 GGGCGGTGGCCAAATCTGTCTCTCCCTTGACCCCTTAAGGAGCTTATTGAGGAGCTG 189
;
; Qy 109 gtcaacatcaccccgaaatcaggcatccctctgcacggcagcattggtgagagctcac 168
;   |||||

```

```
Db 190 AGCAACATCACAAAGACCAGACTCCCTGTGCAACGGCAGCATGTTGAGTGTGGAC 249
Qy 169 ctgaccgcggcatctactgcagctctagaaatctctgatcaatgtctccgactgcagc 228
Db 250 CTGGCCGCTGGCGGTTTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAAATTGCAAT 309
Qy 229 gccatccaaagaccagagatgctgaaagcactgtgctctcaaaagcccgcgaggg 288
Db 310 GCCATCTACAGACCACAGGATATGTGATGGCCCTGTGTAAACCGCAAGGCC----- 360
Qy 289 cagatttccagtgaacgcagccagagacacccaaaaattgaagtgtatccagttggtgaaaaac 348
Db 361 CCCACTACGGTCTCCAGCCTCCCGGATACCAAAATCGAAGTAGGCCACATTATATACAAAA 420
Qy 349 ctgctcaactatgtaagggagtttatcgccatggaatttc 390
Db 421 CTGCTCAGCTACAAAGCAACTGTTTCGCCACGGCCCCCTTC 462

RESULT 14
PCT-US93-07645A-3
; Sequence 3, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-3

Query Match 40.5%; Score 159.2; DB 5; Length 1212;
Best Local Similarity 66.7%; Pred. No. 9e-40;
Matches 268; Conservative 0; Mismatches 113; Indels 21; Gaps 2;
Qy 1 atggcgctgtgtgactgtgtgctcactgtcctcactgcctcggtgacctgctccccc 60
Db 70 ATGGCGCTCTGGGTGACTGCGACTCTGCTCTGCTTGGCTTGGTGTCTCGCCGCCCA 129
Qy 61 agcc-----ctgtgactccctcccaacccctcaaggagctcattgagagctg 108
Db 130 GGGCCGGTGCCAAAGATCTGTGTCTCTCCCTGTGACCTTAAGGAGCTTATTGAGGAGCTG 189
Qy 109 gtaacatcacccagaatacctcctctgcaacggcagcatggtgtggagcgtcaac 168
Db 190 AGCAACATCACAAAGACCAGACTCCCTGTGCAACGGCAGCATGTTGAGTGTGGAC 249
Qy 169 ctgaccgcggcatctactgcagctctagaatctctgatcaatgtctccgactgcagc 228
Db 250 CTGGCCGCTGGCGGTTTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAAATTGCAAT 309
Qy 229 gccatccaaagaccagagatgctgaaagcactgtgctctcaaaagcccgcgaggg 288
Db 310 GCCATCTACAGACCACAGGATATGTGATGGCCCTGTGTAAACCGCAAGGCC----- 360
Qy 289 cagatttccagtgaacgcagccagagacacccaaaaattgaagtgtatccagttggtgaaaaac 348
Db 361 CCCACTACGGTCTCCAGCCTCCCGGATACCAAAATCGAAGTAGGCCACATTATATACAAAA 420
Qy 349 ctgctcaactatgtaagggagtttatcgccatggaatttc 390
Db 421 CTGCTCAGCTACAAAGCAACTGTTTCGCCACGGCCCCCTTC 462
```

```
Db 310 GCATCTACAGGCCAGAGGATATTGCATGGCCTCTGTAAACCGCAAGGCC----- 360
Qy 289 cagatttccagtgaacgcagccagagacacccaaaaattgaagtgtatccagttggtgaaaaac 348
Db 361 CCCACTACGGTCTCCAGCCTCCCGGATACCAAAATCGAAGTAGGCCACATTATATACAAAA 420
Qy 349 ctgctcaactatgtaagggagtttatcgccatggaatttc 390
Db 421 CTGCTCAGCTACAAAGCAACTGTTTCGCCACGGCCCCCTTC 462

RESULT 15
PCT-US93-07645-3
; Sequence 3, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-3

Query Match 40.5%; Score 159.2; DB 5; Length 1212;
Best Local Similarity 66.7%; Pred. No. 9e-40;
Matches 268; Conservative 0; Mismatches 113; Indels 21; Gaps 2;
Qy 1 atggcgctgtgtgactgtgtgctcactgtcctcactgcctcggtgacctgctccccc 60
Db 70 ATGGCGCTCTGGGTGACTGCGACTCTGCTCTGCTTGGCTTGGTGTCTCGCCGCCCA 129
Qy 61 agcc-----ctgtgactccctcccaacccctcaaggagctcattgagagctg 108
Db 130 GGGCCGGTGCCAAAGATCTGTGTCTCTCCCTGTGACCTTAAGGAGCTTATTGAGGAGCTG 189
Qy 109 gtaacatcacccagaatacctcctctgcaacggcagcatggtgtggagcgtcaac 168
Db 190 AGCAACATCACAAAGACCAGACTCCCTGTGCAACGGCAGCATGTTGAGTGTGGAC 249
Qy 169 ctgaccgcggcatctactgcagctctagaatctctgatcaatgtctccgactgcagc 228
Db 250 CTGGCCGCTGGCGGTTTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAAATTGCAAT 309
Qy 229 gccatccaaagaccagagatgctgaaagcactgtgctctcaaaagcccgcgaggg 288
Db 310 GCCATCTACAGGCCACAGGATATGTGATGGCCCTGTGTAAACCGCAAGGCC----- 360
Qy 289 cagatttccagtgaacgcagccagagacacccaaaaattgaagtgtatccagttggtgaaaaac 348
Db 361 CCCACTACGGTCTCCAGCCTCCCGGATACCAAAATCGAAGTAGGCCACATTATATACAAAA 420
```


Qy 349 ctgctcacctatgtaagggaagttttatcgccatggaatttc 390
|||||
Db 421 CTGCTCAGCTACACAAAGCAACTGTTTCGCCACGGCCCTTC 462

Search completed: May 13, 2001, 14:21:17
Job time: 17828 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:07 ; Search time 5997.24 Seconds
(without alignments)
572.478 Million cell updates/sec

Title: US-09-451-527-94
Perfect score: 393
Sequence: 1 atggcgctctgttgactgt.....atggccatggaatttcaga 393

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
- 1: gb_est1:*
 - 2: gb_est2:*
 - 3: gb_est3:*
 - 4: gb_est4:*
 - 5: gb_est5:*
 - 6: gb_est6:*
 - 7: gb_est7:*
 - 8: gb_est8:*
 - 9: gb_est9:*
 - 10: gb_est10:*
 - 11: gb_est11:*
 - 12: gb_est12:*
 - 13: gb_est13:*
 - 14: gb_est14:*
 - 15: gb_est15:*
 - 16: gb_est16:*
 - 17: gb_est17:*
 - 18: gb_est18:*
 - 19: gb_est19:*
 - 20: gb_est20:*
 - 21: gb_est21:*
 - 22: gb_est22:*
 - 23: gb_est23:*
 - 24: gb_est24:*
 - 25: gb_est25:*
 - 26: gb_est26:*
 - 27: gb_est27:*
 - 28: gb_est28:*
 - 29: gb_est29:*
 - 30: gb_est30:*
 - 31: gb_est31:*
 - 32: gb_est32:*
 - 33: gb_est33:*
 - 34: em_estfun:*
 - 35: em_esthum1:*
 - 36: em_esthum2:*
 - 37: em_esthum3:*
 - 38: em_esthum4:*
 - 39: em_esthum5:*
 - 40: em_esthum6:*
 - 41: em_esthum7:*
 - 42: em_esthum8:*
 - 43: em_esthum9:*

- 44: em_esthum10:*
- 45: em_esthum11:*
- 46: em_esthum12:*
- 47: em_esthum13:*
- 48: em_esthum14:*
- 49: em_esthum15:*
- 50: em_esthum16:*
- 51: em_esthum17:*
- 52: em_esthum18:*
- 53: em_esthum19:*
- 54: em_esthum20:*
- 55: em_esthum21:*
- 56: em_esthum22:*
- 57: em_esthum23:*
- 58: em_esthum24:*
- 59: em_esthum25:*
- 60: em_esthum26:*
- 61: em_esthum27:*
- 62: em_esthum28:*
- 63: em_estin1:*
- 64: em_estin2:*
- 65: em_estin3:*
- 66: em_estin4:*
- 67: em_estin5:*
- 68: em_estom1:*
- 69: em_estom2:*
- 70: em_estov1:*
- 71: em_estov2:*
- 72: em_estpl1:*
- 73: em_estpl2:*
- 74: em_estpl3:*
- 75: em_estpl4:*
- 76: em_estpl5:*
- 77: em_estpl6:*
- 78: em_estpl7:*
- 79: em_estpl8:*
- 80: em_estpl9:*
- 81: em_estpl10:*
- 82: em_estro1:*
- 83: em_estro2:*
- 84: em_estro3:*
- 85: em_estro4:*
- 86: em_estro5:*
- 87: em_estro6:*
- 88: em_estro7:*
- 89: em_estro8:*
- 90: em_estro9:*
- 91: em_estro10:*
- 92: em_estro11:*
- 93: em_estro12:*
- 94: em_estro13:*
- 95: em_estro14:*
- 96: em_estro15:*
- 97: em_estro16:*
- 98: em_estro17:*
- 99: em_estro18:*
- 100: em_estro19:*
- 101: em_estro20:*
- 102: gb_est25:*
- 103: gb_est26:*
- 104: gb_est27:*
- 105: gb_est28:*
- 106: gb_est29:*
- 107: gb_est30:*
- 108: gb_est31:*
- 109: gb_est32:*
- 110: gb_est41:*
- 111: gb_est42:*
- 112: gb_est43:*
- 113: gb_est44:*
- 114: gb_est45:*
- 115: gb_est46:*
- 116: gb_est47:*

```
117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*
```

```
190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro1:*
193: em_gss_pro2:*
194: em_gss_rod1:*
195: em_gss_rod2:*
196: em_gss_rod3:*
197: em_gss_rod4:*
198: em_gss_rod5:*
199: em_gss_vrt1:*
200: em_gss_vrt2:*
201: em_gss_vrt3:*
202: gb_gss1:*
203: gb_gss2:*
204: gb_gss3:*
205: gb_gss4:*
206: gb_gss5:*
207: gb_gss6:*
208: gb_gss7:*
209: gb_gss8:*
210: gb_gss9:*
211: gb_gss10:*
212: gb_gss11:*
213: gb_gss12:*
214: gb_gss13:*
215: gb_gss14:*
216: gb_gss15:*
217: gb_gss16:*
218: gb_gss17:*
219: gb_gss18:*
220: gb_gss19:*
221: gb_gss20:*
222: gb_gss21:*
223: gb_gss22:*
224: gb_gss23:*
225: gb_gss24:*
226: gb_gss25:*
227: gb_gss26:*
228: gb_gss27:*
229: gb_gss28:*
230: gb_gss29:*
231: gb_gss30:*
232: gb_gss31:*
233: gb_gss32:*
234: gb_gss33:*
235: gb_gss34:*
```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	43.4	11.0	581	219	AZ305110	1M0005P05
2	40	10.2	463	24	AI712497	AI712497 UI-R-AFL-
3	37.8	9.6	994	231	CNS0402X	AL300678 Tetraodon
4	37	9.4	1016	230	CNS024F6	AL180699 Tetraodon
5	36.8	9.4	576	141	BE907816	BE907816 601501924
6	36.6	9.3	329	146	BF292210	BF292210 WHE2208_A
7	36.6	9.3	925	229	CNS0091P	AL053013 Drosophila
8	36.4	9.3	277	137	BE593226	BE593226 WSL_99_B0
9	36.4	9.3	411	201	AQ001086	AQ001086 CIT-HSP-2
10	36.4	9.3	537	166	BE357229	BE357229 DGL_147_B
11	36	9.2	462	143	BF039993	BF039993 BF250023B
12	35.8	9.1	497	20	AI444326	AI444326 GA_Ea002
13	35.8	9.1	1946	119	AW729623	AW729623 GA_Ea002
14	35.6	9.1	230	167	BE498968	BE498968 WHE0959_G
15	35.6	9.1	537	29	AV387571	AV387571 AV387571
16	35.6	9.1	1070	136	BE536034	BE536034 601062471
17	35.6	9.1	2275	14	AF034173	AF034173 AF034173
18	35.4	9.0	498	150	BF606532	BF606532 273595 MA

27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60 61 62 63 64 65 66 67 68 69 70 71 72 73 74 75 76 77 78 79 80 81 82 83 84 85 86 87 88 89 90 91 92 93 94 95 96 97 98 99 100 101 102 103 104 105 106 107 108 109 110 111 112 113 114 115 116 117 118 119 120 121 122 123 124 125 126 127 128 129 130 131 132 133 134 135 136 137 138 139 140 141 142 143 144 145 146 147 148 149 150 151 152 153 154 155 156 157 158 159 160 161 162 163 164 165 166 167 168 169 170 171 172 173 174 175 176 177 178 179 180 181 182 183 184 185 186 187 188 189 190 191 192 193 194 195 196 197 198 199 200 201 202 203 204 205 206 207 208 209 210 211 212 213 214 215 216 217 218 219 220 221 222 223 224 225 226 227 228 229 230 231 232 233 234 235 236 237 238 239 240 241 242 243 244 245 246 247 248 249 250 251 252 253 254 255 256 257 258 259 260 261 262 263 264 265 266 267 268 269 270 271 272 273 274 275 276 277 278 279 280 281 282 283 284 285 286 287 288 289 290 291 292 293 294 295 296 297 298 299 300 301 302 303 304 305 306 307 308 309 310 311 312 313 314 315 316 317 318 319 320 321 322 323 324 325 326 327 328 329 330 331 332 333 334 335 336 337 338 339 340 341 342 343 344 345 346 347 348 349 350 351 352 353 354 355 356 357 358 359 360 361 362 363 364 365 366 367 368 369 370 371 372 373 374 375 376 377 378 379 380 381 382 383 384 385 386 387 388 389 390 391 392 393 394 395 396 397 398 399 400 401 402 403 404 405 406 407 408 409 410 411 412 413 414 415 416 417 418 419 420 421 422 423 424 425 426 427 428 429 430 431 432 433 434 435 436 437 438 439 440 441 442 443 444 445 446 447 448 449 450 451 452 453 454 455 456 457 458 459 460 461 462 463 464 465 466 467 468 469 470 471 472 473 474 475 476 477 478 479 480 481 482 483 484 485 486 487 488 489 490 491 492 493 494 495 496 497 498 499 500 501 502 503 504 505 506 507 508 509 510 511 512 513 514 515 516 517 518 519 520 521 522 523 524 525 526 527 528 529 530 531 532 533 534 535 536 537 538 539 540 541 542 543 544 545 546 547 548 549 550 551 552 553 554 555 556 557 558 559 560 561 562 563 564 565 566 567 568 569 570 571 572 573 574 575 576 577 578 579 580 581 582 583 584 585 586 587 588 589 590 591 592 593 594 595 596 597 598 599 600 601 602 603 604 605 606 607 608 609 610 611 612 613 614 615 616 617 618 619 620 621 622 623 624 625 626 627 628 629 630 631 632 633 634 635 636 637 638 639 640 641 642 643 644 645 646 647 648 649 650 651 652 653 654 655 656 657 658 659 660 661 662 663 664 665 666 667 668 669 670 671 672 673 674 675 676 677 678 679 680 681 682 683 684 685 686 687 688 689 690 691 692 693 694 695 696 697 698 699 700 701 702 703 704 705 706 707 708 709 710 711 712 713 714 715 716 717 718 719 720 721 722 723 724 725 726 727 728 729 730 731 732 733 734 735 736 737 738 739 740 741 742 743 744 745 746 747 748 749 750 751 752 753 754 755 756 757 758 759 760 761 762 763 764 765 766 767 768 769 770 771 772 773 774 775 776 777 778 779 780 781 782 783 784 785 786 787 788 789 790 791 792 793 794 795 796 797 798 799 800 801 802 803 804 805 806 807 808 809 810 811 812 813 814 815 816 817 818 819 820 821 822 823 824 825 826 827 828 829 830 831 832 833 834 835 836 837 838 839 840 841 842 843 844 845 846 847 848 849 850 851 852 853 854 855 856 857 858 859 860 861 862 863 864 865 866 867 868 869 870 871 872 873 874 875 876 877 878 879 880 881 882 883 884 885 886 887 888 889 890 891 892 893 894 895 896 897 898 899 900 901 902 903 904 905 906 907 908 909 910 911 912 913 914 915 916 917 918 919 920 921 922 923 924 925 926 927 928 929 930 931 932 933 934 935 936 937 938 939 940 941 942 943 944 945 946 947 948 949 950 951 952 953 954 955 956 957 958 959 960 961 962 963 964 965 966 967 968 969 970 971 972 973 974 975 976 977 978 979 980 981 982 983 984 985 986 987 988 989 990 991 992 993 994 995 996 997 998 999 1000 1001 1002 1003 1004 1005 1006 1007 1008 1009 1010 1011 1012 1013 1014 1015 1016 1017 1018 1019 1020 1021 1022 1023 1024 1025 1026 1027 1028 1029 1030 1031 1032 1033 1034 1035 1036 1037 1038 1039 1040 1041 1042 1043 1044 1045 1046 1047 1048 1049 1050 1051 1052 1053 10

```

Db    803 ASAGHSSSACBSSSSSCASCSWASSSSSASSSRSRSGGAGCGAGSSRSSSSSSSSAS 744
Qy    208 atcaatgtctccgactcagcgcccatcaaagaccacagaggatgctgaagcactgtgc 267
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db    743 AGSVVSANSSSSCCSSVSCSVVASMSGCCSBSSSSSSASASSSSSSSSASCASCCTCCTS 684
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Qy    268 tctcaaaagcccggcagcgagatttccagtgaacgcagcgacgagacacc 318
      |:|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db    683 WSCSCTSASMSAARSSSSSSSSSSSSSMASSSASSSASSSSSSSSSSSSSSS 633

RESULT# 8
BE593226
LOCUS       BE593226             277 bp   mRNA           EST          18-AUG-2000
DEFINITION WS1_99_B03_gl_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
            mRNA sequence.
ACCESSION  BE593226
VERSION    BE593226..1 GI:9848299
KEYWORDS   EST.
SOURCE     sorghum.
ORGANISM   Sorghum bicolor
            Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
            Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
            ; Andropogoneae; Sorghum.
REFERENCE  1 (bases 1 to 277)
AUTHORS   Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
            ,L.H.
TITLE      An EST database from Sorghum: water-stressed plants
COMMENT    Unpublished (2000)
            Contact: Cordonnier-Pratt MM
            Department of Botany
            The University of Georgia
            Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
            Tel.: 706 542 1860
            Fax: 706 542 1805
            Email: mmpratt@uga.edu
            Sequences have been trimmed to exclude PolyA, vector and regions
            below Phred quality 16. The threshold for highest quality sequence
            is 20.
Seq primer: PolytMix
High quality sequence start: 5
High quality sequence stop: 246
POLYA=NO.
FEATURES             Location/Qualifiers
     source           1..277
                     /organism="Sorghum bicolor"
                     /db_xref="taxon:4538"
                     /note="Organ: Mix of 5-week old plants on days 7 & 8 after
                     water was withheld; Vector: Lambda zap; Site:1: XhoI;
                     Site:2: EcoRI; The library was made from poly-A RNA in the
                     cloning vector lambda ZAP II. Clones to be sequenced were
                     prepared by mass excision."
BASE COUNT        47 a         81 c         78 g         71 t
ORIGIN
Query Match              9.3%; Score 36.4; DB 137; Length 277;
Best Local Similarity 53.5%; Pred. No. 8;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;
Qy    84 cctcaagagctcattgagagtggttcacatcacccagaatacggcatcccccttgtcaa 143
      |||||
Db    22 CCCCATGGAGGCCTCGGGAGCCCCGGCGACATCGCGCCGTGGTTCCTCTGCAC 81
      |||||
Qy    144 cggcagcatggtgtggagcgtcaacctgccgcggcgcatgtactgtgcgagctctaagtc 203
      |||||
Db    82 CGAGCGCGCGAGTGGGTCAACGGCCAGGTCATCCGCGCCACCGCGGCTACGTGTGATG 141
      |||||
Qy    204 tcgatcataatgtctccagctgc 225
      |||||
Db    142 TCTGATCTTTTAGCTTCTACAGC 163

```

```

RESULT 9
AC001086/c
LOCUS
DEFINITION CIT-HSP-2288N10.TR CIT-HSP Homo sapiens genomic clone 2288N10, DNA
sequence.
ACCESSION
VERSION A0001086
KEYWORDS A0001086.1 GI:3028525
SOURCE
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 411)
AUTHORS Adams M.D., Rounsley S.D., Zhao S., Field C.E., Bass S., Linher K.,
Golden K., Berry K., Granger D., Suh E., Wible C., Shizuya H.,
Simon M. and Venter J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.
FEATURES
Location/Qualifiers
source
1..411
/organism="Homo sapiens"
/db_xref="GDB:7150045"
/db_xref="taxon:9606"
/clone="2288N10"
/clone_lib="CIT-HSP"
/cell_type="Sperm"
/sex="Male"
/notes="Vector: pBelBAC11; Site_1: HindIII; Site_2:
HindIII"
BASE COUNT 120 a 100 c 101 g 90 t
ORIGIN

Query Match 9.3%; Score 36.4; DB 201; Length 411;
Best Local Similarity 48.5%; Pred. No. 8.9; Mismatches 0; Gaps 0;
Matches 100; Conservative 0; Indels 106;

Qy 29 ctctcacctgctcggtgcttgcctcccccagccctgtgactccctccccaaccctca 88
||| ||||| ||||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 287 CCTCGCTGCTGCTGCTGCAAGCCACCCGCGCCAGTGCCTTGTACCGCCCTCT 228
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 89 aggagctcattgaggagctggtcaacatcacccagaatcaggcatccctctgcaacgca 148
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 227 CCCAGACTGGGTCTCTGTGTGGGTGGGGCCACATGGGGTCTGAAAGGCGAGGCTG 168
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 149 gcatggttgagctcaacctgacccgagctagtactgcgagctctagaatctctga 208
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 167 GTGCTGAGGGGCTGTGATGATCAGTCCCGCTCTCTCTTTTGTCTCAGTATCTCACA 108
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 209 tcaatgtctccgactgcagcgccatc 234
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 107 TGAGCTTTTAAAGATCCACTTC 82
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 10
BE357229
LOCUS
DEFINITION DGI_147_B02.g1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
sequence.

```

```

ACCESSION BE357229
VERSION BE357229.1 GI:9298786
KEYWORDS
SOURCE Sorghum bicolor
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
Andropogoneae; Sorghum.
REFERENCE
1 (bases 1 to 537)
AUTHORS Cordonnier-Pratt M., Gingle A., Marsala C., Sudman M. and Pratt
L.H.
TITLE An EST database from Sorghum: dark-grown seedlings
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolyTMix
High quality sequence start: 31
High quality sequence stop: 514
POLYA=NO.
FEATURES
Location/Qualifiers
source
1..537
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGI)"
/notes="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector Lambda Zap II.
Clones to be sequenced were prepared by mass excision."
BASE COUNT 89 a 160 c 176 g 112 t
ORIGIN

Query Match 9.3%; Score 36.4; DB 166; Length 537;
Best Local Similarity 53.5%; Pred. No. 9.6; Mismatches 0; Gaps 0;
Matches 76; Conservative 0; Indels 66;

Qy 84 cctcaaggagctcattgaggagctggtcaacatcacccagaatcaggcatccctctgcaa 143
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 249 CCCCATGGAGAGGCTCGGGAGAGCCCGGCGCATCGCGCGGTTCCTCTGCAC 308
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 144 cggcagcatggtgtgagcgctcaacctgacccgagcgatgtactgcgagctctagaatc 203
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 309 CGACGCCCGCGAGTGGGTCAACGGCCAGGTTCATCGGCCCAACGGCGGTACGTGTGATG 368
||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Qy 204 tctgatcaatgtctccgactgc 225
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 369 TCTGATCTTTAGCTTCTACAGC 390
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 11
BF039993
LOCUS
DEFINITION BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA
clone BP250023B10D12 5', mRNA sequence.
ACCESSION BF039993
VERSION BF039993.1 GI:10757048
KEYWORDS EST.
SOURCE EST.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE
1 (bases 1 to 462)
AUTHORS Lewin H.A., Soares M.B., Rebeiz M., Pardinas J., Liu L. and Larson
J.H.

```



```

DEFINITION GA_Ea0025J07 Gossypium arboreum 7-10 dpa fiber library Gossypium
arboeum cDNA clone GA_Ea0025J07, mRNA sequence.
ACCESSION AW729623
VERSION AW729623.1 GI:7627221
KEYWORDS EST.
SOURCE Gossypium arboreum.
ORGANISM Gossypium arboreum.
REFERENCE 1 (bases 1 to 1946)
AUTHORS Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry
D., Wood,T.C., Leslie,A. and Wilkins,T.A.
TITLE An integrated analysis of the genetics, development, and evolution
of the cotton fiber
JOURNAL Unpublished (2000)
COMMENT Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
Email: rwing@clemson.edu
High quality sequence stop: 1946.

FEATURES
source
1..1946
Location/Qualifiers
/organism="Gossypium arboreum"
/strain="AKA"
/cultivar="8400"
/db_xref="taxon:29729"
/clone="GA_Ea0025J07"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
dpa"
/lab_host="E. coli"
/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"

BASE COUNT 412 a 492 C 495 G 472 T 75 others
ORIGIN

Query Match 9.1%; Score 35.8; DB 119; Length 1946;
Best Local Similarity 52.8%; Pred. No. 20;
Matches 76; Conservative 0; Mismatches 68; Indels 0; Gaps 0;

Qy 183 gtactgcagctctagaaatctgtatcatctctccgactgcagccatccaaaggac 242
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 276 GCACTCGCGACCTATTGTGTGATCATGTCTCTGAGTATCGAGGCACTACACGCAC 217
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 243 ccagaggatgctgaagcaactgtctctcaaaagccgcggcaggcgagattccagtg 302
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 216 ACATAGCTAAACCAAGGAACAGAGAGNTCTCGCACTCTCTAGGCGCAGCGATAATGTGA 157
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 303 acgcagccgagacaccaaattga 326
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 156 CTAGAGTCGACGAACAAGAGAGA 133
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 14
LOCUS BE498968 230 bp mRNA EST 04-AUG-2000
DEFINITION WHE0969_G06_N11ZS Wheat pre-anthesis spike cDNA library Triticum
aestivum cDNA clone WHE0969_G06_N11, mRNA sequence.
ACCESSION BE498968
VERSION BE498968.1 GI:9697585
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
Triticum.
REFERENCE 1 (bases 1 to 230)
AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han
P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J.,

```

```

Seaton,C.L. and Tong,J.C.
The structure and function of the expressed portion of the wheat
genomes - Pre-anthesis spike cDNA library
Unpublished (2000)
Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific
West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: oanders@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low
quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES
source
1..230
Location/Qualifiers
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0969_G06_N11"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/notes="Vector: Lambda Uni-ZAP XR, excised phagemid;
Site_1: EcoRI; Site_2: XhoI; Plants were grown in the
greenhouse. Whole spike with awns trimmed, white, green
and yellow anther were collected and total RNA, and
poly(A) RNA were prepared, a cDNA library was made, and
the cDNA clones were in vivo excised to give pBluescript
phagemids in the TJ Close lab (Choi, Close, Fenton) at
the University of California, Riverside. Plasmid DNA
preparations and DNA sequencing were performed in the OD
Anderson lab (all other authors)."

BASE COUNT 42 a 69 C 74 G 45 T
ORIGIN

Query Match 9.1%; Score 35.6; DB 167; Length 230;
Best Local Similarity 50.6%; Pred. No. 13;
Matches 86; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 20 tggctattgtctcaactgcctcgtggtgcttgcctcccgagccctgtgactccctcc 79
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 61 TCGCATCTCTCTCCCTTCGTCGAGAGATCATCGCGAGATTTTCGGGACCTACTTCC 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 80 caacctcaaggagctcatgaggagctggtcaacatcacccagaaatcaggcatccctct 139
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 121 TGATCTTCGCGGGTGGCGGGGTGACCATCAACAGAGCAATGGGCAGATCAGTTCC 180
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Qy 140 gcaacgcagcatggtgtgagcgctcaacctgacgcgcggcatgtactgc 189
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 181 CCGCGTGGCCATCGTCTGGGGCCTCACCGTGATGGTGATGTACTCC 230
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

RESULT 15
LOCUS AV387571/c 537 bp mRNA EST 29-SEP-2000
DEFINITION AV387571 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
cDNA clone CM026e03_f, mRNA sequence.
ACCESSION AV387571
VERSION AV387571.1 GI:6541787
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadales; Chlamydomonas.
REFERENCE 1 (bases 1 to 537)
AUTHORS Asamizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
TITLE A large scale structural analysis of cDNAs in a unicellular green
alga, Chlamydomonas reinhardtii. I. Generation of 3433
non-redundant expressed sequence tags
JOURNAL DNA Res. 6 (6), 369-373 (1999)

```


GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:33 ; Search time 9342.78 Seconds
(without alignments)
525.651 Million cell updates/sec

Title: US-09-451-527-96
Perfect score: 333
Sequence: 1 agccctgtactccctcccc.....atgcccatgaaatttcaga 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_om.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
14: gb_pl3.*
15: gb_pl4.*
16: em_ba1.*
17: em_ba2.*
18: em_fun.*
19: em_htgo_hum.*
20: em_htgo_inv.*
21: em_htgo_rod.*
22: em_htg_hum1.*
23: em_htg_hum2.*
24: em_htg_hum3.*
25: em_htg_hum4.*
26: em_htg_hum5.*
27: em_htg_hum6.*
28: em_htg_hum7.*
29: em_htg_hum8.*
30: em_htg_inv1.*
31: em_htg_inv2.*
32: em_htg_rod.*
33: em_hum1.*
34: em_hum2.*
35: em_hum3.*
36: em_hum4.*
37: em_hum5.*
38: em_hum6.*
39: em_hum7.*
40: em_hum8.*
41: em_in.*
42: em_om.*
43: em_or.*

- 44: em_ov.*
45: em_pat.*
46: em_ph.*
47: em_pl.*
48: em_ro.*
49: em_sts.*
50: em_sy.*
51: em_un.*
52: em_v1.*
53: gb_sts1.*
54: gb_sts2.*
55: gb_sts3.*
56: gb_sy.*
57: gb_un.*
58: gb_v11.*
59: gb_v12.*
60: gb_htg1.*
61: gb_htg2.*
62: gb_htg3.*
63: gb_htg4.*
64: gb_htg5.*
65: gb_htg6.*
66: gb_htg7.*
67: gb_htg8.*
68: gb_htg9.*
69: gb_htg10.*
70: gb_htg11.*
71: gb_htg12.*
72: gb_htg13.*
73: gb_htg14.*
74: gb_htg15.*
75: gb_htg16.*
76: gb_htg17.*
77: gb_htg18.*
78: gb_htg19.*
79: gb_htg20.*
80: gb_htg21.*
81: gb_htg22.*
82: gb_htg23.*
83: gb_htg24.*
84: gb_htg25.*
85: gb_pr1.*
86: gb_pr2.*
87: gb_pr3.*
88: gb_pr4.*
89: gb_pr5.*
90: gb_pr6.*
91: gb_pr7.*
92: gb_pr8.*
93: gb_pr9.*
94: gb_rol.*
95: gb_ro2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	333	100.0	1302	7	AF244915
2	203.4	61.1	336	9	A29931
3	203.4	61.1	336	10	I58494
4	203.4	61.1	1270	93	HUMIL13A
5	203.4	61.1	1282	92	HSNC30
6	203.4	61.1	1290	10	I34548
7	201.8	60.6	336	9	A29930
8	201.8	60.6	336	10	I58481
9	201.8	60.6	417	88	AF043334
10	201.8	60.6	1297	9	A29948
11	201.8	60.6	1297	10	I58488

```
12 200.2 60.1 384 9 A29950
13 200.2 60.1 384 10 158489
14 198.6 59.6 425 9 AR027065
15 198.6 59.6 425 10 186198
16 198.6 59.6 4410 9 A52326
17 198.6 59.6 4410 9 AR027062
18 198.6 59.6 4410 10 186195
19 179 53.8 343 7 AF072807
20 142 42.6 447 10 158495
21 142 42.6 1207 94 MUSSTCPE
22 142 42.6 1212 10 134549
23 131.4 39.5 443 94 RAFIL13A
24 106.2 31.9 213343 78 AF276990
c 25 71 21.3 3714 93 HUM11DC992
c 26 71 21.3 4600 93 HUM11L3B
27 71 21.3 4740 93 HSU10307
28 71 21.3 5670 93 HSU11120
c 29 71 21.3 50282 85 AC004039
c 30 71 21.3 78489 75 AC074127
c 31 70.6 21.2 3395 93 HUM11DC982
c 32 70 21.0 3520 7 BT132441
c 33 58.4 17.5 78469 75 AC074127
c 34 51.6 15.5 4376 94 MUS11L13A
c 35 49.4 14.8 142732 88 AC084392
c 36 49.4 14.8 159500 94 AC005742
c 37 49.4 14.8 237823 66 AC020886
c 38 40.8 12.3 38390 3 SC2H12
c 39 37 11.1 39739 3 SCD16A
c 40 36.8 11.1 185300 2 AP000063
c 41 36.6 11.0 51440 12 AB025632
c 42 36.4 10.9 1091 94 AB015206
c 43 36.4 10.9 1122 94 MMU18723
c 44 36.4 10.9 2437 3 SAAJ3310
c 45 36.4 10.9 2437 3 SAU77894
```

ALIGNMENTS

```
RESULT 1
LOCUS AF244915 1302 bp mRNA MAM 16-OCT-2000
DEFINITION Canis familiaris interleukin-13 mRNA, complete cds.
ACCESSION AF244915
VERSION AF244915.1 GI:7528273
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
REFERENCE 1 (bases 1 to 1302)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
TITLE Yang,S., Borroughs,K.L. and McDermott,M.J.
JOURNAL Canine interleukin-13: molecular cloning of full-length cDNA and
expression of biologically active recombinant protein
MEDLINE 20485146
PUBMED 11032397
REFERENCE 2 (bases 1 to 1302)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation,
1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES
source
Location/Qualifiers
1..1302
/organism="Canis familiaris"
/db_xref="taxon:9615"
1..51
52..447
/codon_start=1
/product="interleukin-13"
/protein_id="AAF63204.1"
/db_xref="GI:7528274"
/translation="MALMLTVVIALTCLGLASPSVPTSPTLKELIEELVNITQNA
```

```
SLGNSWVSNLTAGMYCAALESILNVDCSATQRTORMLKALCSQKPAAGQISSR
SRDTKIEIVIQLVKNLLFYVRGVRHGNP*
BASE COUNT 337 a 318 c 340 g 307 t
ORIGIN
Query Match 100.0%; Score 333; DB 7; Length 1302;
Best Local Similarity 100.0%; Pred. No. 2.2e-78;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtgaacatcacc 60
Db 112 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGAGCTGTTCAACATCAC 171
Qy 61 cagaatcaggatccctctgcaacgcgacagctggtgagcgtcaacacctgacccgcgc 120
Db 172 CAGATCAGGATCCCTCTGCAACGCGACATGGTGTGGAGCGTCAACCTGACCCGCCGC 231
Qy 121 atgtactgcgagctctagaatctctgtatcaatgtctccgactgcagcgccatccaaagg 180
Db 232 ATGTACTGCGAGCTCTAGAAATCTCTGATCATCTCTCGACTGCAGCGCCATCCAAAGG 291
Qy 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcagggcagatttccagt 240
Db 292 ACCCAGAGGATGCTGAAAGCACTGTGCTCTCAAAAGCCGCGCAGGCGAGATTTCCAGT 351
Qy 241 gaacgcagccgagacacacaaattgaagtgtaccagtgtgtaaaaaacctgtccacctat 300
Db 352 GAACCGACCGGAGACACCAAAATTTGAAGTGTGTTGTTGTTGTTGTTGTTGTTGTTGTT 411
Qy 301 gtaagggagttatcgccatggaatttcaga 333
Db 412 GTAGGGGAGTTTATCGCCATGGAAATTTTCAGA 444
```

RESULT 2

```
LOCUS A29931 336 bp DNA PAT 23-JUN-1995
DEFINITION Sequence coding for the mature cytokine like protein.
ACCESSION A29931
VERSION A29931.1 GI:1249019
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 3 30-SEP-1992;
ELF SANOFI
FEATURES
Location/Qualifiers
source
1..336
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN
Query Match 61.1%; Score 203.4; DB 9; Length 336;
Best Local Similarity 77.8%; Pred. No. 7.5e-44;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;
Qy 2 gccctgtgactccctcccaaccctcaaggagctcattgagagctggtgaacatcacc 61
Db 2 GCCCTGTGCTCCCTCTCTACAGCCCTCAGGAGCTCATTTGAGAGCTGTTCAACATCACCC 61
Qy 62 agaatc---aggatccctctgcaacgcgacagctggtgagcgtcaacacctgacccgcgc 118
Db 62 AGAACCAAGGCTCCGCTCTCGAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121
```


AUTHORS Minty, A.J.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches, Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
 REFERENCE 2 (bases 1 to 1282)
 AUTHORS Minty, A.J., Chalton, P., Derocq, J.M., Dumont, X., Guillemot, J.C., Kaghad, M., Labit, C., Lepiatols, P., Liauzon, P., Miloux, B., Minty, C., Casellas, P., Loison, G., Lupker, J., Shire, D., Ferrare, P. and Caput, D.

TITLE Interleukin-13 is a new human lymphokine regulating inflammatory

JOURNAL and immune responses

MEDLINE Nature 362 (6417), 248-250 (1993)

FEATURES 93211479

source

/organism="Homo sapiens"

/db_xref="taxon:9606"

/chromosome="5q 23-31"

/cell_type="peripheral blood lymphocytes"

15..455

/gene="NC30"

15..116

/gene="NC30"

/product="NC30; alternative"

15..455

/gene="NC30"

/note="alternative; ATG at 15 is an alternative start

codon"

/codon_start=1

/evidence="experimental

/protein_id="CAA48823.1"

/db_xref="GI:580330"

/db_xref="SWISS-PROT:P35225"

/translation="MLPLNPLLLALGALLLTVTALCLGFGSPGVPVPSTALR

ELIEELVNTONKAPLCNGSMVSNLTAGMYCALESINVGCSAIEKTQRLMSG

FCPHKYSAGQFSLHVRDVKIEVAQFVKDLLLHLKLFREGFN"

57..455

/gene="NC30"

/note="alternative; ATG at 15 is an alternative start

codon"

/codon_start=1

/evidence="experimental

/protein_id="CAA48824.1"

/db_xref="GI:673420"

/db_xref="SWISS-PROT:P35225"

/translation="MALLLTVTALCLGFGSPGVPVPSTALRELIEELVNTONK

APLCNGSMVSNLTAGMYCALESINVGCSAIEKTQRLMSGFCPHKYSAGQFSL

HVRDVKIEVAQFVKDLLLHLKLFREGFN"

57..116

/gene="NC30"

/product="NC30; alternative"

117..452

/gene="NC30"

/evidence="experimental

238

/gene="NC30"

/replace="a"

856..860

/note="ATTTA motif"

873..877

/note="ATTTA motif"

1134..1138

/note="ATTTA motif"

1153..1157

/note="ATTTA motif"

1264..1269

341 c 337 g 311 t

BASE COUNT

ORIGIN

Query Match 61.1%; Score 203.4; DB 92; Length 1282;

Best Local Similarity 77.8%; Pred. No. 7e-44;

Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

Qy 2 gccctgtgaactccctcccccacccctcaaggagctcattgagagctgggtcaacatcaccc 61
 Db 118 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTAGGAGCTGGTCAACATCACCC 177
 Qy 62 aqaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgacgcgcg 118
 Db 178 AGAACCAAGAAGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 237
 Qy 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
 Db 238 GCATGTACTGTGCAGCCCTGGGAATCCCTCATCAACGTGTTCAGGCTGCAGTGCATCGAGA 297
 Qy 179 ggaccagagaggtgctgaaagcactgtgtctctcaaaagcccgaggcagcagatttcca 238
 Db 298 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGCAGCTTTTCCA 357
 Qy 239 gtgaacgcagccgagac 298
 Db 358 GCTTCATGTCGAGACACACAAATCGAGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 417
 Qy 299 atgtaaggaggatttatcgccatggaatttca 331
 Db 418 ATTAAAGAAACTTTTTCGCGAGGACGGTTCA 450

RESULT 6

LOCUS

I34548

1290 bp

DNA

Sequence 1 from patent US 5596072.

ACCESSION

I34548

VERSION

I34548.1

GI:1825339

KEYWORDS

Unknown.

ORGANISM

Unclassified.

REFERENCE

1 (bases 1 to 1290)

AUTHORS

Culpepper, J., McKenzie, A., Dang, W. and Zurawski, G.

TITLE

Method of refolding human IL-13

JOURNAL

Patent: US 5596072-A 1 21-JAN-1997;

FEATURES

Location/Qualifiers

1..1290

source

/organism="unknown"

BASE COUNT

308 a 335 c 336 g 311 t

ORIGIN

Query Match

61.1%; Score 203.4; DB 10; Length 1290;

Best Local Similarity 77.8%; Pred. No. 7e-44;

Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

Qy 2 gccctgtgaactccctcccccacccctcaaggagctcattgagagctgggtcaacatcaccc 61

Db 106 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTAGGAGCTGGTCAACATCACCC 165

Qy 62 aqaatc---aggcatccctctgcaacggcagcatggtgtggagcgtcaaacctgacgcgcg 118

Db 166 AGAACCAAGAAGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 225

Qy 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178

Db 226 GCATGTACTGTGCAGCCCTGGGAATCCCTCATCAACGTGTTCAGGCTGCAGTGCATCGAGA 285

Qy 179 ggaccagagaggtgctgaaagcactgtgtctctcaaaagcccgaggcagcagatttcca 238

Db 286 AGACCCAGAGGATGCTGAGCGGATTCTGCCCGCACAAAGTCTCAGCTGGCAGCTTTTCCA 345

Qy 239 gtgaacgcagccgagac 298

Db 346 GCTTCATGTCGAGACACACAAATCGAGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 405

Qy 299 atgtaaggaggatttatcgccatggaatttca 331

Db 405 ATTTAAGAAACTTTTTTCGAGGACGGTTCA 438

RESULT 7

LOCUS A29930 336 bp DNA PAT 23-JUN-1995

DEFINITION Sequence coding for the mature cytokine like protein.

ACCESSION A29930

VERSION A29930.1 GI:1249018

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM artificial sequence.

REFERENCE 1 (bases 1 to 336)

AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le

TITLE Boutellier,C., Lepoint,P., Magazin,M. and Minty,A.

PROTEIN Protein having cytokine type activity, recombinant DNA coding for

JOURNAL this protein, transformed cells and microorganisms

PATENT: EP 0506574-A 2 30-SEP-1992;

ELF SANOFI

FEATURES

source

1. .336

/organism="synthetic construct"

/db_xref="taxon:32630"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 60.6%; Score 201.8; DB 9; Length 336;

Best Local Similarity 77.5%; Pred. No. 2e-43;

Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

Qy 2 gccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcaccc 61

Db 2 gccctgtgctccctctacagccctcaggagctcattgagagctggtcaacatcaccc 61

Qy 62 agaatc---aggcatccctctcaacgagcagcagctggtgagcgtcgaacccgacccg 118

Db 62 AGAACCAGAGGATCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

Qy 119 gcatgtactgcagctctagaaatctctgatcaatgtctccgactgcagcgcattcca 238

Db 122 ACATGTACTGTGCGCCCTGGAAATCCCTGATCAACGTGTGAGCTGCCATCGAGA 181

Qy 179 ggaccagagagctgtaaaagcactgctcctcaaaagcccgagcagcagattcca 238

Db 182 AGACCCAGAGGATGCTAGCGGATTCCTGATCAACGTGTGAGCTGCCATCGAGA 181

Qy 239 gtgaacgagagctgtaaaagcactgctcctcaaaagcccgagcagcagattcca 238

Db 242 GCITGTCATGTCGAGACACCAAAATCGAGTGGCCAGTTTGTAAAGGACCTGCTTAC 301

Qy 299 atgtaaggaggagtttatcgccatggaattcca 331

Db 302 ATTTAAGAAACTTTTTTCGAGGACGGTTCA 334

RESULT 8

LOCUS I58481 336 bp DNA PAT 07-OCT-1997

DEFINITION Sequence 2 from patent US 5652123.

ACCESSION I58481

VERSION I58481.1 GI:2477719

KEYWORDS Unknown.

SOURCE Unknown.

ORGANISM Unclassified.

REFERENCE 1 (bases 1 to 336)

AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le

TITLE Boutellier,C., Lepoint,P., Magazin,M. and Minty,A.

PROTEIN Protein having interleukin 13 activity, recombinant DNA coding for

JOURNAL this protein, transformed cells and microorganisms

PATENT: US 5652123-A 2 29-JUL-1997;

FEATURES

source

1. .336

Location/Qualifiers

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 60.6%; Score 201.8; DB 10; Length 336;

Best Local Similarity 77.5%; Pred. No. 2e-43;

Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

Qy 2 gccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcaccc 61

Db 2 gccctgtgctccctctacagccctcaggagctcattgagagctggtcaacatcaccc 61

Qy 62 agaatc---aggcatccctctcaacgagcagcagctggtgagcgtcgaacccgacccg 118

Db 62 AGAACCAGAGGCTCCCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

Qy 119 gcatgtactgcagctctagaaatctctgatcaatgtctccgactgcagcgcattcca 178

Db 122 ACATGTACTGTGCGCCCTGGAAATCCCTGATCAACGTGTGAGCTGCCATCGAGA 181

Qy 179 ggaccagagagctgtaaaagcactgctcctcaaaagcccgagcagcagattcca 238

Db 182 AGACCCAGAGGATGCTAGCGGATTCCTGATCAACGTGTGAGCTGCCATCGAGA 241

Qy 239 gtgaacgagcagcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 298

Db 242 GCITGTCATGTCGAGACACCAAAATCGAGTGGCCAGTTTGTAAAGGACCTGCTTAC 301

Qy 299 atgtaaggaggagtttatcgccatggaattcca 331

Db 302 ATTTAAGAAACTTTTTTCGAGGACGGTTCA 334

RESULT 9

LOCUS AF043334 417 bp mRNA PRI 21-FEB-1998

DEFINITION Homo sapiens Interleukin 13 precursor (IL13) mRNA, complete cds.

ACCESSION AF043334

VERSION AF043334.1 GI:2905619

KEYWORDS human.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

AUTHORS Jang,J.S. and Kim,B.E.

TITLE Direct Submission

JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea

COMMENT

Nested PCR:

1) first PCR :

forward primer (5'-ctcaatcctctcctgttgca-3')

reverse primer (5'-tagtcaggtcctgtctgc-3')

2) second PCR :

forward primer (5'-ctcatggcgtttttgtgaccag-3')

reverse primer (5'-gatgcttcgaagtttcagttgaa-3').

FEATURES

source

1. .417

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_type="PHA-treated peripheral blood leukocyte"

gene

1. .417

/gene="IL13"

primer_bind

1. .24

/gene="IL13"

/note="second PCR"

/PCR_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles; Deltacycler II from Ericomp"

CDS

4. .402

QY	119	gcattgactgcagctctagaatctctgtatcaatgtctcgaatgcagcgccatccaaa	178
Db	238	ACATGTAAGTGTGACGCCCTGGAATCCCTGTATCAACGTCAGGTCAGTGCATCGACA	297
QY	179	ggaccagagatgactgaaagcaactgtctctcaaaagccgcgcagggcagatttcca	238
Db	298	AGACCCAGAGGATGCTGAGCGGATCTGCCCGCACAAAGGTCTCAGCTGGCAGTTTCCA	357
QY	239	gtgaacgcagcgcagagacacaaaattgaagtgtatccagttggtgaaaaacctgtcacct	298
Db	358	GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGACCTGCTCTTAC	417
QY	299	atgtaagggagtttatcgccatggaattcca	331
Db	418	ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA	450
RESULT 12			
A29950			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
FEATURES			
source			
BASE COUNT			
ORIGIN			
Query Match			
Best Local Similarity			
Matches			
QY	2	gccctgtgactccctcccaaccctcaaggagctcattgagagctgcaacatcccc	61
Db	23	GCCCTGTGCTCCCTCTACGGCCCTCAGGGAGCTCATTTAGGAGCTGGTCAACATCACCC	82
QY	62	agaatc---aggcaccctctgcaacgcagcatggttgagcgtcaacctgaccgcg	118
Db	83	AGAACGAAGGCTCCGCTCTGCAATGGCAGCATGTTATGGAGCATCAACCTGACAGCTG	142
QY	119	gcattgactgcagctctagaatctctgtatcaatgtctcgaatgcagcgccatccaaa	178
Db	143	ACATGTAAGTGTGACGCCCTGGAATCCCTGTATCAACGTCAGGTCAGTGCATCGACA	202
QY	179	ggaccagagatgactgaaagcaactgtgctctcaaaagccgcgcagggcagatttcca	238
Db	203	AGACCCAGAGGATGCTGAGCGGATCTGCCCGCACAAAGGTCTCAGCTGGCAGTTTCCA	262
QY	239	gtgaacgcagcgcagacacaaaattgaagtgtatccagttggtgaaaaacctgtcacct	298
Db	263	GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGACCTGCTCTTAC	322
QY	299	atgtaagggagtttatcgccatggaattcca	331
Db	323	ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA	355
RESULT 13			
158489			

Best Local Similarity 76.9%; Pred. No. 1.4e-42; Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;									
Qy	2	gccctgtgactccctcccccaccctcaaggagctcattgagagctgtggaacatcaccc 61							
Db	65	GCCCTGTGCTCCCTCCAGTACTGCCCTCAGGGAGCTCATTTAGGAGGCTGGTCAACATCACCC 124							
Qy	62	agaatc---aggcatccctctgcaacgcagcatggtgtggagcgtcaacctgaccgcg 118							
Db	125	AGAACCAAGAGGCTCCGCTCTGCAATGCAGCATGGTATGGAGCATCAACCTGACAGCTG 184							
Qy	119	gcattgactgcgcagctctagaatctctgatacttccagactgcagcgccatccaaa 178							
Db	185	GCATGTACTGTGCAGCCCTGGAATCCCTTGATCAAGCTGCAGGTGTCAGTGCATTCGAGA 244							
Qy	179	ggaccagagatgctgaagcactgtctctcaaaagccgcgagggcagatttcca 238							
Db	245	AGACCCAGAGATGCTGAGCGGATTTCTGCCCGCACAGGCTCTCACTGGGCGATTTTCCA 304							
Qy	239	gtgaacgcagcgcgagacaccaaattgaattgacccagttggtgaaaacctgtccacct 298							
Db	305	GCTTGCATGTCGGAGACACCAAAATCGAGGTGGCCCACTTTGTAAAGCACCTGCTCTTAC 364							
Qy	299	atgtaagggggagtttatgcccatggaaatttcca 331							
Db	365	ATTTAAAGAACTTTTTCGCGAGGAGCGGTTCA 397							
RESULT 15									
I86198									
LOCUS	I86198	425 bp	DNA	PAT	10-JUN-1998				
DEFINITION	Sequence 4 from patent US 5700665.								
ACCESSION	I86198								
VERSION	I86198.1 GI:3205916								
KEYWORDS	Unknown.								
SOURCE	Unknown.								
ORGANISM	Unclassified.								
REFERENCE	1 (bases 1 to 425)								
AUTHORS	Legoux, R., Maldonado, P. and Salome, M.								
TITLE	Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine								
JOURNAL	Patent: US 5700665-A 4 23-DEC-1997;								
FEATURES	Location/Qualifiers								
source	1..425								
BASE COUNT	100 a 116 c 110 g 99 t								
ORIGIN									
Query Match: 59.6%; Score 198.6; DB 10; Length 425;									
Best Local Similarity 76.9%; Pred. No. 1.4e-42; Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;									
Qy	2	gccctgtgactccctcccccaccctcaaggagctcattgagagctgtggaacatcaccc 61							
Db	65	GCCCTGTGCTCCCTCCAGTACTGCCCTCAGGGAGCTCATTTAGGAGGCTGGTCAACATCACCC 124							
Qy	62	agaatc---aggcatccctctgcaacgcagcatggtgtggagcgtcaacctgaccgcg 118							
Db	125	AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 184							
Qy	119	gcattgactgcgcagctctagaatctctgatacttccagactgcagcgccatccaaa 178							
Db	185	GCATGTACTGTGCAGCCCTGGAATCCCTTGATCAAGCTGCAGGTGTCAGTGCATTCGAGA 244							
Qy	179	ggaccagagatgctgaagcactgtctctcaaaagccgcgagggcagatttcca 238							
Db	245	AGACCCAGAGATGCTGAGCGGATTTCTGCCCGCACAGGCTCTCACTGGGCGATTTTCCA 304							
Qy	239	gtgaacgcagcgcgagacaccaaattgaattgacccagttggtgaaaacctgtccacct 298							
Db	305	GCTTGCATGTCGGAGACACCAAAATCGAGGTGGCCCACTTTGTAAAGCACCTGCTCTTAC 364							

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:29:54 ; Search time 472.02 Seconds
(without alignments)
411.845 Million cell updates/sec

Title: US-09-451-527-96
Perfect score: 333
Sequence: 1 agccctgtactccctccc.....atgcccatggaatttcaga 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*

- 1: /cgnl_8/gcgdata/geneseq/geneseq/NA1980.DAT.*
- 2: /cgnl_8/gcgdata/geneseq/geneseq/NA1981.DAT.*
- 3: /cgnl_8/gcgdata/geneseq/geneseq/NA1982.DAT.*
- 4: /cgnl_8/gcgdata/geneseq/geneseq/NA1983.DAT.*
- 5: /cgnl_8/gcgdata/geneseq/geneseq/NA1984.DAT.*
- 6: /cgnl_8/gcgdata/geneseq/geneseq/NA1985.DAT.*
- 7: /cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT.*
- 8: /cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT.*
- 9: /cgnl_8/gcgdata/geneseq/geneseq/NA1988.DAT.*
- 10: /cgnl_8/gcgdata/geneseq/geneseq/NA1989.DAT.*
- 11: /cgnl_8/gcgdata/geneseq/geneseq/NA1990.DAT.*
- 12: /cgnl_8/gcgdata/geneseq/geneseq/NA1991.DAT.*
- 13: /cgnl_8/gcgdata/geneseq/geneseq/NA1992.DAT.*
- 14: /cgnl_8/gcgdata/geneseq/geneseq/NA1993.DAT.*
- 15: /cgnl_8/gcgdata/geneseq/geneseq/NA1994.DAT.*
- 16: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT.*
- 17: /cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT.*
- 18: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT.*
- 19: /cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT.*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/NA1999.DAT.*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT.*
- 22: /cgnl_8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	333	100.0	333	21	Canine mature inte
2	333	100.0	333	21	Canine mature inte
3	333	100.0	333	21	Canine mature inte
4	333	100.0	333	21	Canine mature inte
5	333	100.0	1302	21	Canine mature inte
6	333	100.0	1302	21	Canine mature inte
7	317	95.2	330	21	Canine mature inte
8	317	95.2	330	21	Canine mature inte
9	317	95.2	390	21	Canine mature inte
10	317	95.2	390	21	Canine mature inte
11	317	95.2	1269	21	Canine mature inte

C	12	317	95.2	1269	21	255562	Canine interleukin
	13	256	76.9	272	21	255553	Canine interleukin
	14	218	65.5	278	21	255554	Canine interleukin
	15	203.4	61.1	336	13	Q28944	Gly41-Cytokine cod
	16	203.4	61.1	1270	21	F21334	Human low adenosin
	17	203.4	61.1	1270	21	A35212	Human adenosine re
	18	203.4	61.1	1282	21	F21332	Human low adenosin
	19	203.4	61.1	1282	21	A35210	Human adenosine re
	20	203.4	61.1	1290	15	Q56692	Sequence encoding
	21	203.4	61.1	6952	21	F21333	Human low adenosin
	22	203.4	61.1	6952	21	A35211	Human adenosine re
	23	203.4	61.1	14978	21	F21338	Human low adenosin
	24	203.4	61.1	14978	21	A35216	Human adenosine re
	25	201.8	60.6	336	13	Q28943	Asp41-Cytokine cod
	26	201.8	60.6	1237	13	Q28947	Cytokine NC30. Q
	27	142	42.6	1212	15	Q56693	Sequence encoding
	28	71	21.3	5670	21	F21331	Human low adenosin
	29	71	21.3	5670	21	F21337	Human low adenosin
	30	71	21.3	5670	21	A35209	Human adenosine re
	31	71	21.3	5670	21	A35215	Human adenosine re
	32	39	11.7	166	21	255552	Canine interleukin
	33	34	10.2	479	21	C38383	Zea mays DNA fragm
	34	34	10.2	1896	21	248297	S. coelicolor Yesw
	35	33.4	10.0	66	20	232227	Human interleukin
	36	33.4	10.0	772	19	V48405	Dominant-negative
	37	32.4	9.7	717	21	A93373	Enhanced green flu
	38	32.4	9.7	717	21	A93374	Enhanced blue fluo
	39	32.4	9.7	717	21	A93375	Enhanced cyan fluo
	40	32.4	9.7	717	21	A27573	DNA encoding EGFP
	41	32.4	9.7	717	21	A27574	DNA encoding EBFP
	42	32.4	9.7	717	21	A27575	DNA encoding ECFP
	43	32.4	9.7	720	21	C62377	cdNA encoding a gr
	44	32.4	9.7	720	21	Z45642	DNA encoding the m
	45	32.4	9.7	720	21	Z45644	DNA encoding the m

ALIGNMENTS

RESULT 1
255559
ID 255559 standard; cDNA; 333 BP.
XX AC 255559;

14-MAR-2000 (first entry)

Canine mature interleukin-13 (IL-13) clone 80 cDNA.

Interleukin-13; IL-13; antibody; canine; canine; immune response;
immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

Canis familiaris.

WO9961618-A2.

02-DEC-1999.

28-MAY-1999; 99WO-US11942.

29-MAY-1998; 98US-0087306.

(HESK-) HESKA CORP.

Slm G, Yang S, Dreitz MJ, Wonderling RS;

WPI; 2000-072623/06.

P-PSDB; Y58222.

Nucleic acids encoding immunoregulatory proteins from cats or dogs,
useful for treating or preventing e.g. tumors or autoimmune disease

Claim 11; Page 233-234; 264pp; English.

```

XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match 100.0%; Score 333; DB 21; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccccaagagctcattgaggagctggccaacatcacc 60
DB 1 agccctgtgactccctcccaaccccaagagctcattgaggagctggccaacatcacc 60
QY 61 cagaatcaggatccctctgcaacggcagcagatggtgtggagcgtcaacctgacgcgcgc 120
DB 61 cagaatcaggatccctctgcaacggcagcagatggtgtggagcgtcaacctgacgcgcgc 120
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
DB 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
QY 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
DB 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
QY 241 gaacgcagccgagacacccaaattgaagtgtatccagttgtgaaacacctgctcacctat 300
DB 241 gaacgcagccgagacacccaaattgaagtgtatccagttgtgaaacacctgctcacctat 300
QY 301 gtaaggggagttatcgccatggaatttcaga 333
DB 301 gtaaggggagttatcgccatggaatttcaga 333

RESULT 2
255560/c
ID Z55560 standard; cDNA; 333 BP.
XX
AC Z55560;
XX
XX 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX

```

```

PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR P-PSDB; Y58222.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 235; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 100.0%; Score 333; DB 21; Length 333;
Best Local Similarity 100.0%; Pred. No. 1.4e-90;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccccaagagctcattgaggagctggccaacatcacc 60
DB 333 AGCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 274
QY 61 cagaatcaggatccctctgcaacggcagcagatggtgtggagcgtcaacctgacgcgcgcgc 120
DB 273 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACGTGACCCGGGC 214
QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaaagg 180
DB 213 ATGTACTGCGCAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCGAGCGCCATCCAAAGG 154
QY 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
DB 153 ACCCAGAGATGCTGAAAGCAGCTGTGCTCTCAAAAGCCCGCGGACGAGATTTCAGT 94
QY 241 gaacgcagccgagacacccaaattgaagtgtatccagttgtgaaacacctgctcacctat 300
DB 93 GAACGCAGCCGAGACACCAAAATTTGAAGTGATCCAGTTGGTGAATAACCTGCTCACCATT 34
QY 301 gtaaggggagttatcgccatggaatttcaga 333
DB 33 GTAAGGGGAGTTTATCGCCATGGAATTTTCA 1

RESULT 3
255557
ID Z55557 standard; cDNA; 393 BP.
XX

```

255557;
 14-MAR-2000 (first entry)
 Canine interleukin-13 (IL-13) clone 80 cDNA coding region.
 Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 Canis familiaris.
 WO9961618-A2.
 02-DEC-1999.
 28-MAY-1999; 99WO-US11942.
 29-MAY-1998; 98US-0087306.
 (HESK-) HESKA CORP.
 Sim G, Yang S, Dreitz MJ, Wonderling RS;
 WPI; 2000-072623/06.
 P-PSDB; Y58221.
 Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 useful for treating or preventing e.g. tumors or autoimmune disease
 Claim 1i; Page 232-233; 264pp; English.
 Sequences 255552-255560 and 255561-255566 represent cDNA
 sequences encoding canine interleukin-13 (IL-13) clones 80
 and 78 respectively. The invention relates to canine
 IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 colony-stimulating factor (GM-CSF), and nucleotides which encode these
 immunoregulatory proteins. The proteins, their associated
 nucleic acids, specific antibodies and inhibitors may be used as
 vaccines for therapeutic or prophylactic regulation of an immune
 response in animals (particularly cats, dogs, horses and humans).
 They may be used to treat autoimmune or infectious diseases including
 allergies, tumours, inflammation and graft rejection, and to increase
 the response from a co-administered antigen. The nucleotide sequences
 can also be used for the recombinant production of a protein, while
 nucleotide fragments are useful as probes, as amplification primers and
 as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 The proteins may be used to raise antibodies and to screen for
 modulators of activity, while the antibodies may be used in detection,
 and in drug targeting.
 Sequence 393 BP; 93 A; 118 C; 100 G; 82 T; 0 other;

Db 241 accagagagatgtaaaagcaactgtgtctctcaaaagcccgagcgagggcagatttcagat 300
 QY 241 gaacgcagcgagacacacacaaattgaagtgtacatcagttggtgaaacacactgtcacctat 300
 DE |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 301 gaacgcagcgagacacacacaaattgaagtgtacatcagttggtgaaacacactgtcacctat 360
 QY 301 gtaaggagagtttatccatgccatggaatttcaga 333
 DE |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 Db 361 gtaaggagagtttatccatgccatggaatttcaga 393
 RESULT 4
 255558/c
 ID 255558 standard; cDNA; 393 BP.
 XX 255558;
 AC 255558;
 DT 14-MAR-2000 (first entry)
 DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 OS Canis familiaris.
 XX WO9961618-A2.
 PN 02-DEC-1999.
 PD 28-MAY-1999; 99WO-US11942.
 PF 29-MAY-1998; 98US-0087306.
 PR (HESK-) HESKA CORP.
 PA Sim G, Yang S, Dreitz MJ, Wonderling RS;
 PI WPI; 2000-072623/06.
 XX P-PSDB; Y58221.
 DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX Claim 1i; Page 233; 264pp; English.
 PS Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;
 SQ

Query Match 100.0%; Score 333; DB 21; Length 393;
 Best Local Similarity 100.0%; Pred. No. 1.5e-90;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaacccctcaaggagctcattgaggctgtggtcaacatcacc 60
 Db 333 AGCCCTGTGACTCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 274
 QY 61 caaatcagcattccctctgcaacgcagcagctggtgagcgtcaacctgacgcgcgc 120
 Db 273 CAGAAATCAGGATCCCTCTGCAACGGCAGCATGGTGTGGAGCGTCAACCTGACCGCCGC 214
 QY 121 atgtactgcgcagctctagatctctgataatctctccgactgcagcgccatccaaagg 180
 Db 213 ATGTACTGCCAGCTCTAGAACTCTGATCAATCTCTCCGACTGCAGCGCCATCCAAAGG 154
 QY 181 acccagggatgctgaaagcaactgtctctcaaaagccgcggcaggcagattccagt 240
 Db 153 ACCCAGAGGATGCTGAAAGCACTGTCTCTCAAAAGCCGCGGCGAGGCAGATTTCAGT 94
 QY 241 gaacgcagcagagacacacaaatgaagtgtatccagttgtggaataacccctcaccat 300
 Db 93 GAACGCGAGCGAGACACCAAAATTTGAAAGTGATCCAGTTGGTGAATAACCTGCTCACCTAT 34
 QY 301 gtaagggagtttatcgccatggaaatttcaga 333
 Db 33 GTAAGGGAGTTTATCGCCATGGAAATTTTCAGA 1
 RESULT 5
 ID Z55555 standard; cDNA; 1302 BP.
 XX AC Z55555;
 XX DT 14-MAR-2000 (first entry)
 XX DE Canine interleukin-13 (IL-13) clone 80 cDNA.
 XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX OS Canis familiaris.
 FH Key Location/Qualifiers
 FT CDS 52..447
 FT /*tag= a
 FT /product= "Canine IL-13 clone 80"
 PN WO9961618-A2.
 XX PD 02-DEC-1999.
 XX PF 28-MAY-1999; 99WO-US11942.
 XX PR 29-MAY-1998; 98US-0087306.
 XX PA (HESK-) HESKA CORP.
 XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WI: 2000-072623/06.
 XX DR P-PSDB; Y58221.
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease
 XX Claim 11; Page 229-230; 264pp; English.
 XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
 XX sequences encoding canine interleukin-13 (IL-13) clones 80
 XX and 78 respectively. The invention relates to canine
 XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 XX colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 333; DB 21; Length 1302;
 Best Local Similarity 100.0%; Pred. No. 2.4e-90;
 Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaacccctcaaggagctcattgaggctgtggtcaacatcacc 60
 Db 112 agccctgtgactccctcccaacccctcaaggagctcattgaggctgtggtcaacatcacc 171
 QY 61 gagaatcaggcattccctctgcaacgcagcagctggtgagcgtcaacctgacgcgcgc 120
 Db 172 gagaatcaggcattccctctgcaacgcagcagctggtgagcgtcaacctgacgcgcgc 231
 QY 121 atgtactgcgcagctctagatctctgataatctctccgactgcagcgccatccaaagg 180
 Db 232 atgtactgcgcagctctagatctctgataatctctccgactgcagcgccatccaaagg 291
 QY 181 acccagggatgctgaaagcaactgtctctcaaaagccgcggcaggcagattccagt 240
 Db 292 acccagggatgctgaaagcaactgtctctcaaaagccgcggcaggcagattccagt 351
 QY 241 gaacgcagcagagacacacaaatgaagtgtatccagttgtggaataacccctcaccat 300
 Db 352 gaacgcagcagagacacacaaatgaagtgtatccagttgtggaataacccctcaccat 411
 QY 301 gtaagggagtttatcgccatggaaatttcaga 333
 Db 412 gtaagggagtttatcgccatggaaatttcaga 444

RESULT 6

Z55556/c
 ID Z55556 standard; cDNA; 1302 BP.

XX AC Z55556;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-13 (IL-13) clone 80 cDNA complement.

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

FH Key Location/Qualifiers
 FT CDS complement (856..1251)
 FT /*tag= a
 FT /product= "Canine IL-13 clone 80"

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US11942.

XX PR 29-MAY-1998; 98US-0087306.


```
XX PA (HESK-) HESKA CORP.
XX PI
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX KW WPI; 2000-072623/06.
XX DR P-PSDB; Y58221.
XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX PT useful for treating or preventing e.g. tumors or autoimmune disease
XX PS Claim 11; Page 231-232; 264pp; English.
XX CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
XX CC sequences encoding canine interleukin-13 (IL-13) clones 80
XX CC and 78 respectively. The invention relates to canine
XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX CC immunoregulatory proteins. The proteins, their associated
XX CC nucleic acids, specific antibodies and inhibitors may be used as
XX CC vaccines for therapeutic or prophylactic regulation of an immune
XX CC response in animals (particularly cats, dogs, horses and humans).
XX CC They may be used to treat autoimmune or infectious diseases including
XX CC allergies, tumours, inflammation and graft rejection, and to increase
XX CC the response from a co-administered antigen. The nucleotide sequences
XX CC can also be used for the recombinant production of a protein, while
XX CC nucleotide fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for
XX CC modulators of activity, while the antibodies may be used in detection,
XX CC and in drug targeting.
XX SQ Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;

Query Match 100.0%; Score 333; DB 21; Length 1302;
Best Local Similarity 100.0%; Pred. No. 2.4e-90;
Matches 333; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaacccctcaaggagctcattgagagctgtcaacatcacc 60
DB 1191 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTATTGAGAGCTGTCAACATCACC 1132
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcgcgc 120
DB 1131 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGGTGTGAGCGTCAACCTGACCGCGGC 1072
QY 121 atgtactgcgcagctctagaatctctgtatcaatgtctctcgcagctgcagccatccaaagg 180
DB 1071 ATGTACTGCGCAGCTCTAGAAATCTCTGTATCAATGTCTCCGACTGCGAGCGCATCCAAAGG 1012
QY 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcagattccagtt 240
DB 1011 ACCCAGAGATGCTCAAAAGCAGTGTCTCTCAAAAGCCGCGGAGGAGATTTCCAGT 952
QY 241 gaacgcagccgcagacacacaaattgaagtgtatccagttgtaaaaaacctgtccacctat 300
DB 951 GAACGCAGCCGAGACACCAAAATTTGAAGTATCCAGTTGTTGTAAGAAACCTGTCTACCTAT 892
QY 301 gtaagggagtttatgccatggaatttcaga 333
DB 891 GTAAGGGAGTTTATGCCATGCCATGCAAAATTCAGA 859

RESULT 7
Z55565
ID Z55565 standard; cDNA; 330 BP.
XX AC Z55565;
XX DT 14-MAR-2000 (first entry)
```

```
XX DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.
XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX OS Canis familiaris.
XX PN WO9961618-A2.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US11942.
XX PR 29-MAY-1998; 98US-0087306.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX DR P-PSDB; Y58224.
XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX PT useful for treating or preventing e.g. tumors or autoimmune disease
XX PS Claim 11; Page 239-240; 264pp; English.
XX CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
XX CC sequences encoding canine interleukin-13 (IL-13) clones 80
XX CC and 78 respectively. The invention relates to canine
XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX CC immunoregulatory proteins. The proteins, their associated
XX CC nucleic acids, specific antibodies and inhibitors may be used as
XX CC vaccines for therapeutic or prophylactic regulation of an immune
XX CC response in animals (particularly cats, dogs, horses and humans).
XX CC They may be used to treat autoimmune or infectious diseases including
XX CC allergies, tumours, inflammation and graft rejection, and to increase
XX CC the response from a co-administered antigen. The nucleotide sequences
XX CC can also be used for the recombinant production of a protein, while
XX CC nucleotide fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for
XX CC modulators of activity, while the antibodies may be used in detection,
XX CC and in drug targeting.
XX SQ Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 95.2%; Score 317; DB 21; Length 330;
Best Local Similarity 99.1%; Pred. No. 9e-86;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 agccctgtgactccctcccaacccctcaaggagctcattgagagctgtcaacatcacc 60
DB 1 agccctgtgactccctcccaacccctcaaggagctcattgagagctgtcaacatcacc 60
QY 61 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcgcgc 120
DB 61 cagaatcaggcatccctctgcaacggcagcatggtgtgagcgtcaacctgaccgcgcgc 120
QY 121 atgtactgcgcagctctagaatctctgtatcaatgtctctcgcagctgcagccatccaaagg 180
DB 121 atgtactgcgcagctctagaatctctgtatcaatgtctctcgcagctgcagccatccaaagg 180
QY 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcagattccagtt 240
DB 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcagattccagtt 237
QY 241 gaacgcagccgcagacacacaaattgaagtgtatccagttgtaaaaaacctgtccacctat 300
```


CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.

XX Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match 95.2%; Score 317; DB 21; Length 390;
Best Local Similarity 99.1%; Pred. No. 9.6e-86;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 agccctgagctccctcccaaccctcaaggagctcattgagagctgtcaacatcacc 60
Db 61 agccctgagctccctcccaaccctcaaggagctcattgagagctgtcaacatcacc 120
Qy 61 cagaatcaggatccctctgcaacgagcagctggtgtgagcgctcaacctgacccgagc 120
Db 121 cagaatcaggatccctctgcaacgagcagctggtgtgagcgctcaacctgacccgagc 180
Qy 121 atgtactgcagctctagaatctctgatcaatctctccgactgcagcgccatccaaagg 180
Db 181 atgtactgcagctctagaatctctgatcaatctctccgactgcagcgccatccaaagg 240
Qy 181 accagagagctgtaagagcactgtgctctcaaaagccgagcgagatttccagt 240
Db 241 accagagagctgtaagagcactgtgctctcaaaagccgagcgagatttccagt 297
Qy 241 gaacgagcagcagacaccaaattgaagtgtatccagttggtgaaacacctgtcacctat 300
Db 298 gaacgagcagcagacaccaaattgaagtgtatccagttggtgaaacacctgtcacctat 357
Qy 301 gtaaggaggattatcgccatggaatttcaga 333
Db 358 gtaaggaggattatcgccatggaatttcaga 390

RESULT 10
255564/c
ID 255564 standard; cDNA; 390 BP.

AC 255564;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

XX P-PSDB; Y58223.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease

XX Claim 1i; Page 239; 264pp; English.

XX

CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.

XX Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 95.2%; Score 317; DB 21; Length 390;
Best Local Similarity 99.1%; Pred. No. 9.6e-86;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 agccctgagctccctcccaaccctcaaggagctcattgagagctgtcaacatcacc 60
Dy 330 agccctgagctccctcccaaccctcaaggagctcattgagagctgtcaacatcacc 271
Qy 61 cagaatcaggatccctctgcaacgagcagctggtgtgagcgctcaacctgacccgagc 120
Dy 270 cagaatcaggatccctctgcaacgagcagctggtgtgagcgctcaacctgacccgagc 211
Qy 121 atgtactgcagctctagaatctctgatcaatctctccgactgcagcgccatccaaagg 180
Dy 210 atgtactgcagctctagaatctctgatcaatctctccgactgcagcgccatccaaagg 151
Qy 181 accagagagctgtaagagcactgtgctctcaaaagccgagcgagatttccagt 240
Dy 150 accagagagctgtaagagcactgtgctctcaaaagccgagcgagatttccagt 94
Qy 241 gaacgagcagcagacaccaaattgaagtgtatccagttggtgaaacacctgtcacctat 300
Dy 93 gaacgagcagcagacaccaaattgaagtgtatccagttggtgaaacacctgtcacctat 34
Qy 301 gtaaggaggattatcgccatggaatttcaga 333
Dy 33 gtaaggaggattatcgccatggaatttcaga 1

RESULT 11
255561

ID 255561 standard; cDNA; 1269 BP.

AC 255561;

XX 14-MAR-2000 (first entry)

XX Canine interleukin-13 (IL-13) clone 78 cDNA.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

XX Key Location/Qualifiers

XX CDS 57..449

XX /*tag= a

XX /product= "Canine IL-13 clone 78"

|||||
Db 1093 CAGAAATCAGGCATCCCTCTGCAACGCGAGCATGGTGTGGAGCGTCAACCTGACCGCGCGC 1034
QY 121 atgtactgcgagctctagaatctctgatcaatgtctccagactgagcgccatcaaaagg 180
Db 1033 ATGTACTCGCGAGCTCTAGAATCTCTGATCAATGTCTCGACTGCGAGCGCCATCCAAAGG 974
QY 181 acccagagatgctgaagcactgtgctctcaaaagccgagcgagggcagattcccaat 240
Db 973 ACCCAGAGATGCTGAAGCACTGTGCTCTCAAAAGCCCGCGCAGG---GATTTCACAT 917
QY 241 gaacgagccgagacacacaaattgaagtgcattcagttgtgaaacacctgtcacctat 300
Db 916 GAACGCAGCCGAGACACCAAAATTGAAGTGATCCAGTTGGTGAANAACCTGTCACCTAT 857
QY 301 gtaagggagttatcgccatggaatttcaga 333
Db 856 GTAAGGGGAGTTTATCGCCATGGAATTTTCA 824

RESULT 13
Z55553
ID Z55553 standard; cDNA; 272 BP.
XX
AC Z55553;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 228; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targeting.
XX
SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;

Query Match 76.9%; Score 256; DB 21; Length 272;
Best Local Similarity 100.0%; Pred. No. 1.6e-67;
Matches 256; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaacccctcaagagctcattgagagctggtgcaacatcacc 60
Db 17 agccctgtgactccctcccaacccctcaagagctcattgagagctggtgcaacatcacc 76
QY 61 cagaatcaggcatccctctctcaacggcagcagatggtgagcgtcaacactgacgcgcgcg 120
Db 77 cagaatcaggcatccctctctcaacggcagcagatggtgagcgtcaacactgacgcgcgcg 136
QY 121 atgtactgcgagctctagaatctctgatcaatgtctccagctcagcgcgcgcgcgcgcg 180
Db 137 atgtactgcgagctctagaatctctgatcaatgtctccagctcagcgcgcgcgcgcgcg 196
QY 181 acccagagatgctgaagcactgtgctctcaaaagccgagcgagcagatttccagt 240
Db 197 acccagagatgctgaagcactgtgctctcaaaagccgagcgagcagatttccagt 256
QY 241 gaacgagccgagaca 256
Db 257 gaacgagccgagaca 272

RESULT 14
Z55554
ID Z55554 standard; cDNA; 278 BP.
XX
AC Z55554;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) cDNA probe.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 229; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:17 ; Search time 226.02 seconds
(without alignments)
257.246 Million cell updates/sec

Title: US-09-451-527-96

Perfect score: 333

Sequence: 1 agccctgtgactccctccc.....atgcccatggaatttcaga 333

Scoring table: IDENTITY_NUC

Gapop 10.0, Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- Issued Patents.NA.*
1: /cgnl_7/ptodata/1/ina/5A.COMB.seq.*
2: /cgnl_7/ptodata/1/ina/5B.COMB.seq.*
3: /cgnl_7/ptodata/1/ina/6A.COMB.seq.*
4: /cgnl_7/ptodata/1/ina/6B.COMB.seq.*
5: /cgnl_7/ptodata/1/ina/PTCUS.COMB.seq.*
6: /cgnl_7/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	203.4	61.1	336	1	US-08-371-121-24
2	203.4	61.1	1290	1	US-08-012-543-1
3	203.4	61.1	1290	5	PCT-US93-07645A-1
4	203.4	61.1	1290	5	PCT-US93-07645-1
5	201.8	60.6	336	1	US-08-371-121-2
6	201.8	60.6	1297	1	US-08-371-121-15
7	200.2	60.1	384	1	US-08-371-121-17
8	198.6	59.6	425	1	US-08-594-469-4
9	198.6	59.6	425	2	US-08-906-957-4
10	198.6	59.6	4410	1	US-08-594-469-1
11	198.6	59.6	4410	2	US-08-906-957-1
12	142	42.6	447	1	US-08-371-121-26
13	142	42.6	1212	1	US-08-012-543-3
14	142	42.6	1212	5	PCT-US93-07645A-3
15	142	42.6	1212	5	PCT-US93-07645-3
16	33.4	10.0	1322	4	US-09-128-450-27
17	32.4	9.7	720	4	US-09-094-359-3
18	32.4	9.7	720	4	US-09-094-359-7
19	32.4	9.7	720	4	US-09-172-063-11
20	32.4	9.7	720	4	US-09-172-063-13
21	32.4	9.7	762	1	US-08-532-390-40
22	32.4	9.7	762	4	US-08-717-294-40
23	32.4	9.7	768	4	US-09-094-359-11
24	32.4	9.7	850	4	US-09-062-102-2
25	32.4	9.7	972	4	US-09-172-063-27
26	32.4	9.7	972	4	US-09-172-063-29
27	32.4	9.7	1095	4	US-09-085-305-5

28	32.4	9.7	1929	2	US-08-818-253-1	Sequence 1, Appli
29	32.4	9.7	1929	2	US-08-818-253-5	Sequence 5, Appli
30	32.4	9.7	1929	4	US-08-818-252-1	Sequence 1, Appli
31	32.4	9.7	1929	4	US-08-818-252-5	Sequence 5, Appli
32	32.4	9.7	1959	2	US-08-818-253-3	Sequence 3, Appli
33	32.4	9.7	1959	4	US-08-818-252-3	Sequence 3, Appli
34	32.4	9.7	1971	2	US-08-818-253-7	Sequence 7, Appli
35	32.4	9.7	1971	4	US-08-818-252-7	Sequence 7, Appli
36	32.4	9.7	7938	4	US-09-331-581-14	Sequence 14, Appli
37	32	9.6	1926	2	US-08-978-182-2	Sequence 2, Appli
38	32	9.6	1926	2	US-09-205-681-2	Sequence 2, Appli
39	32	9.6	3958	2	US-07-952-853-21	Sequence 21, Appli
40	32	9.6	3958	2	US-08-914-848-21	Sequence 21, Appli
41	31.8	9.5	4184	2	US-08-785-310A-4	Sequence 4, Appli
42	31.8	9.5	35081	2	US-08-752-760A-1	Sequence 1, Appli
43	31.4	9.4	398	4	US-09-060-756-630	Sequence 630, App
44	31.2	9.4	720	4	US-09-094-359-5	Sequence 5, Appli
45	31.2	9.4	720	4	US-09-094-359-9	Sequence 9, Appli

ALIGNMENTS

RESULT 1

US-08-371-121-24

; Sequence 24, Application US/08371121

; Patent No. 5652123

; GENERAL INFORMATION:

; APPLICANT: CAPUT, Daniel

; APPLICANT: FERRARA, Pascual

; APPLICANT: GUILLEMOT, Jean-Claude

; APPLICANT: LEPLATOIS, Pascal

; APPLICANT: MINTY, Adrian

; APPLICANT: KAGHAD, Mourad

; APPLICANT: LABIT-LE BOUTELLER, Christine

; APPLICANT: MAGAZIN, Marilyn

; TITLE OF INVENTION: Protein having a cytokine type

; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/371.121

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/938,161

; FILING DATE: 30-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR92/00280

; FILING DATE: 27-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 00137

; FILING DATE: 08-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 03904

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: Saxe, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 16781/383

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300


```
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match          61.1%; Score 203.4; DB 1; Length 336;
Best Local Similarity 77.8%; Pred. No. 3.8e-55;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 2 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGTTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcaacggcagcagcatggtgtgagcgtcaaacctgaccgcg 118
Db 62 AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGAGGAGCATCAACCTGACAGCTG 121

QY 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
Db 122 GCATGTACTGTGCGAGCCCTCGAATCCCTGTATCAACGCTCAGGCTGAGTGCCCATCGAGA 181

QY 179 ggacccagagatgctgaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 238
Db 182 AGACCCAGAGAGTGTGAGCGGATTTGCCGCGACAGAGTCTCAGCTGGGCGAGTTTCCA 241

QY 239 gtgaacgcagccgcagacacccaaattgaagtgtatccagttggtgaaacacctgctcacct 298
Db 242 GCATTGATGTCGCGAGACACCAAAATCAGGTGGGCCAGTTTGTAAAGGACCTGCTCTTAC 301

QY 299 atgtaagggaggtttatcgccatggaatttca 331
Db 302 ATTTAAAGAAACTTTTTCGGGAGGACGGTTCA 334

RESULT 2
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchemau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
```

```
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
US-08-012-543-1

Query Match          61.1%; Score 203.4; DB 1; Length 1290;
Best Local Similarity 77.8%; Pred. No. 6.3e-55;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 106 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGTTCAACATCACCC 165

QY 62 agaatc---aggcatccctctgcaacggcagcagcatggtgtgagcgtcaaacctgaccgcg 118
Db 166 AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGAGGAGCATCAACCTGACAGCTG 225

QY 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
Db 226 GCATGTACTGTGCGAGCCCTCGAATCCCTGTATCAACGCTGTCAGGCTGCAGTGCATCGAGA 285

QY 179 ggacccagagatgctgaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 238
Db 286 AGACCCAGAGGATGCTGAGCGGATTTGCCGCGACAAAGTCTCAGCTGGGCGAGTTTCCA 345

QY 239 gtgaacgcagccgcagacacccaaattgaagtgtatccagttggtgaaacacctgctcacct 298
Db 346 GCTTGCATGTCGCGAGACACCAAAATCGAGGTGGGCCAGTTTGTAAAGGACCTGCTCTTAC 405

QY 299 atgtaagggaggtttatcgccatggaatttca 331
Db 406 ATTTAAAGAAACTTTTTCGGGAGGACGGTTCA 438

RESULT 3
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
```

;; FILING DATE: 29-JAN-1993
;; PRIORITY APPLICATION DATA:
;; APPLICATION NUMBER: US 07/933416
;; FILING DATE: 21-AUG-1992
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1290 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match. 61.1%; Score 203.4; DB 5; Length 1290;
Best Local Similarity 77.8%; Pred. No. 6.3e-55;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccccacccctcaaggagctcattgaggagctgggtcaacatcaccc 61
DB 106 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 165
QY 62 agaatc---aggcatccctctgcaacgagcagcatggtgtggagcgtcaacacctgaccgcg 118
DB 166 AGAACCAAGAGCTCCGCTCTGCAATGCGAGCATGCTATGGAGCATCAACCTGACAGCTG 225
QY 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
DB 226 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGCAGGCTGCAGTGCATCGAGA 285
QY 179 ggaccagagatgctgaagcactgtgctctcaaaagcccgccagggcagatttcca 238
DB 286 AGACCCAGAGGATGCTGAGCGGATTCGCCCGCAAGGTCACAGTGGCGAGTTTCCA 345
QY 239 gtgaacgcagccgagacacccaaattgaagtgtatccagttgtgaaacacctgctcaact 298
DB 346 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 405
QY 299 atgtaaggaggatttatcgccatggaatttca 331
DB 406 ATTTAAGAAACTTTTTCGCGAGGACGGTTCA 438

RESULT 4
PCT-US93-07645-1
; Sequence 1, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT: Human Interleukin-13
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-1

Query Match 61.1%; Score 203.4; DB 5; Length 1290;
Best Local Similarity 77.8%; Pred. No. 6.3e-55;
Matches 259; Conservative 0; Mismatches 71; Indels 3; Gaps 1;
QY 2 gccctgtgactccctcccccacccctcaaggagctcattgaggagctgggtcaacatcaccc 61
DB 106 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 165
QY 62 agaatc---aggcatccctctgcaacgagcagcatggtgtggagcgtcaacacctgaccgcg 118
DB 166 AGAACCAAGAGCTCCGCTCTGCAATGCGAGCATGCTATGGAGCATCAACCTGACAGCTG 225
QY 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
DB 226 GCATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGCAGGCTGCAGTGCATCGAGA 285
QY 179 ggaccagagatgctgaagcactgtgctctcaaaagcccgccagggcagatttcca 238
DB 286 AGACCCAGAGGATGCTGAGCGGATTCGCCCGCAAGGTCACAGTGGCGAGTTTCCA 345
QY 239 gtgaacgcagccgagacacccaaattgaagtgtatccagttgtgaaacacctgctcaact 298
DB 346 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 405
QY 299 atgtaaggaggatttatcgccatggaatttca 331
DB 406 ATTTAAGAAACTTTTTCGCGAGGACGGTTCA 438

RESULT 5
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:

```
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match      60.6%; Score 201.8; DB 1; Length 336;
Best Local Similarity 77.5%; Pred. No. 1.2e-54;
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaacctcaaggagctcattgaggagctgtgtaacatcaacc 61
DB 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGCTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgacgcgcg 118
DB 62 AGAACCAAGAGGCTCCGCTCTGCAATGCCAGCATGGTATGGAGCATCACTGCACATCG 121

QY 119 gcatgtactgcgcagctctagaatctctgataatgtctccgactgcagcgccatccaaa 178
DB 122 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA 181

QY 179 ggaccagagatgctgaaagcactgtgctctcaaaagccgcggcgagatttccca 238
DB 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCGCCACACAGGTCTCAGCTGGCGAGTTTCCA 241

QY 239 gtgaacgcagcgcagacaccaaattgaagtgtatccagtgtgtaaaacacctgctcaact 298
DB 242 GCTTGTGATGTCAGACACCAAAATGAGGTGGCCCAAGTTTGTAAAGGACCTGCTCTTAC 301

QY 299 atgtaagggagtttatcgccatggaaatttca 331
DB 302 ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 334

RESULT 6
US-08-371-121-15
; Sequence 15, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOIS, Jean-Claude
; APPLICANT: LEPLATOT, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE HOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; * COMPUTER READABLE FORM:
```

```
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938.161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..452
; NAME/KEY: mat_peptide
; LOCATION: 117..452
US-08-371-121-15

Query Match      60.6%; Score 201.8; DB 1; Length 1297;
Best Local Similarity 77.5%; Pred. No. 2e-54;
Matches 258; Conservative 0; Mismatches 72; Indels 3; Gaps 1;

QY 2 gccctgtgactccctcccaaacctcaaggagctcattgaggagctgtgtaacatcaacc 61
DB 118 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGCTCAACATCACCC 177

QY 62 agaatc---aggcatccctctgcaacggcagcatggtgtgagcgtcaacctgacgcgcg 118
DB 178 AGAACCAAGAGGCTCCGCTCTGCAATGCCAGCATGGTATGGAGCATCACTGCAGAGCTG 237

QY 119 gcatgtactgcgcagctctagaatctctgataatgtctccgactgcagcgccatccaaa 178
DB 238 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGAGA 297

QY 179 ggaccagagatgctgaaagcactgtgctctcaaaagccgcggcgagatttccca 238
DB 298 AGACCCAGAGGATGCTGAGCGGATTTCTGCCGCCACACAGGTCTCAGCTGGCGAGTTTCCA 357

QY 239 gtgaacgcagcgcagacaccaaattgaagtgtatccagtgtgtaaaacacctgctcaact 298
DB 358 GCTTGTGATGTCAGACACCAAAATGAGGTGGCCCAAGTTTGTAAAGGACCTGCTCTTAC 417

QY 299 atgtaagggagtttatcgccatggaaatttca 331
DB 418 ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 450
```

RESULT 7
US-08-371-121-17
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascal
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371.121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match 60.1%; Score 200.2; DB 1; Length 384;
Best Local Similarity 77.2%; Pred. No. 4.1e-54;
Matches 257; Conservative 0; Mismatches 73; Indels 3; Gaps 1;

QY 2 gccctgtactccctcccccaaccctcaaggagctcattgagagctggtcaacatcaccc 61
Db 23 gccctgtgctccctctcagccgctcaggagctcattgaggagctggtcaacatcaccc 82
QY 62 agaatac---aggatccctctcgaagcagcatggtgtgagagctcaacctgacgcgcg 118
Db 83 AGAACCAAGGCTCCGCTCTCAATGGCAGCATGTTATGGAGCATCAACCTGACAGCTG 142

QY 119 gcatgtactgcagctcttagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
Db 143 ACATGTACTGTGAGCCCTCGAATCCTGATCAACGTTGTCAGGTGTCAGTCCCATCGAGA 202
QY 179 ggaccagagagtgctgaaagcactgtgctctcaaaagcccgagcgagggcagattcca 238
Db 203 AGACCCAGAGATGCTGAGCGGATTCTGCCCGCACAGGTCTCAGCTGGGAGCTTTTCCA 262
QY 239 gtgaacgcagcgagagacacacaaaattgaagtgtatccagttggtgaaaaacctgtcacct 298
Db 263 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 322
QY 299 atgaaggaggagtttatcgcatggaaattcca 331
Db 323 ATTAAAGAAACTTTTTCGCGAGGACGGTTCA 355

RESULT 8
US-08-594-469-4
; Sequence 4, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-4

Query Match 59.6%; Score 198.6; DB 1; Length 425;
Best Local Similarity 76.9%; Pred. No. 1.4e-53;
Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 2 gccctgtactccctcccccaaccctcaaggagctcattgagagctggtcaacatcaccc 61
Db 65 GCCTGTGCTCCCTCAGTACTGCTCCCTCAGGAGGCTCATTGAGGAGCTGCTCAACATCACCC 124

Qy	62	agaatc---aggcatccctctgcaacagcgagcatggtgtggaggtgcaacctgaccgcg	118
Db	125	AGAACCAAGAGGCTCGGCTCTGCAATGGCAGCATGGTATGAGCATCAACCTGACAGCTG	184
Qy	119	gcatgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgccatccaaa	178
Db	185	GCATGTACTGTGTCAGCCCTGGAAATCCCTGATCAACGTGTGAGGTGCGCATCGAGA	244
Qy	179	ggaccagagatgctgaaagcacgtgtctctcaaaagccgcgagcgagcgagatttcca	238
Db	245	AGACCCAGAGGATGCTGACGGGATTCTGCCGGCACAAGGTCTCAGCTGGGCGAGTTTCCA	304
Qy	239	gtgaacgcagcgcagacacacccaaaattgaagtgcacgttggtagaaacacctgctcaact	298
Db	305	GCTTCATGCTCCGAGACACCAAAATCGAGGTGCCCATTTGTAAAGGACCTGCTCTTAC	364
Qy	299	atgtaaggggagtttatcgccatgaaatttca	331
Db	365	ATTTAAGAAACTTTTTCGAGGGACGGTTCA	397

RESULT 9
 US-08-906-957-4
 ; Sequence 4, Application US/08906957
 ; Patent No. 5856142
 ; GENERAL INFORMATION:
 ; APPLICANT: LEGOUX, Richard
 ; APPLICANT: MALDONADO, Paul
 ; APPLICANT: SALOME, Marc
 ; TITLE OF INVENTION: Method for the extraction of
 ; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
 ; TITLE OF INVENTION: presence of arginine
 ; NUMBER OF SEQUENCES: 9
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Bacon & Thomas
 ; STREET: 625 Slaters Lane - Fourth Floor
 ; CITY: Alexandria
 ; STATE: Virginia
 ; COUNTRY: USA
 ; ZIP: 22314
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.25
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/906,957
 ; FILING DATE: 06-AUG-1997
 ; CLASSIFICATION: 435
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: 08/594,469
 ; FILING DATE:
 ; APPLICATION NUMBER: FR 95 01083
 ; FILING DATE: 31-JAN-1995
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: FICHTER, Richard E
 ; REGISTRATION NUMBER: 26,382
 ; REFERENCE/DOCKET NUMBER: REF/LEGOUX
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (703) 683-0500
 ; TELEFAX: (703) 683-1080
 ; INFORMATION FOR SEQ ID NO: 4:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 425 base pairs
 ; TYPE: nucleic acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: linear
 ; MOLECULE TYPE: DNA (genomic)
 US-08-906-957-4

Query Match 59.6% Score 198.6; DB 2; Length 425;

Best Local Similarity 76.9%; Pred. No. 1.4e-53;
Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

Qy 2 gccctgtactccctcccccaaccctcaagagcattcaggagctggtcaacatcaccc 61
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 65 GCCCTGTGCCCTCCCAAGTACTGCCCTCAGGGAGCTCATTCAGGAGCTGGTCAACATCACCC 124
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 62 agaatac---aggcatccctctgcacaacggcagcatggttggagcgctcaaacctgaccgccg 118
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 125 AGAACCAAGAGGCTCGCTCTGCATTCGAATGGCAGCATGTTATGGAGCATCAACTGACAGCTG 184
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 119 gcatgtactgcgcagctcttagaatctctctgatcaatgtctcccagctgcagcgccatccaaa 178
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 185 GCATGTACTGTGCAGCCCTGGAAATCCCTGATCAACGTGTCAAGCTGCAGTGCCATCGAGA 244
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 179 gaacccaagaagtgtgaagcaactgtgtctctcaaaagccgcggcagggcagattttcaa 238
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 245 AGACCCAGAGGATGTGACGGGATTCTGCCCCACAAAGGTCTCAGCTGGGAGTTTTTCCA 304
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 239 gtgaacgcagccgcagacacccaaaattgaagtcatcagttggtgaaaaaacctgctcacct 298
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 305 GCTTGCATGTCGAGACACCAAATCGAGTGGCCCAGTTGTAAAGGACCTGCTCTTAC 364
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 299 atgtaagggaggtttatgcgatgccaatggaatttca 331
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 365 ATTTAAGAAAACCTTTTTCGCGAGGACGCGTTCA 397
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

RESULT 10
US-08-594-469-1
; Sequence 1, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594.469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26.382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)

Query Match 59.6%; Score 198.6; DB 2; Length 425;

US-08-594-469-1

```

Query Match          59.6%; Score 198.6; DB 1; Length 4410;
Best Local Similarity 76.9%; Pred. No. 3.2e-53;
Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 2 gccctgtactccctcccaaacctcaaggagctcattgaggagctggtcaacatcaccc 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 402 GCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCAATGAGGAGCTGGTCAACATCACCC 461

QY 62 agaatac---aggcatccctctgcaacggcagcatggtgagagctcaaacctgaccgcg 118
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 462 AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGTATGAGAGCATCAACCTGACAGCTG 521

QY 119 gcatgtactgagctctagatctctgataatctctccgactgagcgccatccaaa 178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 522 GCATGTACTGTGCAGGCCCTGGAATCCCTGATCAACGTGTGAGGAGCTGGTCAACATCACCC 461

QY 179 ggaaccagaggtgtaagacactgtctctcaaaagccgcgagcgccatccaaa 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 582 AGACCCAGAGGATGCTGAGCGGATTCGCCCGCACCAAGGTCTCAGCTGGCAGTTTCCA 641

QY 239 gtgaacgcagcgagacacacaaattgaaagtatccagttggtgaaacacctgctcacct 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 642 GCTTCATGTCGAGACACCAAAATCGAGTGGCGCCAGTTTGTAAAGGACCTGCTCTTAC 701

QY 299 atgtaagggagtttatccctggaatttca 331
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 702 ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA 734

RESULT 11
US-08-594-469-1
; Sequence 1, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:

```

```

; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-906-957-1

Query Match          59.6%; Score 198.6; DB 2; Length 4410;
Best Local Similarity 76.9%; Pred. No. 3.2e-53;
Matches 256; Conservative 0; Mismatches 74; Indels 3; Gaps 1;

QY 2 gccctgtactccctcccaaacctcaaggagctcattgaggagctggtcaacatcaccc 61
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 402 GCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCAATGAGGAGCTGGTCAACATCACCC 461

QY 62 agaatac---aggcatccctctgcaacggcagcatggtgagagctcaaacctgaccgcg 118
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 462 AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGTATGAGAGCATCAACCTGACAGCTG 521

QY 119 gcatgtactgagctctagatctctgataatctctccgactgagcgccatccaaa 178
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 522 GCATGTACTGTGCAGGCCCTGGAATCCCTGATCAACGTGTGAGGAGCTGGTCAACATCACCC 461

QY 179 ggaaccagaggtgtaagacactgtctctcaaaagccgcgagcgccatccaaa 238
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 582 AGACCCAGAGGATGCTGAGCGGATTCGCCCGCACCAAGGTCTCAGCTGGCAGTTTCCA 641

QY 239 gtgaacgcagcgagacacacaaattgaaagtatccagttggtgaaacacctgctcacct 298
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 642 GCTTCATGTCGAGACACCAAAATCGAGTGGCGCCAGTTTGTAAAGGACCTGCTCTTAC 701

QY 299 atgtaagggagtttatccctggaatttca 331
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 702 ATTTAAGAAACTTTTTCGCGAGGGACGGTTCA 734

RESULT 12
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 26:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 447 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-371-121-26

Query Match 42.6%; Score 142; DB 1; Length 447;
Best Local Similarity 67.0%; Pred. No. 9.2e-36;
Matches 221; Conservative 0; Mismatches 100; Indels 9; Gaps 1;

QY 1 agccctgtgactcctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 60
Db 121 AGATCTGTGTCTCTCCCTCTCACCTTAAGCAGCTTATTGAGGAGCTGAGCAACATCACA 180

QY 61 cagaatcaggcatcctctgcaaggagcagatggtgtagagcgtcaacccagccgcgc 120
Db 181 CAAGACCAGACTCCCTCTGTGCAAGCGCAGCATGTTGAGTGGAGTGGACCTGGCCGCTGC 240

QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactcagcgccatccaaagg 180
Db 241 GGGTCTGTGTAGCCCTGGATTCTCTGNCCCAACATCTCCATTGCAATGCCATCTACAGG 300

QY 181 acccagaggtgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
Db 301 ACCCAGAGGATATTGCATGGCTCTGTAAACCGCAAGGCC-----CCCACTACGGTTC 351

QY 241 gaacgcagcgcagcaccacaaatgaagtgatccagttggtgaaaaaacctgctcacctat 300
Db 352 TCCAGCCTCCCGATACCAAAATCGAAGTAGCCCACTTTATACAAAAAAGTCTCAGCTAC 411

QY 301 gtaagggagtttatcgccatggaaatttc 330
Db 412 ACAAGCAACTGTTTCGCCACGCGCCCTTC 441

RESULT 13
US-08-012-543-3
; Sequence 3, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 70..465
US-08-012-543-3

Query Match 42.6%; Score 142; DB 1; Length 1212;
Best Local Similarity 67.0%; Pred. No. 1.3e-35;
Matches 221; Conservative 0; Mismatches 100; Indels 9; Gaps 1;

QY 1 agccctgtgactcctcccaacccctcaaggagctcattgaggagctggtcaacatcacc 60
Db 142 AGATCTGTGTCTCTCCCTCTCACCTTAAGCAGCTTATTGAGGAGCTGAGCAACATCACA 201

QY 61 cagaatcaggcatcctctgcaaggcagcagatggtgtagagcgtcaacccagccgcgc 120
Db 202 CAAGACCAGACTCCCTCTGTGCAAGCGCAGCATGTTGAGTGGAGTGGACCTGGCCGCTGC 261

QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactcagcgccatccaaagg 180
Db 262 GGGTCTGTGTAGCCCTGGATTCTCTGNCCCAACATCTCCAAATTCGAATGCCATCTCAGG 321

QY 181 acccagaggtgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
Db 322 ACCCAGAGGATATTGCATGGCTCTCTAACCGCAAGGCC-----CCCACTACGGTTC 372

QY 241 gaacgcagcgcagcaccacaaatgaagtgatccagttggtgaaaaaacctgctcacctat 300
Db 373 TCCAGCCTCCCGATACCAAAATCGAAGTAGCCCACTTTATACAAAAAAGTCTCAGCTAC 432

QY 301 gtaagggagtttatcgccatggaaatttc 330
Db 433 ACAAGCAACTGTTTCGCCACGCGCCCTTC 462

RESULT -14
PCT-US93-07645A-3
; Sequence 3, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:

```

; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; PCT-US93-07645A-3

Query Match 42.6%; Score 142; DB 5; Length 1212;
Best Local Similarity 67.0%; Pred. No. 1.3e-35;
Matches 221; Conservative 0; Mismatches 100; Indels 9; Gaps 1;

Qy 1 agccctgtgactccctcccaaccctcaaggagctcattgagagctgtgtaacatcacc 60
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 AGATCTGTCTCTCCCTCTGACCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 201

Qy 61 cagaatcaggcatccctctgcaacgagcagcatgtgtgagcgtcaacctgacgcgcgc 120
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 202 CAAGACCAAGACTCCCTCTGCAACGGCAGCATGGTATGGAGTGTGACCTGGCGCTGGC 261

Qy 121 atgtactgcgcagctctagaatctctgataatgtctccgactgcagcgccatccaaagg 180
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 262 GGGTCTGTGTAGCCCTCGATTCCCTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321

Qy 181 acccagagagctgtaaaagcactgtgtctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 322 ACCCAGAGGATATTGCATGGCTCTGTAAACCCCAAGGCC-----CCCACTACGGTC 372

Qy 241 gaacgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 TCCAGCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTTATAACAAAACCTGCTCAGCTAC 432

Qy 301 gtaaggggagttatcgccatggaatttc 330
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 433 ACAAGCAACTGTTTCGCCACGCGCCCTTC 462

RESULT 15
PCT-US93-07645-3
; Sequence 3, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
```

```

; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; PCT-US93-07645-3

Query Match 42.6%; Score 142; DB 5; Length 1212;
Best Local Similarity 67.0%; Pred. No. 1.3e-35;
Matches 221; Conservative 0; Mismatches 100; Indels 9; Gaps 1;

Qy 1 agccctgtgactccctcccaaccctcaaggagctcattgagagctgtgtaacatcacc 60
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 142 AGATCTGTCTCTCCCTCTGACCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 201

Qy 61 cagaatcaggcatccctctgcaacgagcagcatgtgtgagcgtcaacctgacgcgcgc 120
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 202 CAAGACCAAGACTCCCTCTGCAACGGCAGCATGGTATGGAGTGTGACCTGGCGCTGGC 261

Qy 121 atgtactgcgcagctctagaatctctgataatgtctccgactgcagcgccatccaaagg 180
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 262 GGGTCTGTGTAGCCCTCGATTCCCTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321

Qy 181 acccagagagctgtaaaagcactgtgtctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 322 ACCCAGAGGATATTGCATGGCTCTGTAAACCCCAAGGCC-----CCCACTACGGTC 372

Qy 241 gaacgcagcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgcgc 300
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 373 TCCAGCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTTATAACAAAACCTGCTCAGCTAC 432

Qy 301 gtaaggggagttatcgccatggaatttc 330
|| ||||| ||| ||| ||||| ||||| ||||| ||||| ||||| |||||
Db 433 ACAAGCAACTGTTTCGCCACGCGCCCTTC 462
```

Search completed: May 13, 2001, 14:21:21
Job time: 17832 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:15 ; Search time 5997.24 Seconds
(without alignments)
485.077 Million cell updates/sec

Title: US-09-451-527-96
Perfect score: 333
Sequence: 1 agccctgtgactccctcccc.....atcgccatggaatttcaga 333

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est33:*
26: gb_est34:*
27: gb_est35:*
28: gb_est36:*
29: gb_est37:*
30: gb_est38:*
31: gb_est39:*
32: gb_est40:*
33: gb_estba:*
34: em_estfun:*
35: em_esthum1:*
36: em_esthum2:*
37: em_esthum3:*
38: em_esthum4:*
39: em_esthum5:*
40: em_esthum6:*
41: em_esthum7:*
42: em_esthum8:*
43: em_esthum9:*

- 44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estin5:*
68: em_estom1:*
69: em_estom2:*
70: em_estov1:*
71: em_estov2:*
72: em_estpl1:*
73: em_estpl2:*
74: em_estpl3:*
75: em_estpl4:*
76: em_estpl5:*
77: em_estpl6:*
78: em_estpl7:*
79: em_estpl8:*
80: em_estpl9:*
81: em_estpl10:*
82: em_estro1:*
83: em_estro2:*
84: em_estro3:*
85: em_estro4:*
86: em_estro5:*
87: em_estro6:*
88: em_estro7:*
89: em_estro8:*
90: em_estro9:*
91: em_estro10:*
92: em_estro11:*
93: em_estro12:*
94: em_estro13:*
95: em_estro14:*
96: em_estro15:*
97: em_estro16:*
98: em_estro17:*
99: em_estro18:*
100: em_estro19:*
101: em_estro20:*
102: gb_est25:*
103: gb_est26:*
104: gb_est27:*
105: gb_est28:*
106: gb_est29:*
107: gb_est30:*
108: gb_est31:*
109: gb_est32:*
110: gb_est41:*
111: gb_est42:*
112: gb_est43:*
113: gb_est44:*
114: gb_est45:*
115: gb_est46:*
116: gb_est47:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	37	11.1	1016	230	CNS024F6	AL180699 Tetradon
2	36.4	10.9	277	137	BE593226	BE593226 WSI_99_B0
3	36.4	10.9	537	166	BE357229	BE357229 DGI_147_B
4	36	10.8	462	143	BF039993	BF039993 BP250023B
5	35.8	10.8	497	20	A144326	A1444326 fb47hl2.y
6	35.8	10.8	1946	119	AW729623	AW729623 GA_Ea002
7	35.6	10.7	2275	14	AF034173	AF034173 AF034173
8	35.4	10.6	498	150	BF606532	BF606532 273595 MA
9	34.4	10.3	507	138	BE705147	BE705147 SC02_08f0
10	34.2	10.3	535	161	BE032541	BE032541 131940 MA
11	34.2	10.3	546	161	BE032543	BE032543 131942 MA
12	34.2	10.3	570	24	A1746678	A1746678 ul06b05.y
13	34.2	10.3	965	217	AZ201624	AZ201624 SP_0053_A
14	34	10.2	370	166	BE363650	BE363650 WSI_64_G1
15	34	10.2	562	166	BE361027	BE361027 DGI_69_A0
16	34	10.2	929	143	BF037598	BF037598 601461167
17	33.8	10.2	341	163	BE127683	BE127683 DEPAL1432
18	33.6	10.1	577	166	BE402120	BE402120 CSB004F06


```

Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 24 cctcaaggagctcattgaggagctgtgtaacataccaccagaatcaggcatccctctgcaa 83
DB 22 CCCCATGGAGAGGCTCGGGAGCCGCGGACATCGCGCGGTGTCGGGTTCCTCTGCAC 81
QY 84 cggcagcatggttgagagctcaacctgagccgcggtatgtactgacgagctctagaatc 143
DB 82 CGACGCCCGCGAGTGGTCAACGCCAGGTATCCCGGCCAACCGCGGTACGTGTGATG 141
QY 144 ttgatcaatgtctccgactgc 165
DB 142 TCATGATCTTTAGCTTCTACAGC 163

RESULT 3
BE357229
LOCUS DGI_147_B02.g1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
DEFINITION BE357229 537 bp mRNA EST 20-JUL-2000
ACCESSION BE357229
VERSION BE357229.1 GI:9298786
KEYWORDS EST.
SOURCE Sorghum bicolor
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
; Andropogoneae; Sorghum.
1 (bases 1 to 537)
REFERENCE Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
AUTHORS L.H.
TITLE An EST database from Sorghum: dark-grown seedlings
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolyTMix
High quality sequence start: 31
High quality sequence stop: 514
POLYA-No. Location/Qualifiers
FEATURES
source
1..537
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGI)"
/notes="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
BASE COUNT 89 a 160 c 176 g 112 t
ORIGIN

Query Match 10.9%; Score 36.4; DB 166; Length 537;
Best Local Similarity 53.5%; Pred. No. 4.5;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

QY 24 cctcaaggagctcattgaggagctgtgtaacataccaccagaatcaggcatccctctgcaa 83
DB 249 CCCCATGGAGAGGCTCGGGAGCCGCGGACATCGCGCGGTGTCGGGTTCCTCTGCAC 308
QY 84 cggcagcatggttgagagctcaacctgagccgcggtatgtactgacgagctctagaatc 143
DB 309 CGACGCCCGCGAGTGGTCAACGCCAGGTATCCCGGCCAACCGCGGTACGTGTGATG 368
QY 144 ttgatcaatgtctccgactgc 165

```

```

||||||| | | | | | | |
Db 369 TCTGATCTTTAGCTTCTACAGC 390

RESULT 4
BF039993
LOCUS BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA
DEFINITION clone BP250023B10D12 5', mRNA sequence.
ACCESSION BF039993
VERSION BF039993.1 GI:10757048
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;
Bovidae; Bovinae; Bos.
1 (bases 1 to 462)
REFERENCE Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
AUTHORS J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGG
BACKWARD: ATTAACCTCACTAAAG
Insert Length: 462 Std Error: 0.00
Plate: BP250023B10 row: D column: 12
Seq primer: AGCGATACCAATTTCCACAGGA
High quality sequence stop: 462.
Location/Qualifiers
FEATURES
source
1..462
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250023B10D12"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/notes="Organ: placenta; Vector: pMT73pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 110 a 153 c 123 g 73 t
ORIGIN

Query Match 10.8%; Score 36; DB 143; Length 462;
Best Local Similarity 47.9%; Pred. No. 5.6;
Matches 102; Conservative 0; Mismatches 111; Indels 0; Gaps 0;

QY 25 ctaaggagctcattgaggagctgtgtaacataccaccagaatcaggcatccctctgcaa 84
DB 113 CTGATGGAGTTCAGTGAGCACCTGGCCATCATCTCTGGAGGACGCGCTCCGACATCAGC 172
QY 85 ggcagcatggttgagagctcaacctgagccgcggtatgtactgacgagctctagaatc 144
DB 173 TCCACTCTCGGCAACCAACATCAACACGCGGAGTGTCTCCCATTCAGCTGGACACC 232
QY 145 ctgatcaatgtctccgactgcagcgccatccaaaggaccagaggatgctgaaagcactg 204

```

BASE COUNT	126 a	167 c	121 g	83 t
ORIGIN				
Query Match	10.8%;	Score 35.8;	DB 20;	Length 497;
Best Local Similarity	57.7%;	Pred. No. 6.5;		
Matches	64;	Conservative	0;	Mismatches 47; Indels 0; Gaps 0;
Qy	184	cgagagatgctgaaagcactgtgctctcaaaagccgcgagcgagcgagatttccagtga	243	
Db	422	CAGAGGATGCTGAGAGATTTCAGGTTCCGCGACGACGCGGAGTGGAGAGGGCTGGATGG	363	
Qy	244	cgacgcgcgagacacccaattgaagtgcattgcacagttggtgaaacacctgctc	294	
Db	362	TTCAGAGTCCCGCCACTTTTGTAGTCTGCTCAGTGTGTCGAGAACCAACGTC	312	
RESULT	6			
LOCUS	AW729623/c	1946 bp	mrna	EST 16-NOV-2000
DEFINITION	GA_Ea0025J07 Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0025J07, mRNA sequence.			
ACCESSION	AW729623	AW729623.1	GI:7627221	
KEYWORDS	EST.			
SOURCE	Gossypium arboreum.			
ORGANISM	Gossypium arboreum.			
REFERENCE	Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Malvales; Malvaceae; Gossypium.			
AUTHORS	Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry D., Wood,T.C., Leslie,A. and Wilkins,T.A.			
TITLE	An integrated analysis of the genetics, development, and evolution of the cotton fiber			
JOURNAL	Unpublished (2000)			
COMMENT	Contact: Wing RA Clemson University Genomics Institute Clemson University 100 Jordan Hall, Clemson, SC 29634, USA Tel: 864 656 7288 Fax: 864 656 4293 Email: rwing@clemson.edu			
FEATURES	High quality sequence stop: 1946.			
source	Location/Qualifiers			
	1..1946			
	/organism="Gossypium arboreum"			
	/strain="AKA"			
	/cultivar="8400"			
	/db_xref="taxon:29729"			
	/clone="GA_Ea0025J07"			
	/clone_lib="Gossypium arboreum 7-10 dpa fiber library"			
	/tissue_type="Fibers isolated from bolls harvested 7-10 dpa"			
	/lab_host="E. coli"			
	/notes="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"			
BASE COUNT	412 a	492 c	495 g	472 t
ORIGIN	75 others			
Query Match	10.8%;	Score 35.8;	DB 119;	Length 1946;
Best Local Similarity	52.8%;	Pred. No. 9.5;		
Matches	76;	Conservative	0;	Mismatches 68; Indels 0; Gaps 0;
Qy	123	gtactgcgcgactagaattctctgataatgtctccgactgcagcgccatcccaagagac	182	
Db	276	GCACTGCGGACCTCTATTTGTGTGTATCTATGTCTCTCAGTATCGAGCGCACTACAGCAC	217	
Qy	183	ccagagatgctaaaaacactgtgctctcaaaagccgcgagcgagatttccagtga	242	
Db	216	ACATAGCTAAACCAAGAACAGAGAGNCTCGGCACTCTCGTAGCGCGCAAGTAAATGTGA	157	
Qy	243	acgcgacgcgagacacccaattga	266	

[illegible]

```

source
1. 535
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      121 a   151 c   168 g   95 t
ORIGIN

Query Match      10.3%; Score 34.2; DB 161; Length 535;
Best Local Similarity 55.5%; Pred. No. 19;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;

QY 4 cctgtgactccctcccaacacctcaagagagctctattgaggagctggttcacacatcacccag 63
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 227 CCTGTACCACCGGGTCTACGATGACAAAGGGCAATGAGAAAGACATCACCGTGGCCGAC 286

QY 64 aatcagacatccctctcaacgcagcatggtgtggagcgtcaacctgaccgcgcggcat 122
||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 287 GATGAGGCGATCCGCCCAACACCACCATGAGGCGCTGGCCAAACTGAAGCCTCGCTT 345

RESULT 11
BE032543
LOCUS BE032543 546 bp mRNA EST 09-JUL-2000
DEFINITION 131942 MARC 1P1G Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE032543
VERSION BE032543.1 GI:8327552
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
REFERENCE 1 (bases 1 to 546)
AUTHORS Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing, bases called and alt trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -mismatch 12 options.
PCR Primers
FORWARD: AGGAACAGCTATGACCAT
BACKWARD: GTTTCCCGAGTCACGACG
Plate: 63 row: E column: 10
Seq primer: ATTTAGTGACACTATAG.
Location/Qualifiers
1. 546
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC 1P1G"
/tissue_type="pooled"
/lab_host="DH10B"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI;
Library made from pooled tissue from day 11, 13, 15, 20,
and 30 embryos."
BASE COUNT      125 a   152 c   169 g   98 t   2 others
ORIGIN

Query Match      10.3%; Score 34.2; DB 161; Length 546;

```



```

QY 141 atctctgatcaatgt 155
Db 637 ACTACTCTTCACGGT 623

RESULT 14
BE363650
LOCUS BE363650 370 bp mRNA EST 20-JUL-2000
DEFINITION WSI_64_GL0_A002 Water-stressed 1 (WS1) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BE363650
VERSION BE363650.1 GI:9305207
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 370)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: water-stressed plants
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: Polymix
High quality sequence start: 32
High quality sequence stop: 368
POLYA=yes.
FEATURES
source Location/Qualifiers
1..370
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Water-stressed 1 (WS1)"
/note="Organ: Mix of 5-week old plants on days 7 & 8 after
water was withheld; Vector: Lambda Zap; Site.1: XhoI;
Site.2: EcoRI; The library was made from poly-A RNA in the
cloning vector lambda ZAP II. Clones to be sequenced were
prepared by mass excision."
BASE COUNT 76 a 110 c 130 g 54 t
ORIGIN

Query Match 10.2%; Score 34; DB 166; Length 370;
Best Local Similarity 56.1%; Pred. No. 20;
Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 13 ccctcccaaccctcaaggagctcattgagagctgtcaacatcacccaggaatcaggca 72
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 54 CCTTCGGCGAGGTCAGGACGTCAGAGCGCGCTGGACGAGTCCACGAGCAGACCGC 113

QY 73 tccctctgcaaggcagcatggtgtggagcgctcaacctgacccgcgcatgtac 126
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114 TCCTTCGGCTTCCTCACCCTTCCTTGAGCGCGAGGACGCCGCCCTGCCATGGAC 167

RESULT 15
BE361027
LOCUS BE361027 562 bp mRNA EST 20-JUL-2000
DEFINITION DGL_69_A02_b1_A002 Dark Grown 1 (DGL) Sorghum bicolor cDNA, mRNA
sequence.
ACCESSION BE361027
VERSION BE361027.1 GI:9302584
KEYWORDS EST.

```

```

sorghum.
Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 562)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: dark-grown seedlings
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: JEN REV
High quality sequence stop: 560
POLYA=no.
FEATURES
source Location/Qualifiers
1..562
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGL)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site.1: XhoI; Site.2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."
BASE COUNT 130 a 174 c 187 g 71 t
ORIGIN

Query Match 10.2%; Score 34; DB 166; Length 562;
Best Local Similarity 56.1%; Pred. No. 22;
Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 13 ccctcccaaccctcaaggagctcattgagagctgtgtcaacatcacccaggaatcaggca 72
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 171 CCTTCGGCGAGGTCAGGACGTCAGAGCGCGCTGGACGAGTCCACGAGCAGACCGC 230

QY 73 tccctctgcaaggcagcatggtgtggagcgctcaacctgacccgcgcatgtac 126
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 231 TCCTTCGGCTTCCTCACCCTTCCTTGAGCGCGAGGACGCCGCCCTGCCATGGAC 284

```

Search completed: May 13, 2001, 11:40:22
Job time: 16497 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:20:35 ; Search time 9342.78 Seconds
(without alignments)
2003.155 Million cell updates/sec

Title: US-09-451-527-99

Perfect score: 1269

Sequence: 1 ccagctacgacctgctgc.....gaaaaaaaaaaaaaaaaa 1269

Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

GenEmbl.*

1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_em.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
14: gb_pl3.*
15: gb_pl4.*
16: gb_ba1.*
17: gb_ba2.*
18: em_fun.*
19: em_htgo_hum.*
20: em_htgo_inv.*
21: em_htgo_rod.*
22: em_htg_hum1.*
23: em_htg_hum2.*
24: em_htg_hum3.*
25: em_htg_hum4.*
26: em_htg_hum5.*
27: em_htg_hum6.*
28: em_htg_hum7.*
29: em_htg_hum8.*
30: em_htg_inv1.*
31: em_htg_inv2.*
32: em_htg_rod.*
33: em_htg_rod.*
34: em_hum1.*
35: em_hum2.*
36: em_hum3.*
37: em_hum4.*
38: em_hum5.*
39: em_hum6.*
40: em_hum7.*
41: em_in.*
42: em_or.*
43: em_or.*

44: em_ov.*
45: em_pat.*
46: em_ph.*
47: em_pl.*
48: em_ro.*
49: em_sts.*
50: em_sy.*
51: em_un.*
52: em_vi.*
53: gb_sts1.*
54: gb_sts2.*
55: gb_sts3.*
56: gb_sy.*
57: gb_un.*
58: gb_vil.*
59: gb_vil.*
60: gb_htg1.*
61: gb_htg2.*
62: gb_htg3.*
63: gb_htg4.*
64: gb_htg5.*
65: gb_htg6.*
66: gb_htg7.*
67: gb_htg8.*
68: gb_htg9.*
69: gb_htg10.*
70: gb_htg11.*
71: gb_htg12.*
72: gb_htg13.*
73: gb_htg14.*
74: gb_htg15.*
75: gb_htg16.*
76: gb_htg17.*
77: gb_htg18.*
78: gb_htg19.*
79: gb_htg20.*
80: gb_htg21.*
81: gb_htg22.*
82: gb_htg23.*
83: gb_htg24.*
84: gb_htg25.*
85: gb_pr1.*
86: gb_pr2.*
87: gb_pr3.*
88: gb_pr4.*
89: gb_pr5.*
90: gb_pr6.*
91: gb_pr7.*
92: gb_pr8.*
93: gb_pr9.*
94: gb_rol.*
95: gb_ro2.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1251	98.6	1302	7	AF244915
2	887	69.9	213343	78	AF276990
3	408.4	32.2	213343	78	AF276990
4	362	28.5	1270	93	HOMIL13A
5	362	28.5	1282	92	HSNC30
6	362	28.5	1290	10	I34548
7	360.4	28.4	1297	9	A29948
8	360.4	28.4	1297	10	I58488
9	235.6	18.6	417	88	AF043334
10	229.2	18.1	3520	7	BTAL132441
11	216.4	17.1	1212	10	I34549
					AF244915 Canis fam
					AF276990 Canis fam
					AF276990 Canis fam
					L06801 Homo sapien
					X69079 H.sapiens i
					I34548 Sequence 1
					A29948 Coding sequ
					I58488 Sequence 15
					AF043334 Homo sapi
					AJ132441 Bos tauru
					I34549 Sequence 3

Db 901 GGTTTAGAGTCCCTGGGAATAAGCACTGCTGTTAAATTCGTACCTCACTGGGATC 960

Qy 963 ctggggccgacacaggggacagagaaaggtcagagatgctgctcttctgccaactca 1022

Db 961 CTGGGGCCGACACAGGGGACAGAGAAAGGGTCAGAGATGCTGCTTCTGCCACTCA 1020

Qy 1023 gcagctggccctcagccagcagtaattattgttttctctgtatttaaaagtaagaaa 1082

Db 1021 GCAGCTGCGCCCTCACCCCAAGCAGTAATTTATTTGTTTCTCTGATTTAAAGTTAAGAAA 1080

Qy 1083 taaatatgttatcaaaagtgtaataatatagaaagtagcctctaaaggctgcatttg 1142

Db 1081 TAAAAATATGTTATCAAGAGTTAATAATATAAGAAGCTAGCCTAAAAGGCTGCATTG 1140

Qy 1143 gtgtgtgtggccagccggggcggtg999ggaggggtgtgttcactgaatgtgctcttt 1202

Db 1141 GTGTGTGTGGCCAGCCGGGGCGGTGGGGGGAGGGTGTCTCAATGTGCTCTTT 1200

Qy 1203 cactgactttgtcaaaactggagccagcaataaaagatggtgacaagagaaaaa 1262

Db 1201 CACTGACTTTGTCAANCCTGGAGCCAGAAATAAAGATGGTGACAGAGAAAAA 1260

Qy 1263 aaaaaa 1269

Db 1261 AAAAAA 1267

RESULT 2

AF276990/c

LOCUS AF276990 213343 bp DNA HTG 29-SEP-2000

DEFINITION Canis familiaris chromosome 4 clone RPCI-81 390C13, *** SEQUENCING

IN PROGRESS ***, 25 ordered pieces.

ACCESSION AF276990

VERSION AF276990.1 GI:9964079

KEYWORDS HTG; HTGS_PHASE2.

SOURCE dog.

ORGANISM Canis familiaris

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.

1 (bases 1 to 213343)

Dubchak, I., Brudno, M., Loots, G.G., Pachter, L., Mayor, C., Rubin, E.M., and Frazer, K.A.

Active conservation of noncoding sequences revealed by three-way species comparisons

Genome Res. 10 (9), 1304-1306 (2000)

20442524

PUBMED 10984448

2 (bases 1 to 213343)

Blankespoor, C.M., Dean, W.B. and Lewis, K.D.

Direct Submission

Submitted (10-JUN-2000) Genome Sciences Department, Lawrence Berkeley National Laboratory, 1 Cyclotron Road, Berkeley, CA 94720, USA

COMMENT

* NOTE: This is a 'working draft' sequence. It currently

* consists of 25 contigs. Gaps between the contigs

* are represented as runs of N. The order of the pieces

* is believed to be correct as given, however the sizes

* of the gaps between them are based on estimates that have

* provided by the submittor.

* This sequence will be replaced

* by the finished sequence as soon as it is available and

* the accession number will be preserved.

* 1 16269: contig of 16269 bp in length

* 16270 gap of unknown length

* 24613: contig of 8344 bp in length

* 24614 gap of unknown length

* 28694: contig of 4081 bp in length

* 28695 gap of unknown length

* 31694: contig of 3000 bp in length

* 31695 gap of unknown length

* 32391: contig of 697 bp in length

* 32392 gap of unknown length

* 32392 gap of unknown length

* 36539 gap of unknown length

* 39567: contig of 3029 bp in length

* 39568 gap of unknown length

* 41164: contig of 1597 bp in length

* 41165 gap of unknown length

* 56023: contig of 14859 bp in length

* 56024 gap of unknown length

* 56825: contig of 13802 bp in length

* 69826 gap of unknown length

* 71104: contig of 1279 bp in length

* 72258: contig of 1154 bp in length

* 72259 gap of unknown length

* 73132: contig of 874 bp in length

* 73133 gap of unknown length

* 88901: contig of 15769 bp in length

* 88902 gap of unknown length

* 96587: contig of 7686 bp in length

* 96588 gap of unknown length

* 105542: contig of 8955 bp in length

* 105543 gap of unknown length

* 108418: contig of 2876 bp in length

* 108419 gap of unknown length

* 113668: contig of 5250 bp in length

* 113669 gap of unknown length

* 116446: contig of 2778 bp in length

* 116447 gap of unknown length

* 148107: contig of 31660 bp in length

* 148107 gap of unknown length

* 155037: contig of 931 bp in length

* 155038 gap of unknown length

* 170050: contig of 15013 bp in length

* 170051 gap of unknown length

* 196830: contig of 26780 bp in length

* 196831 gap of unknown length

* 202835: contig of 6005 bp in length

* 202836 gap of unknown length

* 213343: contig of 10508 bp in length.

FEATURES

source

1. 213343

/organism="Canis familiaris"

/db_xref="taxon:9615"

/clone="RPCI-81 390C13"

BASE COUNT 60084 a 42812 c 44046 g 66392 t 9 others

ORIGIN

Query Match 69.9%; Score 887; DB 78; Length 213343;

Best Local Similarity 99.0%; Pred. No. 9.1e-226;

Matches 904; Conservative 0; Mismatches 5; Indels 4; Gaps 1;

Qy 344 gatttccagtgaacgcagcagcagacacacaaatgaagtgatccagttggtgaaaaacct 403

Db 112101 GATTTCAGTGAACGCAGCGAGACACCAAATTTGAAGTGTATCCAGTTGGTGAAACCT 112042

Qy 404 gctcacctatgaaggaggttatcccatggaatttcagatgaagcatgaaacatta 463

Db 112041 GCTCACCTATGTAGGGGAGTTTATCGCCATGGAAATTTTCAGATGAACGAAACCTA 111982

Qy 464 gcatccttatctgtagaccagacactgaccacttaagtccagatctcttcttcctcg 523

Db 111981 GCATCCTTATCTGTAGACCCAGACCTGACCACCTTAAGTTCAGATTCATTTTCTTCCG 111922

Qy 524 acgtacaaaattcttagggaggtg999gggggggagaaacacattctcctcagctggacct 583

Db 111921 ACGTCAAAAATTTCTTAGGG---GGGGGGGGGGAAGAACCATTTCTCAGCTGGACCT 111866

Qy 584 cagcctgcacgcgctgctccatgagctgagccagccagcccccctgcttggatgcatgg 643

Db 111865 CAGCCTGCACCGCTGCTCCATGGAGCTGAGCCAGCCAGCCCTGCTTGTGTCATGGG 111806

Qy 644 gccagcgggtggccctcctcctcgctctgcatctcatcaacgtgagggaaagcactgcat 703


```
QY 644 gccagcgggtggtccctccctcgtctgctcacttcatcaacgctgagggagaaacactgcat 703
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113727 GCCAGCGGGGTGGCTTCCTCGTCTGCACCTTCATCAACGCTGAGGGAAACGACTGCAT 113786

QY 704 cccatgactgtccctcctcagagcaaatgctcagcattacagtgaggcagatatgtgtg 763
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113787 CCCATGACTGTCCCTCCTCAGAGCAAAAGTCAGCATTACAGTGGAGGCAGATATGTGTG 113846

QY 764 ggaaggggtctgtgtacctgtggagtgagcagacagatgtttctcttagccttatttat 823
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113847 GGAGGGGGTCTTGCTGTACCTTGGGAGTGGCACAGACATGTTCTTCTTAAGCCCTTATTTAT 113906

QY 824 tattgtgttatttaaacaaagtctcttctgttctgtgtgggacagggagtgcttggag 883
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113907 TATTGTGTCTTATTAAACAAGTGTGTTGTTGCTGCGGAACAGGGAGTGGCTTGGAG 113966

QY 884 ctggggggccagtgactcgggttttagagagtcctcctgggaataagcactgtgtgtaaaatt 943
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 113967 CTGGGGCCAGTGACTCGGCTTTAGAGAGTCCCTGGGAATAAGCAC TGTGTGTAATAATT 114026

QY 944 ctgctacctactgggacctgtggggccacacaggggacagagagaaggggtcagagatgc 1003
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 114027 CTGCTACCTCACTGGGATCGTGGGCCGACACAGGGGACAGGAGAAGGGTCAGAGATGC 114086

QY 1004 tgcctc 1009
|||||
Db 114087 TGCTGT 114092

RESULT 4
LOCUS HUM113A 1270 bp mRNA PRI 22-JUL-1993
DEFINITION Homo sapiens interleukin 13 mRNA, complete cds.
ACCESSION L06801
VERSION L06801.1 GI:186275
KEYWORDS cytokine; growth factor; interleukin 13; regulatory protein.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 1270)
AUTHORS McKenzie,A.N.J., Culpepper,J.A., de Waal Malefyt,R., Briere,F.,
Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de
Vries,J.E., Banchereau,J. and Zurawski,G.R.
TITLE Interleukin-13, a T cell-derived cytokine that regulates human
monocyte and B cell function
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)
MEDLINE 93234572
FEATURES
source Location/Qualifiers
1..1270
/organism="Homo sapiens"
/db_xref="taxon:9606"
45..443
/codon_start=1
/product="interleukin 13"
/protein_id="AAA36107.1"
/db_xref="GI:186276"
/translation="MALLLTTVIALTCLGGFASPGVPPSTALRELIELYNITONOK
APLCNGSMVWSINLTAGMYCALESILNVSCSALEKRTQMLSGFCPHKVSAGQFSSL
HVRDTKEVAQFVKDLLHLKLFREGFNP"
polya_site 1270
BASE COUNT 288 a 335 c 336 g 311 t
ORIGIN

Query Match 28.5%; Score 362; DB 93; Length 1270;
Best Local Similarity 66.0%; Pred. No. 8.4e-86;
Matches 777; Conservative 0; Mismatches 290; Indels 111; Gaps 13;

QY 26 cctcgctcctcgtcattggtcctcagcctcgtctgtgtgactgtgttcattgc 85
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 14 CCTCAATCCTCTCCTGTTGGCACTGGGCTCATGGGCTTTTGTGTGACACCGGTCATTCG 73
```


Db 1145 AA-----ATATATAATATTAGCAAGAGTAAATA 1175

|||||

```

RESULT      5
HSCN30      1282 bp      mRNA      17-FEB-1997
LOCUS       H.sapiens interleukin-13 mRNA.
DEFINITION  X69079
ACCESSION   X69079.1 GI:297787
KEYWORDS    lymphokine.
SOURCE      human.
ORGANISM    Homo sapiens
REFERENCE   1 (bases 1 to 1282)
AUTHORS     Minty,A.J.
TITLE       Direct Submission
JOURNAL     Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches,
MEDLINE     Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
FEATURES    2 (bases 1 to 1282)
            1 (bases 1 to 1282)
            2 (bases 1 to 1282)
            3 (bases 1 to 1282)
            4 (bases 1 to 1282)
            5 (bases 1 to 1282)
            6 (bases 1 to 1282)
            7 (bases 1 to 1282)
            8 (bases 1 to 1282)
            9 (bases 1 to 1282)
            10 (bases 1 to 1282)
            11 (bases 1 to 1282)
            12 (bases 1 to 1282)
            13 (bases 1 to 1282)
            14 (bases 1 to 1282)
            15 (bases 1 to 1282)
            16 (bases 1 to 1282)
            17 (bases 1 to 1282)
            18 (bases 1 to 1282)
            19 (bases 1 to 1282)
            20 (bases 1 to 1282)
            21 (bases 1 to 1282)
            22 (bases 1 to 1282)
            23 (bases 1 to 1282)
            24 (bases 1 to 1282)
            25 (bases 1 to 1282)
            26 (bases 1 to 1282)
            27 (bases 1 to 1282)
            28 (bases 1 to 1282)
            29 (bases 1 to 1282)
            30 (bases 1 to 1282)
            31 (bases 1 to 1282)
            32 (bases 1 to 1282)
            33 (bases 1 to 1282)
            34 (bases 1 to 1282)
            35 (bases 1 to 1282)
            36 (bases 1 to 1282)
            37 (bases 1 to 1282)
            38 (bases 1 to 1282)
            39 (bases 1 to 1282)
            40 (bases 1 to 1282)
            41 (bases 1 to 1282)
            42 (bases 1 to 1282)
            43 (bases 1 to 1282)
            44 (bases 1 to 1282)
            45 (bases 1 to 1282)
            46 (bases 1 to 1282)
            47 (bases 1 to 1282)
            48 (bases 1 to 1282)
            49 (bases 1 to 1282)
            50 (bases 1 to 1282)
            51 (bases 1 to 1282)
            52 (bases 1 to 1282)
            53 (bases 1 to 1282)
            54 (bases 1 to 1282)
            55 (bases 1 to 1282)
            56 (bases 1 to 1282)
            57 (bases 1 to 1282)
            58 (bases 1 to 1282)
            59 (bases 1 to 1282)
            60 (bases 1 to 1282)
            61 (bases 1 to 1282)
            62 (bases 1 to 1282)
            63 (bases 1 to 1282)
            64 (bases 1 to 1282)
            65 (bases 1 to 1282)
            66 (bases 1 to 1282)
            67 (bases 1 to 1282)
            68 (bases 1 to 1282)
            69 (bases 1 to 1282)
            70 (bases 1 to 1282)
            71 (bases 1 to 1282)
            72 (bases 1 to 1282)
            73 (bases 1 to 1282)
            74 (bases 1 to 1282)
            75 (bases 1 to 1282)
            76 (bases 1 to 1282)
            77 (bases 1 to 1282)
            78 (bases 1 to 1282)
            79 (bases 1 to 1282)
            80 (bases 1 to 1282)
            81 (bases 1 to 1282)
            82 (bases 1 to 1282)
            83 (bases 1 to 1282)
            84 (bases 1 to 1282)
            85 (bases 1 to 1282)
            86 (bases 1 to 1282)
            87 (bases 1 to 1282)
            88 (bases 1 to 1282)
            89 (bases 1 to 1282)
            90 (bases 1 to 1282)
            91 (bases 1 to 1282)
            92 (bases 1 to 1282)
            93 (bases 1 to 1282)
            94 (bases 1 to 1282)
            95 (bases 1 to 1282)
            96 (bases 1 to 1282)
            97 (bases 1 to 1282)
            98 (bases 1 to 1282)
            99 (bases 1 to 1282)
            100 (bases 1 to 1282)
            101 (bases 1 to 1282)
            102 (bases 1 to 1282)
            103 (bases 1 to 1282)
            104 (bases 1 to 1282)
            105 (bases 1 to 1282)
            106 (bases 1 to 1282)
            107 (bases 1 to 1282)
            108 (bases 1 to 1282)
            109 (bases 1 to 1282)
            110 (bases 1 to 1282)
            111 (bases 1 to 1282)
            112 (bases 1 to 1282)
            113 (bases 1 to 1282)
            114 (bases 1 to 1282)
            115 (bases 1 to 1282)
            116 (bases 1 to 1282)
            117 (bases 1 to 1282)
            118 (bases 1 to 1282)
            119 (bases 1 to 1282)
            120 (bases 1 to 1282)
            121 (bases 1 to 1282)
            122 (bases 1 to 1282)
            123 (bases 1 to 1282)
            124 (bases 1 to 1282)
            125 (bases 1 to 1282)
            126 (bases 1 to 1282)
            127 (bases 1 to 1282)
            128 (bases 1 to 1282)
            129 (bases 1 to 1282)
            130 (bases 1 to 1282)
            131 (bases 1 to 1282)
            132 (bases 1 to 1282)
            133 (bases 1 to 1282)
            134 (bases 1 to 1282)
            135 (bases 1 to 1282)
            136 (bases 1 to 1282)
            137 (bases 1 to 1282)
            138 (bases 1 to 1282)
            139 (bases 1 to 1282)
            140 (bases 1 to 1282)
            141 (bases 1 to 1282)
            142 (bases 1 to 1282)
            143 (bases 1 to 1282)
            144 (bases 1 to 1282)
            145 (bases 1 to 1282)
            146 (bases 1 to 1282)
            147 (bases 1 to 1282)
            148 (bases 1 to 1282)
            149 (bases 1 to 1282)
            150 (bases 1 to 1282)
            151 (bases 1 to 1282)
            152 (bases 1 to 1282)
            153 (bases 1 to 1282)
            154 (bases 1 to 1282)
            155 (bases 1 to 1282)
            156 (bases 1 to 1282)
            157 (bases 1 to 1282)
            158 (bases 1 to 1282)
            159 (bases 1 to 1282)
            160 (bases 1 to 1282)
            161 (bases 1 to 1282)
            162 (bases 1 to 1282)
            163 (bases 1 to 1282)
            164 (bases 1 to 1282)
            165 (bases 1 to 1282)
            166 (bases 1 to 1282)
            167 (bases 1 to 1282)
            168 (bases 1 to 1282)
            169 (bases 1 to 1282)
            170 (bases 1 to 1282)
            171 (bases 1 to 1282)
            172 (bases 1 to 1282)
            173 (bases 1 to 1282)
            174 (bases 1 to 1282)
            175 (bases 1 to 1282)
            176 (bases 1 to 1282)
            177 (bases 1 to 1282)
            178 (bases 1 to 1282)
            179 (bases 1 to 1282)
            180 (bases 1 to 1282)
            181 (bases 1 to 1282)
            182 (bases 1 to 1282)
            183 (bases 1 to 1282)
            184 (bases 1 to 1282)
            185 (bases 1 to 1282)
            186 (bases 1 to 1282)
            187 (bases 1 to 1282)
            188 (bases 1 to 1282)
            189 (bases 1 to 1282)
            190 (bases 1 to 1282)
            191 (bases 1 to 1282)
            192 (bases 1 to 1282)
            193 (bases 1 to 1282)
            194 (bases 1 to 1282)
            195 (bases 1 to 1282)
            196 (bases 1 to 1282)
            197 (bases 1 to 1282)
            198 (bases 1 to 1282)
            199 (bases 1 to 1282)
            200 (bases 1 to 1282)
            201 (bases 1 to 1282)
            202 (bases 1 to 1282)
            203 (bases 1 to 1282)
            204 (bases 1 to 1282)
            205 (bases 1 to 1282)
            206 (bases 1 to 1282)
            207 (bases 1 to 1282)
            208 (bases 1 to 1282)
            209 (bases 1 to 1282)
            210 (bases 1 to 1282)
            211 (bases 1 to 1282)
            212 (bases 1 to 1282)
            213 (bases 1 to 1282)
            214 (bases 1 to 1282)
            215 (bases 1 to 1282)
            216 (bases 1 to 1282)
            217 (bases 1 to 1282)
            218 (bases 1 to 1282)
            219 (bases 1 to 1282)
            220 (bases 1 to 1282)
            221 (bases 1 to 1282)
            222 (bases 1 to 1282)
            223 (bases 1 to 1282)
            224 (bases 1 to 1282)
            225 (bases 1 to 1282)
            226 (bases 1 to 1282)
            227 (bases 1 to 1282)
            228 (bases 1 to 1282)
            229 (bases 1 to 1282)
            230 (bases 1 to 1282)
            231 (bases 1 to 128
```

```

misc_feature      856. .860
                  /note="ATTTA motif"
misc_feature      873. .877
                  /note="ATTTA motif"
misc_feature     1134. 1138
                  /note="ATTTA motif"
misc_feature     1153. 1157
                  /note="ATTTA motif"
polyA_signal     1264. 1269
BASE COUNT      293 a 341 c 337 g 311 t
ORIGIN
Query Match      28.5%; Score 362; DB 92; Length 1282;
Best Local Similarity 66.0%; Pred. No. 8.5e-86;
Matches 777; Conservative 0; Mismatches 290; Indels 111; Gaps 13;

Qy 26 cctcgctcctctgcattgctctgggctccatgcgtctggttgactcgtggtcattgc 85
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 26 CCTCAATCCCTCTCTGTTGGCAGCTGGGCCTCATGGCGCTTTTGTGTGACACGGTCATGTC 85

Qy 86 tctcaactgcctcgttggtcctgctctcccagagccctgctgactcctcccacccctcaa 145
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 86 TCTCAGTTGCCTTGGCGGCTTTGGCTCCCCAGGCCCTGTGCTCCCTCTCAGGCCCTCAG 145

Qy 146 ggagctcattgagagctggtgtaacatcaaccagaatc---aggcatcctctctgcacgg 202
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 146 GGAGCTCATTTGAGGAGCTGGTCAACATCACCCAGAACCCAGAGGCTCGGCTCTGCAATGG 205

Qy 203 cagcatggttgagagctcaactgaccgcggcatgactgacgcagctctagaatctct 262
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 206 CAGCATGGTATGGAGCATCAACCTGACAGCTGGCATGTACTGTGAGCCCTGGAAATCCCT 265

Qy 263 gatcaatgtctccgactgcagcgccatccaaagaccagggaggtgctgaaagcactgtg 322
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 266 GATCAACGTGTGAGGCTGCAGTGCATCGAAGAACCCAGAGGATGCTGAGCGGATCTG 325

Qy 323 ctctcaaaagccgcgggcagg---gatttcagtgaaagcagccgagacacccaaaattga 379
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 326 CCGGCACAAAGGTCTTCAGCTGGGCAAGTTTCCAGCTTCGATGTCCGAGACACCAAAATCGA 385

Qy 380 agtgatccagttggtgaaacacctgctcaactatgtaagggaggtttatgcgcattgaaa 439
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 386 GGTGGCCCGAGTTTGTAAAGNACCTGCTCTACATTTTAAGNAACTTTTTCGCGAGGACG 445

Qy 440 ttccagatgaagcatgaaacacttagcatcctctatctgtagaccac-gacctgacacatta 498
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 446 GTTCAACTGAAACTTCGAA----AGCATCATTTATTCAGAGACAGGACCTGACTATTGA 501

Qy 499 agttccagattcatttttcttccagacgtcacaaatttcttagggaggtgggggg----- 553
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 502 AGTTGCAAGATTCATTTTCTTTCTGATGTCAAAAATGCTTGGGTAGCGCGGAAGGAGGG 561

Qy 554 ---ggggggaacatttctcagctggagcctcagcctgcacgcctgcctccctcattggag 610
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 562 TTAGGGAGGGGTAAATTCCTTAGCTTAGACCTCAGCCTGTGCTGCCCGTCTTCAGCCCT- 620

Qy 611 ctgagccagcagccacctgccttggtgcatggggccagccgggtggocctcctccctc- 669
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 621 ---AGCCGACCTCAGCCTTCCCTCTGCCAGGGCTCAGCCTGGTGGGCCCTCTCTGCC 676

Qy 670 ----tgcaacttcaacagctgaggaagcactgcatcccatgactgctcccctccctcag 725
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 677 AGGCCCTTGAGCTCGGTGGAGCCAGGGATGACATGTCCCTACACCCCTGCCCTGCCCTAG 736

Qy 726 agcaaatgtagcattacagtggagg-----cagatatgtgaggaggggg---- 771
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 737 AGCACACTGTAGCATTACAGTGGGTGCCCCCTTGGCCAGACATGTGGTGGGACAGGACC 796

Qy 772 -----tctgtctgactcgtggagtggaagacagaatgtttcttcttagcctta 818
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 797 CACTTTCACACAGGCAACTGAGCAGACAGACGACTCAGGCACACTTCTCTCTGGCTTA 856

```


Qy 263 gatcaatgtctccgactcagcgccatcaaaagaccagagagatgctaaagcactgtg 322
Db 266 GATCAACGTGTGAGCTGCAGTGCCTGAGAGAGACCCAGAGATGCTGAGCGGATTCGTG 325
Qy 323 ctctcaaaagcccgccgagcagg---gatttccagtgaaacgagccgagacacacaaattga 379
Db 326 CCCGCACAAAGTCTCAGCTGGCAGCTTTTCCAGCTTGATGTCGAGACACCAAAATCGA 385
Qy 380 agtgatccagttggtgaaaaacctcaacctatgaagggaggtttatcgccatgaa 439
Db 386 GGTGGCCAGGTTTGAAGGAGCTGCTCTTACATTTAAAGAAACTTTTCGGCAGGAGC 445
Qy 440 ttccagatgaagcatgaaaacttagaccttatctgttagacca-gacctgacacctta 498
Db 446 GTTCAACTGAACACTTCGAA---AGCATCATTTATTTGCAGACAGGAGCTGACTATTGA 501
Qy 499 agttccagatcatctttcttccagcagtcacaaattctctagggaggtggggggg----- 553
Db 502 AGTTGCAGATTCATTTTCTTCTGATGTCAAAATGCTTTGGGTAGGCGGAGGAGG 561
Qy 554 ---gggggagaaaccttccctcagctgggacccctcagcctgcacccgctccctccatggag 610
Db 562 TTAGGAGGGGTAAATTCCTTAGCTTAGACCTCAGCCTGTGCTGCCGCTCTTCAGCCT- 620
Qy 611 ctgagccagcagccctcgtctgttgatggggcccaagccgggtggccctcctcctcgc- 669
Db 621 ---AGCCGACCTCAGCCTTCCTTCCCTTGCCAGGCTCAGCCTGGTGGGCTCCTCTGTCC 676
Qy 670 ---tgacctcatcaacgctgaggaagcagctgcacctcagctgcacctcctcag 725
Db 677 AGGGCCCTGAGCTCGGTGGACCCAGGATGATGTCCTACACCCCTCCCTGCCCTAG 736
Qy 726 agcaagtgcagcattacagtgagg-----cagatatgtgtggagggg----- 771
Db 737 AGCACACTGTAGCATACAGTGGTGGCCCTTCCACACATGTGGTGGGACAGGAGC 796
Qy 772 -----tcttgcgtacctggagtgagtgagcagacacatgttcttcttagcctta 818
Db 797 CACTTCACACACAGCAACTGAGGACAGACAGCAGCTCAGGCACACATCTCTTGGTCTTA 856
Qy 819 ttattattgtgttattaaacagtgcttctgttgggtgagggagggagtg--- 875
Db 857 TTTATTTATTTGTGTATTAATAGTGTGTTTGTACCGTGGGGATGGGGAAGACT 916
Qy 876 -----gcttgagctggggccagctgactcgggttaga----- 910
Db 917 GTGGCTGTGGCAGCTTGAGCCCAAGGTTTCAGAGACTCAGGCCCCCAGCACTAAGCAGT 976
Qy 911 -----gagtcctgggaaataagcactgtgtgtataattctgctactcactggat 961
Db 977 GGACCCAGGAGTCCCTGTAATAAGTACTGTGTACAGAATTCGTCTACCTCAGTGGGT 1036
Qy 962 cctggggcc-----gacacaggggacagagaaagggtagagatgctgctt 1010
Db 1037 CTTGGGGCTCGGAGCCCTCATCCGAGGAGGCTCAGGAGAGGGGAGAGACAGCCGCTCT 1096
Qy 1011 gctgcactcagcagctggccctcagccaagcagtaatttcttcttcttctgtatt 1070
Db 1097 GTCTCCAGCAGCAGCAGCAGCTCTCAGCCACAGAGTAATTTATTTGTTTCTCTCGTATT 1156
Qy 1071 aaagttaagaaataaataatgttatcaagagtaata 1108
Db 1157 AA-----ATATTAAATATGTTAGCAAGAGTAAATA 1187

RESULT 9
AF043334
LOCUS AF043334 417 bp mRNA PRI 21-FEB-1998
DEFINITION Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.
ACCESSION AF043334
VERSION AF043334.1 GI:2905619
KEYWORDS

SOURCE human.
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
1 (bases 1 to 417)
AUTHORS Jang, J.-S. and Kim, B.E.
TITLE Direct Submission
JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea
COMMENT Nested PCR:
1) first PCR :
forward primer (5'-ctcaatccctctcctgttgca-3')
reverse primer (5'-tagtcagggtcctgtctctgc-3')
2) second PCR :
forward primer (5'-ctcatggcgtctttgttgaccacg-3')
reverse primer (5'-gatgttcgaagtctcagttgaa-3').
FEATURES
Location/Qualifiers
1..417
/organism="Homo sapiens"
/db_xref="taxon:9606"
/cell_type="PHA-treated peripheral blood leukocyte"
gene 1..417
/genes="IL13"
primer_bind 1..24
/genes="IL13"
/note="second PCR"
/PCR_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles; DeltaCycler II from Ericomp"
CDS 4..402
/genes="IL13"
/codon_start=1
/product="interleukin 13 precursor"
/protein_id="AAC03535.1"
/db_xref="GI:2905620"
/translation="MALLTIVALTCLGFSFGPPVPPPTALRELIELVNITQNK
APLCNGSMVSNLTAGMYCAALESINVSQSAIEKTRMLGFGCPHKVSAGQFSSL
HYRDTKIEVAQFVKDLLHLKLKLFREGFN"
sig_peptide 4..63
mat_peptide 64..399
/genes="IL13"
/product="interleukin 13"
primer_bind complement(394..417)
/note="second PCR"
BASE COUNT 91 a 121 c 108 g 97 t
ORIGIN
Query Match 18.6%; Score 235.6; DB 88; Length 417;
Best Local Similarity 76.8%; Pred. No. 4.3e-52;
Matches 315; Conservative 0; Mismatches 89; Indels 6; Gaps 2;
Qy 56 catggcgctcgtgtgactgtgtcattgtctctcacctgcctcgtggtgcttgcctccc 115
Db 3 CATGGCGCTTTTGTGACACGCGTCAATTGCTCTCATTGCCTTGGCGCTTTGCCCTCCC 62
Qy 116 gagccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcac 175
Db 63 AGCCCTGTGCCCTCCCTCTACAGCCCTCAGGGAGCTCATTTGAGGAGCTGGTCAACATCAC 122
Qy 176 ccagaatc---aggcatccctctgcaacgagcagcatggtgtggcgctcaacctgaccgc 232
Db 123 CCAGAACCAAGAGCTCCGCTCTGCAATGGCAGCATGGTTGGAGCATCAACCTGACAGC 182
Qy 233 cggcatgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatcca 292
Db 183 TGGCATGTACTGTGACGCCCTTGGAAATCCCTGATCAACGTGTGAGGCTGCAGTGCATCGA 242
Qy 293 aaggaccagagatgctgaaagcactgtctctcaaaagcccgagcag---gatttc 349
Db 243 GAAGACCCAGAGGATGTGGCGGATTTCTGCCCGCACAAAGGCTCTCAGCTGGCAGTTTC 302

[illegible]

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:29:55 ; Search time 472.02 Seconds
(without alignments)
1569.464 Million cell updates/sec

Title: US-09-451-527-99
Perfect score: 1269
Sequence: 1 ccagctacgacctgctgc.....gaaaaaaaaaaaaaaaaaaaaa 1269

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*
1: /cgnl_8/gcgdata/geneseq/geneseq/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseq/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseq/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseq/NA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseq/NA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseq/NA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseq/NA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseq/NA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseq/NA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseq/NA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseq/NA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseq/NA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseq/NA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseq/NA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1269	100.0	1269	21 255561	Canine interleukin
2	1269	100.0	1269	21 255562	Canine interleukin
3	1251	98.6	1302	21 255555	Canine interleukin
4	1251	98.6	1302	21 255556	Canine interleukin
5	390	30.7	390	21 255563	Canine interleukin
6	390	30.7	390	21 255564	Canine interleukin
7	377	29.7	393	21 255557	Canine interleukin
8	377	29.7	393	21 255558	Canine interleukin
9	362	28.5	1270	21 F21334	Human low adenosin
10	362	28.5	1270	21 A35212	Human adenosine re
11	362	28.5	1282	21 F21332	Human low adenosin

12	362	28.5	1282	21 A35210	Human adenosine re
13	362	28.5	1290	15 Q56692	Sequence encoding
14	362	28.5	6952	21 F21333	Human low adenosin
15	362	28.5	6952	21 A35211	Human adenosine re
16	362	28.5	14978	21 F21338	Human low adenosin
17	362	28.5	14978	21 A35216	Human adenosine re
18	358.8	28.3	1297	13 Q28947	Cytokine NC30. Q
19	330	26.0	330	21 Z55565	Canine mature inte
20	330	26.0	330	21 Z55566	Canine mature inte
21	317	25.0	333	21 Z55559	Canine mature inte
22	317	25.0	333	21 Z55560	Canine mature inte
23	278	21.9	278	21 Z55554	Canine interleukin
24	256	20.2	272	21 Z55553	Canine interleukin
25	216.4	17.1	1212	15 Q56693	Sequence encoding
26	187.4	14.8	336	13 Q28944	gly41-Cytokine cod
27	185.8	14.6	336	13 Q28943	Asp41-Cytokine cod
28	166	13.1	5670	21 F21331	Human low adenosin
29	166	13.1	5670	21 F21337	Human low adenosin
30	166	13.1	5670	21 A35209	Human adenosine re
31	166	13.1	5670	21 A35215	Human adenosine re
32	155	12.2	166	21 Z55552	Canine interleukin
33	60.4	4.8	255	19 X11363	Human biallelic po
34	60.4	4.8	255	19 X11365	Human biallelic po
35	60.4	4.8	255	19 X11367	Human biallelic po
36	60.4	4.8	255	19 X11369	Human biallelic po
37	60.4	4.8	255	19 X11371	Human biallelic po
38	59.6	4.7	102	13 Q28941	Cytokine signal se
39	58.4	4.6	251	19 X11362	Human biallelic po
40	58.4	4.6	251	19 X11364	Human biallelic po
41	58.4	4.6	251	19 X11366	Human biallelic po
42	58.4	4.6	251	19 X11368	Human biallelic po
43	58.4	4.6	251	19 X11370	Human biallelic po
44	44.6	3.5	60	13 Q28942	Cytokine signal se
45	40.8	3.2	2460	11 Q05086	plasmid pZPC13 enc

ALIGNMENTS

RESULT	1
Z55561	
ID	Z55561 standard; cDNA; 1269 BP.
AC	Z55561;
XX	
XX	
DT	14-MAR-2000 (first entry)
XX	
DE	Canine interleukin-13 (IL-13) clone 78 cDNA.
XX	
KW	Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX	
OS	Canis familiaris.
XX	
FH	Key Location/Qualifiers
CDS	57..449
FT	/*tag= a
FT	/product= "Canine IL-13 clone 78"
XX	
PN	W09961618-A2.
XX	
PD	02-DEC-1999.
XX	
PF	28-MAY-1999; 99WO-US11942.
XX	
PR	29-MAY-1998; 98US-0087306.
XX	
PA	(HESK-) HESKA CORP.
XX	
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX	
DR	WPI; 2000-072623/06.
DR	P-PSDB; Y58223.

CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airways, including lung disease and diseases whose secondary
CC effects afflict the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasise to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.

XX
SQ Sequence 1270 BP; 288 A; 335 C; 336 G; 311 T; 0 other;

	Query Match	28.5%; Score 362; DB 21; Length 1270;
	Best Local Similarity	66.0%; Pred. No. 3e-89;
	Matches	777; Conservative 0; Mismatches 290; Indels 111; Gaps 13;
QY	26	cctcgctcctctgcattgcttgggtccatagcgctctggttgactgtggttcattgc 85
Db	14	cctcaa tctctctctgttgac tgggacctcatggccttttgtgaccaggctattgc 73
QY	86	tctcaactgctcgttggtccttgcctcccagcgcctgtgactcctccccaaacctcaa 145
Db	74	tctcaactgcttggcgcttgcctccccaggccctgtgctcctctcacagccctcag 133
QY	146	ggagctcaattgagagcttggtcaacataccccaagaatc ---aggcatcctctctgcaacgg 202
Db	134	ggagctcaattgagagcttggtcaacataccccaagaacaggaagctcgcctctgcaatgg 193
QY	203	cagcatggttgggagcgtcaacctgaacccgcgcgcgatgtactgcagctctagaatctct 262
Db	194	cagcatggttatggagcatcaaccttgacagcttggcattgtactgtcagccctcggaaacctc 253
QY	263	gatacaattgtctcgcactgcagcgccatccaaaggaccaccagagagtgtgtgaagcactgtg 322
Db	254	gateaacgtgtcaggctgcagtgccatcgagaagaccagagatgtctgagcgggatctgtg 313
QY	323	ctctcaaaaagccgcggcagg --gatttcagtgaa cgcagcgcagacaccaaaaaattga 379
Db	314	ccgcacaaaggtctcagctgggcaggtttccagctgtgcattgcgcagacaccaaaattga 373
QY	380	agtgatccagctgggtgaaaaacctgctcaactatgtgaaggggaggtttatgccctgaaaa 439
Db	374	gg tggcccaagtgtgaaaggacctgtcttacatttaaaagaaccttttctgcggaggacg 433
QY	440	tttcagatgaagcatgaaaacttagcatcctctattctgtagaccac -gacctgaaccattta 498
Db	434	gttcaactgaaactcgaa ----agcatcata ttgtcagagacaggaacctgactattga 489
QY	499	agttccagattcaatttttcttctcgaagcgtaca aaattctctaggagggtgggggg --- 553
Db	490	agttgcagattcaatttttcttctctgattgacaaaatgtcttgggtaggcgggaaggaggg 549
QY	554	---ggggggagaacatttctctcagctgggacctcagcctgcacgcctgctccatggag 610
Db	550	ttagggggagggtaaaaattctcttagcttagacctcagcctgtgtcgcgcgctcttcagacct - 608
QY	611	ctgagccagccacccctgcttgggtcatggggcccgagccgggtgagccctctccgtc - 669

D	b	609	----	agcgcaactcagccttcccccttgccagggctcagcctggtggtgggcctcctctgtcc	604
Q	y	670	----	tgcacttcatcaacgctgagggaaagcactgcacccatgactgtccctcctctcag	725
D	b	665	agggcccttgagctcggtagccagggatgacatgtccctacacccctccctctgcccctag	724	
Q	y	726	agcaagtgcagcattaccatggagg-----cagatatgtgtggtggaggggg-----	771	
D	b	725	agcacactgtagcattacagtgggtgcgccctctgcacagacatgtggtgggacagggacc	784	
Q	y	772	-----tcttgcgtgacctgggagtgccacagacatgtttcttcttagcctta	818	
D	b	785	cacttcacacacagggcaactgaggcagacagcagctcaggcacactctcttgggtcta	844	
Q	y	819	tttattatgtgtgtatttaaacaagtgtctttgtttgtctggggacagggagtg---	875	
D	b	845	tttattatgtgtgtatttaaagtgtgtttgtcaccgttggggattgggggaagact	904	
Q	y	876	-----gcttgagctggtgggcccagctgactcgggtttaga-----	910	
D	b	905	gtggctgtggcacttggagccaaaggttcagagactcaggccccagcactaaagcagt	964	
Q	y	911	-----gagtcctcctgggaataagcactgtgtgtaaatctctcactcactcgggat	961	
D	b	965	ggaccccaggagtcctcgtgtaatagtactgtgtacagaaatctctgctactcactgggt	1024	
Q	y	962	cctggggccc-----gacacaggggacaggaagaagagtcagagatcgtcctt	1010	
D	b	1025	cctggggcctcggagcctcactccgagggcagggttcaggagaggggcagaaacagccgctct	1084	
Q	y	1011	gtctgccactcagcagctggccctcagcccaagcagtaattattgttttctctgtattt	1070	
D	b	1085	gtctgccagccagcagccagctctcagcccaacagagtaattattgttttctcgtattt	1144	
Q	y	1071	aaagttaagaataaataatgtttatcaagaagttaata	1108	
D	b	1145	aa-----atattaaatgttagcaagagtttaata	1175	
RESULT 11					
F	I	D21332	standard; DNA; 1282 BP.		
XX	XX	AC	F21332;		
XX	XX	DT	14-MAR-2001 (first entry)		
XX	XX	DE	Human low adenosine antisense oligonucleotide related sequence #2899.		
KW	KW	KW	Low adenosine antisense oligonucleotide; phosphorothioate; allergy;		
KW	KW	KW	human; airway disorder; bronchoconstriction; lung inflammation;		
KW	KW	KW	surfactant depletion; respiratory; bronchodilator; antiinflammatory;		
KW	KW	KW	immunosuppressive; antialasthmatic; analgesic; hypotensive; cyostatic;		
KW	KW	KW	respiratory obstruction; pulmonary obstruction; impeded respiration;		
KW	KW	KW	surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;		
KW	KW	KW	respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;		
KW	KW	KW	pulmonary hypertension; emphysema; pulmonary transplantation rejection		
KW	KW	KW	chronic obstructive pulmonary disease; pulmonary infection; bronchitis		
XX	XX	OS	cancer; ss.		
XX	XX	OS	Homo sapiens.		
XX	XX	PN	WO2000062736-A2.		
XX	XX	PD	26-OCT-2000.		
XX	XX	PF	24-MAR-2000; 2000WO-US08020.		
XX	XX	PR	06-APR-1999; 99US-0127958.		
XX	XX	PA	(UYEC-) UNIV EAST CAROLINA.		
XX	XX	PA	(NYCE/) NYCE J W.		

RESULT 15
A35211 ID A35211 standard; DNA; 6952 BP.
XX AC A35211;
XX AC A35211;
XX DT 28-JUL-2000 (first entry)
XX XX Human adenosine receptor related polynucleotide 2nd SEQ ID NO:85.
DE DE
XX KW Human; adenosine receptor; low adenosine antisense oligonucleotide;
KW phosphorothioate; impaired respiration; inflammation; allergy;
KW allergic disease; bronchoconstriction; inhibitor; antiinflammatory;
KW antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway;
KW lung disease; ischaemic condition; pulmonary vasoconstriction; asthma;
KW respiratory distress syndrome; pain; cystic fibrosis; emphysema;
KW pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
KW cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.
XX KW
XX OS Homo sapiens.
XX OS
XX PN WO200009525-A2.
XX XX
XX XX 24-FEB-2000.
XX XX
XX PF 03-AUG-1999; 99WO-US17712.
XX XX
XX PR 03-AUG-1998; 98US-0095212.
XX XX
XX PA (UYEC-) UNIV EAST CAROLINA.
XX XX
XX PT Nyce JW;
XX PT
XX DR WPI; 2000-205971/18.
XX XX
XX PT New antisense oligonucleotides useful for treating e.g. pulmonary
PT vasoconstriction, inflammation, allergies, asthma, hypertension, or
PT bronchitis, emphysema, respiratory distress syndrome, ischemia or
PT cancers -
XX PT
XX PS Disclosure; Page 1250-1251; 1343pp; English.
XX XX
CC CC The present invention describes a new composition comprising an antisense
CC oligonucleotide (ON) with low adenosine (up to 15%), which targets
CC nucleic acids involved in bronchoconstriction, allergies, and/or
CC inflammation. The ON can have antiinflammatory, antiallergic,
CC antiasthmatic, cytostatic and analgesic activities. The compositions are
CC useful for the treatment of diseases associated with inflammation,
CC impaired airflow, including lung disease and diseases whose secondary
CC effects affect the lungs of a subject. They can be used for treating
CC e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, asthma,
CC impeded respiration, respiratory distress syndrome, pain, cystic
CC fibrosis, pulmonary hypertension, emphysema, chronic obstructive
CC pulmonary disease (COPD), and cancers such as leukaemias, lymphomas,
CC carcinomas, and cancers which may metastasize to the lungs, including
CC breast and prostate cancer. The reduction of the adenosine content of the
CC ONs reduces side effects. The A-containing ONs break down with the
CC release of deoxyadenosine which activates adenosine receptors causing
CC bronchoconstriction and inflammation. A32313 to A35312 represent the
CC nucleotide sequences given in the sequence listing from the present
CC invention, which correspond to SEQ ID NO:1 to 2815, and then the last
CC 185 sequences are also called SEQ ID NO:1 to 185, but the sequences
CC differ from the previously named sequences. SEQ ID NO:11 to 1680 (A32323
CC to A33992) are specifically claimed ONs from the present invention.
CC N.B. Sequences given in the disclosure of the present invention do not
CC match up with their corresponding SEQ ID NO: sequences given in the
CC sequence listing.
XX CC
SQ Sequence 6952 BP; 1536 A; 2017 C; 1919 G; 1480 T; 0 other;

Query Match 28.5%; Score 362; DB 21; Length 6952;

[illegible]

Db 6707 cctggggcctcggagcctcatccgagggcaggggtcagggaggggcagaacagccgctcct 6766
 Qy 1011 gtctgccaactcagcagctggccctcagcccaagcagtaatttattgtttttccttgttat 1070
 Db 6767 gtctgccaagccagcagcctctcagcccaagcagtaatttattgtttttcctcgtatt 6826
 Qy 1071 aaagttaagaaataaaataatgttatcaagaggttaata 1108
 Db 6827 aa-----atatataatagttagcaaaagagtttaata 6857

Search completed: May 13, 2001, 14:30:23
 Job time: 18338 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:21 ; Search time 226.02 Seconds
(without alignments)
980.315 Million cell updates/sec

Title: US-09-451-527-99
Perfect score: 1269
Sequence: 1 cagcctacgactgcctgc.....gaaaaaaaaaaaaaaaaa 1269

Scoring table:
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgnl_7/ptodata/1/ina/5A-COMB.seq:*
2: /cgnl_7/ptodata/1/ina/5B-COMB.seq:*
3: /cgnl_7/ptodata/1/ina/6A-COMB.seq:*
4: /cgnl_7/ptodata/1/ina/6B-COMB.seq:*
5: /cgnl_7/ptodata/1/ina/PCTUS-COMB.seq:*
6: /cgnl_7/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	362	28.5	1290	1 US-08-012-543-1	Sequence 1, Appli
2	362	28.5	1290	5 PCT-US93-07645A-1	Sequence 1, Appli
3	362	28.5	1290	5 PCT-US93-07645-1	Sequence 1, Appli
4	360.4	28.4	1297	1 US-08-371-121-15	Sequence 15, Appli
5	216.4	17.1	1212	1 US-08-012-543-3	Sequence 3, Appli
6	216.4	17.1	1212	5 PCT-US93-07645A-3	Sequence 3, Appli
7	216.4	17.1	1212	5 PCT-US93-07645-3	Sequence 3, Appli
8	193.4	15.2	384	1 US-08-371-121-17	Sequence 17, Appli
9	191.6	15.1	425	1 US-08-594-469-4	Sequence 4, Appli
10	191.6	15.1	425	2 US-08-906-957-4	Sequence 4, Appli
11	191.6	15.1	4410	1 US-08-594-469-1	Sequence 1, Appli
12	191.6	15.1	4410	2 US-08-906-957-1	Sequence 1, Appli
13	187.4	14.8	336	1 US-08-371-121-24	Sequence 24, Appli
14	185.8	14.6	336	1 US-08-371-121-2	Sequence 2, Appli
15	185.4	14.6	447	1 US-08-371-121-26	Sequence 26, Appli
16	59.6	4.7	102	1 US-08-371-121-10	Sequence 10, Appli
17	54.6	4.3	96	1 US-08-371-121-9	Sequence 9, Appli
18	44.6	3.6	7218	1 US-08-232-463-14	Sequence 14, Appli
19	44.6	3.5	60	1 US-08-371-121-12	Sequence 12, Appli
20	39.6	3.1	54	1 US-08-371-121-11	Sequence 11, Appli
21	39.4	3.1	7218	1 US-08-232-463-14	Sequence 14, Appli
22	38.8	3.1	1576	2 US-09-197-378-1	Sequence 1, Appli
23	36	2.8	740	2 US-08-713-000-8	Sequence 8, Appli
24	36	2.8	740	2 US-08-975-316-8	Sequence 8, Appli
25	36	2.8	740	4 US-09-211-710-8	Sequence 8, Appli
26	36	2.8	741	2 US-08-975-316-58	Sequence 58, Appli
27	36	2.8	972	1 US-07-915-934-1	Sequence 1, Appli

Sequence 1, Appli
Sequence 19, Appli
Sequence 18, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 26, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 11, Appli
Sequence 1, Appli
Sequence 52, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 13, Appli
Sequence 27, Appli
Sequence 3, Appli
Sequence 9, Appli
US-08-325-743-1
US-08-814-052-19
US-08-814-052-18
US-08-939-218A-1
PCT-US95-06815-1
US-08-706-037-26
US-08-940-661A-1
US-09-083-485-1
US-09-005-397-26
US-08-909-965C-11
US-08-955-937A-1
US-08-306-691B-52
US-08-095-728B-1
PCT-US92-02320A-1
US-08-892-747-13
US-09-138-450-27
US-08-496-855A-3
PCT-US91-02311-9

ALIGNMENTS

RESULT 1
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Bancheureau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cdna

Db 665 AGGCCCTGAGCTCGGTGGACCCAGGATGACATGTCCCTACACCCCTCCCTGCCCTAG 724
Qy 726 agcaaatgacagcattacagtggag-----cagatatgtggtggggggg----- 771
Db 725 AGCACACTGAGCTAGTACAGTGGTGGCCCTCCCTGCCAGACATGTGTGGACAGGGACC 784
Qy 772 -----ctgtgctactctggagtgacagacacatgtttctcttagcctta 818
Db 785 CACTTCACACACAGGCACTAGGACAGACAGCAGTCTAGGACACACTTCTTGTGCTTA 844
Qy 819 ttattattgtgtatttaaaacaaagtcttctgttggctggtgggacagggagtg--- 875
Db 845 TTTATTATTGTGTATTATTAATGAGTGTCTTGTCTACCCGTGGGGATTGGGAAGACT 904
Qy 876 -----gcttgagctggggcccgactgactcgggtttaga----- 910
Db 905 GTGGCTGCTGGCAGCTTGAGGCAAGGTTTACAGACTCAGGCGCCCAACAGCAGT 964
Qy 911 -----gagtcctgggaataagcactgtgtgtaaaattctgactcactcagtgat 961
Db 965 GGACCCAGGAGTCCCTGGTAATAGTACTGTGTACAGAAATTCGTACTCTACCTGGGGT 1024
Qy 962 cctggggcc-----gacacaggggacagagagaaaggtcagagatgctgctct 1010
Db 1025 CTGGGGCTCGGAGCTCATCCGAGCAGGCTCAGGAGAGGGGACAGACAGCCCTCT 1084
Qy 1011 gtctgcaactcagcagctg9ccctcagccagcagagatatttattgtttctctgtatt 1070
Db 1085 GTCTGCAGCAGCAGCAGCAGCTCTCAGCAACGAGTAATTTATTGTTTTTCTCGTATT 1144
Qy 1071 aaagttaaagaaataaataatgttatcaaaagttta 1108
Db 1145 AA-----ATATTAAATATGTTAGCAAGAGTTAATA 1175

RESULT 4

US-08-371-121-15
; Sequence 15, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLENOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA: PCT/FR92/00280
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1297 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 15..452
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: 117..452
US-08-371-121-15

Query Match 28.4%; Score 360.4; DB 1; Length 1297;

Best Local Similarity 65.9%; Pred. No. 6.2e-98;

Matches 776; Conservative 0; Mismatches 291; Indels 111; Gaps 13;

Qy 26 cctcgctcctcctgctggtggtccatggcgctctggtgactgtgtgctattgc 85
Db 26 CCTCAATCCTCTCTCTTGGCACTGGGCTCATGGGCTTTTGTGGACCAAGTCAATGC 85
Qy 86 tctacactgctcgtggtggtcctcccgagcctgactcctcccccacccctcaa 145
Db 86 TCTCACTTGGCTTGGCGGCTTTGCCCTCCCGAGGCTGTGCTCTACAGCCCTCAG 145
Qy 146 ggagctcattgagggctggtcaacataccacagatc---aggcatcctcctgcaacgg 202
Db 146 GGAGCTCATTTGAGGAGCTGGTCAACATCACCCAGAACCAAGAGCTCTGCAATGG 205
Qy 203 cagcatggtgagcgcaacctaaccggtgctgactgctgagctctagaatctct 262
Db 206 CAGCATGTGTATGGACATCAACCTGACCTGACATGTACTGTGAGCCCTGGAATCCCT 265
Qy 263 gatcaatgtctccgactgcagcgccatccaaaggaccagagagatgctgaaagcactgtg 322
Db 266 GATCAACGTGTGAGGCTGAGTGCCATCGAGAAGACCCAGAGGATGCTGAGCGATTCTG 325
Qy 323 ctctcaaaagcccgcgag---gatttcagtgaaocagcagcagacacccaattga 379
Db 326 CCCGCACAAAGGTCTCAGCTGGGACGTTTTTCCAGCTTGTATGTCGAGACACCAAAATCGA 385
Qy 380 agtgcattcagttgtgaaaaacactgactcactatgaaggaggtttatcgcattgaaa 439
Db 386 GGTGCCCCAGTTTGTAAAGGACCTGCTCTTACATTTAAAGAAACTTTTTTCGGAGGGAG 445
Qy 440 ttctcagatgaagcagaaacttagcattcttagtagaccca-gacctgaccactta 498
Db 446 GTTCAACTGAACCTTCGAA---AGCATCATTTTTCGAGACAGACAGGACCTGACATTTGA 501
Qy 499 agttccagattcatttttcttccagctgcaaaatttttagggaggtggtggg--- 553
Db 502 AGTTGCAGATTCTTTTCTTCTGATGCAAAAATGCTTGGGTAGGGGGAAGGAGGG 561
Qy 554 ---gggggagaaacatttctcctcagctggtggacactgacccctgacctccatgagag 610
Db 562 TTAGGGAGGGGTAAAAATTCCTTAGCTTAGACCTCAGCCTGTGCTGCCCGCTTTCAGCCT- 620

Qy	583	cgc	tgg	gga	gaa	gac	tgc	atccccatgc	gtac	gtccctctctcag	agcaaa	gtgcagcatta	742							
Db	649	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	693							
Qy	743	c	---	agt	gag	gcac	at	atg	tgt	ggg	agg	gggt	ctt	gct	tac	ctggag	gtgcac	aga	798	
Db	694	ccg	tga	gtcc	agcc	tgt	ggc	ctgtg	ccac	cac	agg	gcac	act	gag	gcagg	cac	gcac	gttgag	753	
Qy	799	cat	gtt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	ctt	858	
Db	754	cac	at	ttt	ttc	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	ttt	812	
Qy	859	gct	ggg	gac	agg	agg	tgg	ctt	gg	agc	tgg	ggg	gcc	agg	gact	cgg	gtt	taag	-----	910
Db	813	atc	ccg	gtg	ggg	gac	at	gggt	ttg	ctgt	at	gccc	t	g	ggg	ggc	tcc	agc	at	872
Qy	911	---	---	agt	ccc	t	gg	aa	ta	ag	ca	ct	gt	gt	ta	aa	at	ct	g	965
Db	873	gct	ct	g	gg	gt	cc	ct	gg	ca	at	at	tt	act	gt	at	aac	t	932	
Qy	966	ggg	-----	ccg	aca	cg	ggg	ac	gag	gaa	agg	tc	ag	at	gt	g	ct	ct	g	1019
Db	933	agg	tc	ca	ccc	ac	gg	cag	gag	at	gg	gg	g	g	g	g	g	g	992	
Qy	1020	tc	ag	cag	ct	gg	cc	ct	cag	cc	ag	cag	ta	at	tt	at	gt	tt	1079	
Db	993	gc	ag	ca	acc	ag	cc	ct	cag	gc	at	ga	aa	ta	act	tt	at	tt	1047	
Qy	1080	aa	ta	aa	at	at	gt	tt	ca	ag	agt	ta	aa	ta	at	at	at	at	1139	
Db	1048	gt	at	ta	aa	at	ag	ct	ta	ca	ag	gt	ta	at	at	at	at	at	1107	
Qy	1140	tt	g	gt	t	gt	t	g	g	c	g	g	c	g	g	g	g	g	1199	

RESULT 6

```

PCT-US93-07645A-3
; Sequence 3, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1212 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-3

```

Qy	1020	tcagcagctggccctcagccagcagcgttaatttattgttttttctctgtattttaagttaag	1079
Db	993	GCAGCAGCAGCCGCGCCGACGCATGAATAACTTATTGTT-----TTGTTCTTATATTTAAA	1047
Qy	1080	aaataaataatgttatcaaaagtttaataatatagaagagtagcgtaaaggctgcac	1139
Db	1048	GTATTAAATAGCTTAGCAAAAGAGTTAATAATATATGGAAGAATGGCCTGTTACACCTCAAG	1107
Qy	1140	ttggtgtgtgtggccagcgcggggcggggtgggggggaggggtgtgtcactgaaatgtgctc	1199
Db	1108	GTGATGTCTAGTGAATG-----GGGGGAGGGTGGTGGGTTTGTCACTGAACAAACTT	1159
Qy	1200	ttcactgactttgtccaactggaagccagaaataaaagatggtgcacaagagaaaaa	1255
Db	1160	TT---CATTTAGCTGTCAAACCTAGAAACCGGAAATAAAGATGGTGACAGATAAAAA	1212

RESULT

7

PCT-US93-07645-3

Sequence 3, Application PC/TUS9307645

GENERAL INFORMATION:

APPLICANT:

TITLE OF INVENTION: Human Interleukin-13

NUMBER OF SEQUENCES: 6

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Macintosh

OPERATING SYSTEM: Macintosh 6.0.5

SOFTWARE: Microsoft Word 5.1a

CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US93/07645

FILING DATE: 19930818

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/012543

FILING DATE: 01-FEB-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/010977

FILING DATE: 29-JAN-1993

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/933416

FILING DATE: 21-AUG-1992

INFORMATION FOR SEQ ID NO: 3:

SEQUENCE CHARACTERISTICS:

LENGTH: 1212 base pairs

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

PCT-US93-07645-3

RESULT 8
US-08-371-121-17
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual


```

Db 196 ATCGAGAGACCCAGGAGGATGCTGACCGGATTTCTGCCCGCACAGGTTCTCAGCTGGGCAG 255
Qy 345 attccagtgaaacgagcagcagacacaccaaattgaagtgatccagttggtgaaaaacctg 404
Db 256 TTTTCCAGCTTCATGTCGAGACACCAAAATCGAGGTGGCCCGCTGTTGTAAAGGACCTG 315
Qy 405 ctcaacctatgaagggggtttatccgcacatggaatttcagatgaagcagatgaaaa 459
Db 316 CTCCTACATTTAAAGAAACTTTTTTCGAGGGAGCTTCAACTGAAACTTCGAAA 370

RESULT 9
US-08-594-469-4
; Sequence 4, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-4

```

Qy	111	tccccgagccctgtactcctcccacaccctcaaggagctcattgagagctggccaac	170
Db	16	TCCCCAGGCCCTTGCCCTCCTACGGCCCTCAGGAGCTCATTCAGGAGCTGGTCAAC	75
Qy	171	atcacccagaatc---aggcatcctctgaaacgcagcatggttgtagcgctcaacctg	227
Db	76	ATCACCCAGAACCAGAAGGCTCGCGTCTGCATTGGCAGCATGTTAGGACATCAACTTG	135
Qy	228	acgcgcggcatgtactgcgcagctctagaaatctctgatcaatgtctccgactgcagcgcc	287
Db	136	ACAGCTGACATGTACTGTGCAGCCCTGGAATCCCTCATCAACGTGTCAGGCTGCAGTGCC	195
Qy	288	atccaaaggaccacagagatgtctgaagcaactgtgtctctcaaagccccgcgcagg---	344

	Query Match	15.1%	Score 191.6;	DB 1;	Length 425;	
	Best Local Similarity	74.9%;	Pred. No.	9e-48;		
	Matches	268;	Conservative	0;	Mismatches	84; Indels 6; Gaps
<hr/>						
QY	108	gcctcccgagcgcctgactcccaccctcaaggagtcattgagagctgggtc	167			
DG	55	GCTTCGTGGCCCTTGCGCTCCCAGTACTGCCCTCAGSGAGCTCATTTAGGAGCTGGTC	114			
<hr/>						
QY	168	aacatcacccagaatc---aggcatccccctctgccagcgagcatggttggtagcgctaac	224			
DG	115	AACATCACCCAGAACCCAGAGGCTCGGCCTGCAATTGGCAGCATGATAATGGAGCATCAAC	174			
<hr/>						
QY	225	ctgacgcgcgcgatgtactgcygcagtctagnaatctctgtcataatgtctccgactgcagc	284			

Db 175 CTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCTGATCAACCTGTGTCAGGCTGCAGT 234
Qy 285 gccatccaaagagaccagagagatgtgaaagcaactgtgtctctcaaaagcccgcgagcag- 343
Db 235 GCCATCGAAGAACCCAGAGAGATGCTGACGCGATTCTGCCCGCACAAAGGTCTCAGCTGGG 294
Qy 344 --gattccagtgaaagcagccgagacacacaaattgaagtgtatccagttggtgaaaac 401
Db 295 CAGTTTTTCAGCTTGCATGCTCCGAGACACCAAAATCGAGGTGCGCCAGCTTGTAAAGGAC 354
Qy 402 ctgctcacctatgaaggaggttatccatgccatggaaatttcagatgaagcatgaaaa 459
Db 355 CTGCTCTTACATTTAAAGAACTTTTCCGAGGAGCGGTTCACCTGAAACTTCGAAA 412

RESULT 10
US-08-906-957-4
; Sequence 4, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-4

Query Match 15.1%; Score 191.6; DB 2; Length 425;
Best Local Similarity 74.9%; Pred. No. 9e-48;
Matches 268; Conservative 0; Mismatches 84; Indels 6; Gaps 2;

Qy 108 gcctcccgagccctgtactcctcccccacccctcaagagctcattgaggagctggc 167
Db 55 GCCTCCGCTGGCCCTGTGCTCCCACTACTGCCCTCCAGGAGCTCATTCAGGAGCTGGTC 114

Qy 168 aacatcccccagaatc--aggeatccctctgcaacggcagcatggtgtggaggtcaac 224
Db 115 AACATCCCCAGAACCCAGAGGCTCCGCTCTGCAATGCGACGATGGTATGGAGCATCAAC 174
Qy 225 ctgaccgccgagcatgtactgcgagctctagaattctctgatcaatgtctccgactgcagc 284
Db 175 CTGACAGCTGGCATGTACTGTGACGCCCTGGAATCCCTGATCAACCTGTGAGGCTGCAGT 234
Qy 285 gccatccaaagagaccagagagatgtgaaagcaactgtgtctctcaaaagcccgcgagcag- 343
Db 235 GCCATCGAAGAACCCAGAGAGATGCTGAGCGGATTTCTGCCCGCACAAAGGTCTCAGCTGGG 294
Qy 344 --gattccagtgaaagcagccgagacacacaaattgaagtgtatccagttggtgaaaac 401
Db 295 CAGTTTTTCAGCTTGCATGCTCCGAGACACCAAAATCGAGGTGCGCCAGCTTGTAAAGGAC 354
Qy 402 ctgctcacctatgaaggaggttatccatgccatgaaatttcagatgaagcatgaaaa 459
Db 355 CTGCTCTTACATTTAAAGAACTTTTTCGCGAGGAGCGGTTCACCTGAAACTTCGAAA 412

RESULT 11
US-08-594-469-1
; Sequence 1, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-1

Query Match 15.1%; Score 191.6; DB 1; Length 4410;
Best Local Similarity 74.9%; Pred. No. 4.1e-47;
Matches 268; Conservative 0; Mismatches 84; Indels 6; Gaps 2;

QY 108 gctccccgagccctgtgactccctcccccaaccctcaaggagctcattgagagctggtc 167
DB 392 GCCTTCCTGGCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCATTTAGAGAGCTGGTC 451
QY 168 aacatcacccagagatc---aggcatccctctgcaacggcagcagctggtgtgagcgtcaac 224
DB 452 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCAGTGTATGAGCATCAAC 511
QY 225 ctgacccgagcagtgactgcaagctctagaatctctgtatcaatgtctccagctgaagc 284
DB 512 CTGACAGCTGGCATGTACTGTGACAGCCCTGGAATCCCTGTGATCAACGCTGTCAAGGCTGCAGT 571
QY 285 gccatcaaaaggaccagagagatgctgaaagcactgtgctctcaaaaggccgcgcagc- 343
DB 572 GCATCGAAGAGACCCAGAGATGCTGAGGGATTTCTGCCCGCACAGGCTCTCAGCTGGG 631
QY 344 --gattccagtgaaagcagcagcagacacacaaatgaagtgtatccagctggtgaaac 401
DB 632 CAGTTTTCCAGCTGATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGAC 691
QY 402 ctgctccatgttaaggaggagttatcgccatgaaatttcagatgaagcagatgaaa 459
DB 692 CTGCTCTTACATTTAAAGAAACTTTTTCGGGAGGAGCGGTTCAACTGAAACTTCGAAA 749

RESULT 12
US-08-906-957-1
; Sequence 1, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,459
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-906-957-1

Query Match 15.1%; Score 191.6; DB 2; Length 4410;
Best Local Similarity 74.9%; Pred. No. 4.le-47;
Matches 268; Conservative 0; Mismatches 84; Indels 6; Gaps 2;
QY 108 gcctccccgagccctgtgactccctcccccaaccctcaaggagctcattgagagctggtc 167
DB 392 GCCTTCCTGGCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCATTTAGAGAGCTGGTC 451
QY 168 aacatcacccagagatc---aggcatccctctgcaacggcagcagctggtgtgagcgtcaac 224
DB 452 AACATCACCCAGAACAGAGGCTCCGCTCTGCAATGGCAGCAGTGTATGAGCATCAAC 511
QY 225 ctgacccgagcagtgactgcaagctctagaatctctgtatcaatgtctccagctgaagc 284
DB 512 CTGACAGCTGGCATGTACTGTGACAGCCCTGGAATCCCTGTGATCAACGCTGTCAAGGCTGCAGT 571
QY 285 gccatcaaaaggaccagagagatgctgaaagcactgtgctctcaaaaggccgcgcagc- 343
DB 572 GCATCGAAGAGACCCAGAGATGCTGAGGGATTTCTGCCCGCACAGGCTCTCAGCTGGG 631
QY 344 --gattccagtgaaagcagcagcagacacacaaatgaagtgtatccagctggtgaaac 401
DB 632 CAGTTTTCCAGCTGATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGAC 691
QY 402 ctgctccatgttaaggaggagttatcgccatgaaatttcagatgaagcagatgaaa 459
DB 692 CTGCTCTTACATTTAAAGAAACTTTTTCGGGAGGAGCGGTTCAACTGAAACTTCGAAA 749

RESULT 13
US-08-371-121-24
; Sequence 24, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match 14.8%; Score 187.4; DB 1; Length 336;
Best Local Similarity 76.9%; Pred. No. 1.4e-46;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
Qy 118 gccctgtactccctccccaacccctcaaggagctcaattgaggagctggtcaacatcaccc 177
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61
Qy 178 agaatc---aggatccctctcaacgagcagcatgtgtggagcgtcaacctgacgcgcg 234
Db 62 AGAACCAAGAGCTCGCTCTGCATGGCAGCATGTTGAGGAGCTCAACCTGACAGCTG 121
Qy 235 gcatgtactgcgcagctctagatctctctgataatctctccgactgcagcgccatccaaa 294
Db 122 GCATGTACTGTGCACGCCCTTGAATCCCTCATCAACGTGTGAGGAGCTGCAGTGCATCGAGA 181
Qy 295 ggaccacagagatgctgaaagcactgctctcaaaaagccgcgcgcgcgcgcgcgcgcgc 351
Db 182 ACACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAGGTTCTCAGCTGGCGAGTTTCCA 241
Qy 352 gtgaacgcagcgcagacacacaaatgaagtatccagttgtgtaaaaacctgctcacct 411
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTGTAAAGGACCTGCTCTTAC 301
Qy 412 atgtaagggagttatgcgcataatggaatttca 444
Db 302 ATTTAAAGAACTTTTCCGAGGGACGGTTCA 334

RESULT 14
US-08-371-121-2
Sequence 2, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTELLER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371.121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match 14.6%; Score 185.8; DB 1; Length 336;
Best Local Similarity 76.6%; Pred. No. 4.2e-46;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;
Qy 118 gccctgtactccctccccaacccctcaaggagctcaattgaggagctggtcaacatcaccc 177
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61
Qy 178 agaatc---aggatccctctcaacgagcagcatgtgtgagcgtcaacctgacgcgcg 234
Db 62 AGAACCAAGAGCTCGCTCTGCAATGGCAGCATGTTGAGGAGCTCAACCTGACAGCTG 121
Qy 235 gcatgtactgcgcagctctagatctctgataatctctccgactgcagcgccatccaaa 294
Db 122 ACATGTACTGTGCAGCCCTTGAATCCCTCATCAACGTGTGAGGAGCTGCAGTGCATCGAGA 181
Qy 295 ggaccacagagatgctgaaagcactgctctcaaaaagccgcgcgcgcgcgcgcgcgcgc 351
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAGGTTCTCAGCTGGCGAGTTTCCA 241
Qy 352 gtgaacgcagcgcagacacacaaatgaagtatccagttgtgtaaaaacctgctcacct 411
Db 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTGTAAAGGACCTGCTCTTAC 301
Qy 412 atgtaagggagttatgcgcataatggaatttca 444
Db 302 ATTTAAAGAACTTTTCCGAGGGACGGTTCA 334

RESULT 15
US-08-371-121-26
Sequence 26, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:30:23 ; Search time 472.02 Seconds
(without alignments)
482.341 Million cell updates/sec

Title: US-09-451-527-102

Perfect score: 390

Sequence: 1 atggcgctcgttgactgt.....atgcccatggaatttcaga 390

Scoring table:

IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*

1: /cgnl_8/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseqn/NA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseqn/NA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseqn/NA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseqn/NA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseqn/NA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseqn/NA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseqn/NA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseqn/NA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseqn/NA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseqn/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	390	100.0	390	21	255563 Canine interleukin
2	390	100.0	390	21	255564 Canine interleukin
3	390	100.0	1269	21	255561 Canine interleukin
4	390	100.0	1269	21	255562 Canine interleukin
5	377	96.7	393	21	255557 Canine interleukin
6	377	96.7	393	21	255558 Canine interleukin
7	377	96.7	1302	21	255555 Canine interleukin
8	377	96.7	1302	21	255556 Canine interleukin
9	330	84.6	330	21	255565 Canine mature inte
10	330	84.6	330	21	255566 Canine mature inte
11	317	81.3	333	21	255559 Canine mature inte

c	12	317	81.3	333	21	255560 Canine mature inte
	13	278	71.3	278	21	255554 Canine interleukin
	14	256	65.6	272	21	255553 Canine interleukin
	15	230.8	59.2	1270	21	F21334 Human low adenosin
	16	230.8	59.2	1270	21	A35212 Human adenosine re
	17	230.8	59.2	1282	21	F21332 Human low adenosin
	18	230.8	59.2	1282	21	A35210 Human adenosine re
	19	230.8	59.2	1290	15	Q56692 Sequence encoding
	20	230.8	59.2	6952	21	F21333 Human low adenosin
	21	230.8	59.2	6952	21	A35211 Human adenosine re
	22	230.8	59.2	14978	21	F21338 Human low adenosin
	23	230.8	59.2	14978	21	A35216 Human adenosine re
	24	229.2	48.8	1297	13	Q28947 Cytokine NC30. Q
	25	187.4	47.6	336	13	Q28944 Gly41-Cytokine cod
	26	185.8	43.2	1212	15	Q56693 Asp41-Cytokine cod
	27	168.6	43.2	1212	15	Q56693 Sequence encoding
	28	101.8	26.1	5670	21	F21331 Human low adenosin
	29	101.8	26.1	5670	21	F21337 Human low adenosin
	30	101.8	26.1	5670	21	A35209 Human adenosine re
	31	101.8	26.1	5670	21	A35215 Human adenosine re
	32	99	25.4	166	21	255552 Canine interleukin
	33	44.6	11.4	60	13	Q28942 Cytokine signal se
	34	44.6	11.4	102	13	Q28941 Cytokine signal se
	35	40.8	10.5	2460	11	Q06086 Plasmid pZPC13 enc
	36	37.2	9.5	66	20	Z32227 Human interleukin
	37	35.8	9.2	2249	18	T74283 Cellulose binding
	38	35.8	9.2	2300	18	T74282 Laccase gene. MYC
	39	35.8	9.2	3187	17	T10922 Myceliophthora the
	40	35.8	9.2	3192	18	T72106 M. thermophila lac
	41	35.8	9.2	3192	18	T63318 Dominant-negative
	42	35.8	9.2	3192	21	Z24236 Human neuronal nic
	43	34.4	8.8	772	19	V48405 Human neuronal nic
	44	34.4	8.8	1521	12	Q14288 Human neuronal nic
	45	34.4	8.8	2448	15	V12201

ALIGNMENTS

RESULT 1

255563
ID Z55563 standard; cDNA; 390 BP.

XX AC Z55563;

XX XX Z55563;

XX DF 14-MAR-2000 (first entry)

XX DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region.

XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; Immune response;
KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US11942.

XX PR 29-MAY-1998; 98US-0087306.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; Y58223.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX PS Claim 11; Page 238-239; 264pp; English.


```

Db 30 AGGGAGTTTATCGCCATGGAATTTTCAGA 1
|||||
RESULT 3
ID 255561 standard; cDNA; 1269 BP.
XX 255561;
XX 14-MAR-2000 (first entry)
XX Canine interleukin-13 (IL-13) clone 78 cDNA.
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX Key Location/Qualifiers
XX CDS 57..449
XX /*tag= a
XX /product= "Canine IL-13 clone 78"
XX WO9961618-A2.
XX 02-DEC-1999.
XX 28-MAY-1999; 99WO-US11942.
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI: 2000-072623/06.
XX P-PSDB; Y58223.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX Claim 11; Page 235-236; 264pp; English.
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;
XX Query Match 100.0%; Score 390; DB 21; Length 1269;
XX Best Local Similarity 100.0%; Pred. No. 2.8e-102;
XX Matches 390; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 atggcgctctgttgactgtggtcattgctctcacctgcctcgggtggccttgcctcccg 60

```

```

Db 57 atggcgctctgttgactgtggtcattgctctcacctgcctcgggtggccttgcctcccg 116
Qy 61 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcacaacc 120
Db 117 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcacaacc 176
Qy 121 cagaatcaggcatccctctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 180
Db 177 cagaatcaggcatccctctctgcaacggcagcatggtgtgagcgtcaacctgaccgcggc 236
Qy 181 atgtactgcgagctctagaatctctgataatgtctccgactgcagcgcctcccaagg 240
Db 237 atgtactgcgagctctagaatctctgataatgtctccgactgcagcgcctcccaagg 296
Qy 241 acccagagtgctgaaagcactgtgctctcaaaagccgcgcgagggatttccagtga 300
Db 297 acccagagtgctgaaagcactgtgctctcaaaagccgcgcgagggatttccagtga 356
Qy 301 cgcagccgagacacccaaattgaagtgtatccagttggtgaaacacctgtcaccctatga 360
Db 357 cgcagccgagacacccaaattgaagtgtatccagttggtgaaacacctgtcaccctatga 416
Qy 361 agggagtttattccatgcaatggaatttcaga 390
Db 417 agggagtttattccatgcaatggaatttcaga 446

RESULT 4
ID 255562/C
XX 255562 standard; cDNA; 1269 BP.
XX 255562;
XX 14-MAR-2000 (first entry)
XX Canine interleukin-13 (IL-13) clone 78 cDNA complement.
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX Key Location/Qualifiers
XX CDS complement (821..1213)
XX /*tag= a
XX /product= "Canine IL-13 clone 78"
XX WO9961618-A2.
XX 02-DEC-1999.
XX 28-MAY-1999; 99WO-US11942.
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI: 2000-072623/06.
XX P-PSDB; Y58223.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX Claim 11; Page 237-238; 264pp; English.
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline

```


ID 255558 standard; cDNA; 393 BP.
XX
AC 255558;
XX
DT 14-MAR-2000 (first entry)
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region complement.
XX
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI: 2000-072623/06.
XX
XX P-PSDB; Y58221.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 233; 264pp; English.
XX
XX Sequences 255552-255560 and 255561-255566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX can also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for
XX modulators of activity, while the antibodies may be used in detection,
XX and in drug targeting.
XX
XX Sequence 393 BP; 82 A; 100 C; 118 G; 93 T; 0 other;

Query Match 96.7%; Score 377; DB 21; Length 393;
Best Local Similarity 99.2%; Pred. No. 1e-98;
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 atggcgctggtgactggtgctcattgctcctcactgcctcggtgctcctcccg 60
DB 393 ATGGCGCTGCTGGTGAAGTGGTCAATGCTCTCACCTGCCCTGGCTGCTCCCG 334
QY 61 agccctgactcctcccaaccctcaaggagctcattgagagctggtgaacatcacc 120
DB 333 AGCCCTGTGACTCCCTCCCAACCCCAAGAGAGCTATTGAGGAGCTGCTCAACATCACC 274
QY 121 cagaatcagcgcctcctctgcaacgacgacgctggtggaagcgtcaacgtgacgcggc 180
DB 273 CAGAAATCAGCATCCCTCTCTCAACGCGGACGATGCTGTGGAGCGGTCAACCTGACCGCGGC 214

QY 181 atgtactgcagctctagaatctctgatcaatgctccgactgcagcgccatccaaag 240
DB 213 ATGTACTGGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCGCCATCCAAAG 154
QY 241 acccagagtgctgaagcactgtgctctcaaaagcccgcgcgag---gattccagt 297
DB 153 ACCCAGAGGATGCTGAAGCACTGTGCTCTCAAAAGCCCGCGCAGGCGAGATTCCAGT 94
QY 298 gaacgagcccgagacacccaaaattgaagtgtccagtgtggtgaaacacctgtccacctat 357
DB 93 GAACGAGCCGAGACACCAAAATTCGAAGTGATCCAGTTGCTGTTGTTGAAAAACCTGCTCACCTAT 34
QY 358 gtaagggagatttatcgccatggaatattcaga 390
DB 33 GTAAGGGAGTTTATCGCCATGGAATTTTACA 1
RESULT 7
255555
ID 255555 standard; cDNA; 1302 BP.
XX
AC 255555;
XX
XX 14-MAR-2000 (first entry)
XX
XX Canine interleukin-13 (IL-13) clone 80 cDNA.
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX Key Location/Qualifiers
XX CDS 52..447
XX /*tag= a
XX /product= "Canine IL-13 clone 80"
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI: 2000-072623/06.
XX
XX P-PSDB; Y58221.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 229-230; 264pp; English.
XX
XX Sequences 255552-255560 and 255561-255566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX can also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and

Db	241	cgcagcgcagacacccaattgaagtatccagttggtgaaaaaacctgctcacctatgta	300
Qy	361	aggggagttatcccgatggaaatttcaga	390
Db	301	aggggagttatcccgatggaaatttcaga	330
RESULT 10			
ID	255566/c		
XX	255566 standard; cDNA; 330 BP.		
XX	255566;		
AC	255566;		
DT	14-MAR-2000 (first entry)		
XX	Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.		
DE			
XX	Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;		
KW	immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.		
KW			
XX	Canis familiaris.		
OS			
XX			
PN	W09961618-A2.		
XX			
XX	02-DEC-1999.		
XX			
XX	28-MAY-1999; 99WO-US11942.		
XX			
PR	29-MAY-1998; 98US-0087306.		
XX			
PA	(HESK-) HESKA CORP.		
XX			
PI	Sim G, Yang S, Dreitz MJ, Wonderling RS;		
XX			
DR	WPI; 2000-072623/06.		
DR	P-PSDB; Y58224.		
XX			
PT	Nucleic acids encoding immunoregulatory proteins from cats or dogs,		
PT	useful for treating or preventing e.g. tumors or autoimmune disease		
XX			
PS	Claim 11; Page 241; 264pp; English.		
XX			
CC	Sequences 255552-255560 and 255561-255566 represent cDNA		
CC	sequences encoding canine interleukin-13 (IL-13) clones 80		
CC	and 78 respectively. The invention relates to canine		
CC	IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or		
CC	feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline		
CC	interferon-alpha (IFN-alpha) and feline granulocyte macrophage		
CC	colony-stimulating factor (G-CSF), and nucleotides which encode these		
CC	immunoregulatory proteins. The proteins, their associated		
CC	nucleic acids, specific antibodies and inhibitors may be used as		
CC	vaccines for therapeutic or prophylactic regulation of an immune		
CC	response in animals (particularly cats, dogs, horses and humans).		
CC	They may be used to treat autoimmune or infectious diseases including		
CC	allergies, tumours, inflammation and graft rejection, and to increase		
CC	the response from a co-administered antigen. The nucleotide sequences		
CC	can also be used for the recombinant production of a protein, while		
CC	nucleotide fragments are useful as probes, as amplification primers and		
CC	as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).		
CC	The proteins may be used to raise antibodies and to screen for		
CC	modulators of activity, while the antibodies may be used in detection,		
CC	and in drug targeting.		
XX			
SQ	Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;		
Query Match			
Best Local Similarity		84.6%;	Score 330; DB 21; Length 330;
Matches 330; Conservative		0;	Pred. No. 2.7e-85;
		0;	Mismatches
		0;	Indels
		0;	Gaps
Qy	61	agcccttgactccctcccccaacctcaagagagctcattgaggagctgggtcaacatcacc	120
Db	330	AGCCCTGTGACTTCCTCCCAACCCCTCAAGGAGCTCATTTAGGAGCTGGTCAACATCACC	271

QY 121 cagaatcaggcatccctctgcaacggcagcagctggtgtggagcgtcaacctgaccgccggc 180
|||||
Db 270 CAGANTCAGGATCCCTCTGCAACGGCAGCATGGTGTGGAGGCTCAACCTGACCCCGC 211
QY 181 atgtactgcgagctctagaatctctgatcaatgtctcgcgactgcagcgcctccaaagg 240
|||||
Db 210 ATGTACTGCGCAGCTCTAGAACTCTGTGATCAATGTCTCGACTGCGAGCCCAAGG 151
QY 241 accgagagatgctgaaagcactgtgctctcaaaagccgcggcgggatttccagtga 300
|||||
Db 150 ACCCAGAGCATGCTCAAGACACTGTGCTCTCAAAAGCCGCGCAGGGATTTCAGTGAA 91
QY 301 cgcgcgcgagcaccacaaatgaagtgatccagtgctgggtgaaagaaacgtctccctatga 360
|||||
Db 90 CGCAGCCGAGACACCAAAATTTGAAGTGATCCAGTTGGTGTGAAACCTGCTACCTATGTA 31
QY 361 agggaggtttatcgccatggaaatttcaga 390
|||||
Db 30 AGGCAGTTTATCCCATGGAAATTTTCAGA 1

RESULT 11
Z55559
ID Z55559 standard; cDNA: 333 BP.
AC Z55559;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
WPI: 2000-072623/06.
DR P-PSDB; Y58222.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 11; Page 233-234; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and

CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
XX and in drug targeting.
SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;
Query Match 81.3%; Score 317; DB 21; Length 333;
Best Local Similarity 99.1%; Pred. No. 1.4e-81;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 61 agccctgtgactccctcccccacccctcaaggagagctcattgagagctggtcaacatcacc 120
|||||
Db 1 agccctgtgactccctcccccacccctcaaggagctcattgagagctggtcaacatcacc 60
QY 121 cagaatcaggcatccctctgcaacggcagcagcatggtgtggagcgtcaacctgaccgccgc 180
|||||
Db 61 cagaatcaggcatccctctgcaacggcagcagcatggtgtggagcgtcaacctgaccgccgc 120
QY 181 atgtactgcgagctctagaatctctgatcaatgtctcgcgactgcagcgcctccaaagg 240
|||||
Db 121 atgtactgcgagctctagaatctctgatcaatgtctcgcgactgcagcgcctccaaagg 180
QY 241 accgagagatgctgaaagcactgtgctctcaaaagccgcggcagg ---gatttccagt 297
|||||
Db 181 accgagagatgctgaaagcactgtgctctcaaaagccgcggcagg ---gatttccagt 240
QY 298 gaacgcagcgcgagacacccaaattgaagtgtatccagttggtgaaacacctgctcacctat 357
|||||
Db 241 gaacgcagcgcgagacacccaaattgaagtgtatccagttggtgaaacacctgctcacctat 300
QY 358 gtaaggggagtttatcgccatggaaatttcaga 390
|||||
Db 301 gtaaggggagtttatcgccatggaaatttcaga 333

RESULT 12
Z55560/c
ID Z55560 standard; cDNA: 333 BP.
XX
AC Z55560;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
WPI: 2000-072623/06.
DR P-PSDB; Y58222.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 11; Page 235; 264pp; English.
XX
CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 81.3%; Score 317; DB 21; Length 333;
 Best Local Similarity 99.1%; Pred. No. 1.4e-81;
 Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
 Qy 61 agcctgtgactcctcccaaccctcaaggagctcattgagagctgggtcaacatcacc 120
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 333 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 274
 Qy 121 cagaatcaggatccctctgcaacgacgagcatggtgtggagcgtcaacctgaccgcggc 180
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 273 CAGAATCAGGCAATCCCTCTGTCAACGGCAGCATGCTGTGGAGCGCTCAACCTGACCGCGGC 214
 Qy 181 atgtactgcgagctagaatctctgatcaatgtctccgactgcagcgccatccaagg 240
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 213 ATGTACTGGCGAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCGCGGCATCCAAGG 154
 Qy 241 accagagagatgctgaagcactgtgctctcaaaagcccgcgagcgtg--gatttcag 297
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 153 ACCCAGAGATGCTGAAGACACTGTGCTCTCAAAAGCCCGCGGCGAGGATTCACGT 94
 Qy 298 gaacgcagccgagacaccaaattgaagtgtatccagttggtgaaacacctgctcacctat 357
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 93 GAACGAGCCGAGACACCAAAATGAAGTGCATCCAGTTGCTGAAAAACCTGCTCACCTAT 34
 Qy 358 gtaagggagtttatcgccatgaaatttcaga 390
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 33 GTAAGGGGAGTTATCGCCATGGAAATTTTCAGA 1

RESULT 13
 255554
 ID 255554 standard; cDNA; 278 BP.
 XX AC 255554;
 XX
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-13 (IL-13) cDNA probe.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 XX 28-MAY-1999; 99WO-US11942.
 XX

PR 29-MAY-1998; 98US-0087306.
 XX (HESK-) HESKA CORP.
 PA
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX WPI; 2000-072623/06.
 DR
 XX
 PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 XX
 PS Claim 1i; Page 229; 264pp; English.
 XX
 CC Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 278 BP; 58 A; 93 C; 69 G; 58 T; 0 other;

Query Match 71.3%; Score 278; DB 21; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.9e-70;
 Matches 278; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 atggcgctctggtgactgtgctcattgtctcactgcctcggtggtgcttgcctcccg 60
 Db 1 atggcgctctggtgactgtgctcattgtctcactgcctcggtggtgcttgcctcccg 60
 Qy 61 agcctgtgactcctcccaaccctcaaggagctcattgagagctggtcacaatcacc 120
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 61 agcctgtgactcctcccaaccctcaaggagctcattgagagctggtcacaatcacc 120
 Qy 121 cagaatcaggatccctctgcaacgacgagcatggtgtggagcgtcaacctgaccgcggc 180
 Db |||||||||||||||||||||||||||||||||||||||||||||||||||||||
 121 cagaatcaggatccctctgcaacgacgagcatggtgtggagcgtcaacctgaccgcggc 180
 Qy 181 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaagg 240
 Db 181 atgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaagg 240
 Qy 241 accagagagatgctgaaagcactgtgctctcaaaagcc 278
 Db 241 accagagagatgctgaaagcactgtgctctcaaaagcc 278

RESULT 14
 255553
 ID 255553 standard; cDNA; 272 BP.
 XX AC 255553;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;

immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
Canis familiaris.
W09961618-A2.
02-DEC-1999.
28-MAY-1999; 99WO-US11942.
29-MAY-1998; 98US-0087306.
(HESK-) HESKA CORP.
Sim G, Yang S, Dreitz MJ, Wonderling RS;
WPI; 2000-072623/06.
Nucleic acids encoding immunoregulatory proteins from cats or dogs,
useful for treating or preventing e.g. tumors or autoimmune disease
-
Claim 11; Page 228; 264pp; English.
Sequences 255552-255560 and 255561-255566 represent cDNA
sequences encoding canine interleukin-13 (IL-13) clones 80
and 78 respectively. The invention relates to canine
IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
interferon-alpha (IFN-alpha) and feline granulocyte macrophage
colony-stimulating factor (GM-CSF), and nucleotides which encode these
immunoregulatory proteins. The proteins, their associated
nucleic acids, specific antibodies and inhibitors may be used as
vaccines for therapeutic or prophylactic regulation of an immune
response in animals (particularly cats, dogs, horses and humans).
They may be used to treat autoimmune or infectious diseases including
allergies, tumours, inflammation and graft rejection, and to increase
the response from a co-administered antigen. The nucleotide sequences
can also be used for the recombinant production of a protein, while
nucleotide fragments are useful as probes, as amplification primers and
as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
The proteins may be used to raise antibodies and to screen for
modulators of activity, while the antibodies may be used in detection,
and in drug targeting.
Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;
Query Match 65.6%; Score 256; DB 21; Length 272;
Best Local Similarity 98.9%; Pred. No. 3 8e-64;
Matches 269; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
Qy 45 tggccttgctcccccagagccctgtgactccctcccaaccctcaaggagctcattgagga 104
Db 1 tggccttgctcccccagagccctgtgactccctcccaaccctcaaggagctcattgagga 60
Qy 105 gctgggtcaacatcccccagagatcaggcatccctctgcaacggcagcatggtgtgagcgt 164
Db 61 gctgggtcaacatcccccagagatcaggcatccctctgcaacggcagcatggtgtgagcgt 120
Qy 165 caacctgacccgagcctgactgcgcagctctagaatctctgatcaatgtctccgactg 224
Db 121 caacctgacccgagcctgactgcgcagctctagaatctctgatcaatgtctccgactg 180
Qy 225 cagcgccatccaaaggagccagagatgctgaaagcactgtgctctcaaaagcccgcgcc 284
Db 181 cagcgccatccaaaggagccagagatgctgaaagcactgtgctctcaaaagcccgcgcc 240
Qy 285 agg---gattccagtgtaacgacgacggagaca 313
Db 241 agggcagatcttcagtgtaacgacgacggagaca 272
RESULT 15

F21334
ID F21334 standard; DNA; 1270 BP.
XX
AC F21334;
XX
DT 14-MAR-2001 (first entry)
XX
DE Human low adenosine antisense oligonucleotide related sequence #2901.
XX
KW Low adenosine antisense oligonucleotide; phosphorothioate; allergy;
human; airway disorder; bronchoconstriction; lung inflammation;
surfactant depletion; respiratory; bronchodilator; antiinflammatory;
immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic;
respiratory obstruction; pulmonary obstruction; impeded respiration;
surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS;
respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis;
pulmonary hypertension; emphysema; pulmonary transplantation rejection;
chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
cancer; ss.
XX
OS Homo sapiens.
XX
PN W0200062736-A2.
XX
PD 26-OCT-2000.
XX
PF 24-MAR-2000; 2000WO-US08020.
XX
PR 06-APR-1999; 99US-0127958.
XX
PA (UYEC-) UNIV EAST CAROLINA.
PA (NYCE/) NYCE J W.
XX
NYce JW;
WPI; 2000-679539/66.
Low adenosine (A) content antisense oligonucleotides which do not
trigger adenosine receptors during metabolism, useful e.g. for treating
cancers and respiratory obstructions -
Disclosure; Page 1336; 1592pp; English.
The present invention describes low adenosine (A) content antisense
oligonucleotides and compositions (I) comprising them. In the antisense
oligonucleotides the A is replaced by a 'Universal' or alternative base.
(I) can have respiratory, bronchodilator, antiinflammatory, analgesic,
immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.
The antisense oligonucleotides and (I) can be used to down-regulate the
expression and or activity of target polypeptides associated with
lung/respiratory disorders and malignancies, such as stimulating and
activating peptide factors and transmitters, transcription factors,
immunoglobulins and antibodies, antibody receptors, cytokines and
chemokines, endogenously produced specific and non-specific enzymes,
binding proteins, adhesion molecules and their receptors, cytokine and
chemokine receptors, adenosine receptors, bradykinin receptors, central
nervous system (CNS) and peripheral nervous and non-nervous system
receptors, CNS and peripheral nervous and non-nervous system peptide
transmitters, defensins, growth factors, vasoactive peptides and
receptors, binding proteins and malignancy associated proteins. The
antisense oligonucleotides may be used in this way to treat disorders
including respiratory obstruction (especially pulmonary obstruction
and/or bronchoconstriction) and/or lung inflammation, allergy(ies)
and/or surfactant hypoproduction which are associated with a disease or
condition selected from pulmonary vasoconstriction, inflammation
allergies, asthma, impeded respiration, respiratory distress syndrome
(RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary
hypertension, emphysema, chronic obstructive pulmonary disease (COPD),
pulmonary transplantation rejection, pulmonary infections, bronchitis,
and/or cancer. F18434 to F21543 represent human polynucleotide fragments
and antisense oligonucleotides used in the exemplification of the
present invention.

Search completed: May 13, 2001, 14:30:24
Job time: 18339 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:41 ; Search time 226.02 Seconds
(without alignments)
301.279 Million cell updates/sec

Title: US-09-451-527-102
Perfect score: 390
Sequence: 1 atggcgtctgttgactgt.....atgcgcattggaatttcaga 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgnl_7/prodata/1/ina/5A_COMB.seq.*
2: /cgnl_7/prodata/1/ina/5B_COMB.seq.*
3: /cgnl_7/prodata/1/ina/6A_COMB.seq.*
4: /cgnl_7/prodata/1/ina/6B_COMB.seq.*
5: /cgnl_7/prodata/1/ina/PCTUS_COMB.seq.*
6: /cgnl_7/prodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	230.8	59.2	1290	1	US-08-012-543-1
2	230.8	59.2	1290	5	PCT-US93-07645A-1
3	230.8	59.2	1290	5	PCT-US93-07645-1
4	229.2	58.8	1297	1	US-08-371-121-15
5	188	48.2	384	1	US-08-371-121-17
6	187.4	48.1	336	1	US-08-371-121-24
7	186.2	47.7	425	1	US-08-594-469-4
8	186.2	47.7	425	2	US-08-906-957-4
9	186.2	47.7	4410	1	US-08-594-469-1
10	186.2	47.7	4410	2	US-08-906-957-1
11	185.8	47.6	336	1	US-08-371-121-2
12	168.6	43.2	447	1	US-08-371-121-26
13	168.6	43.2	1212	1	US-08-012-543-3
14	168.6	43.2	1212	5	PCT-US93-07645A-3
15	168.6	43.2	1212	5	PCT-US93-07645-3
16	44.6	11.4	60	1	US-08-371-121-12
17	44.6	11.4	102	1	US-08-371-121-10
18	39.6	10.2	54	1	US-08-371-121-11
19	39.6	10.2	96	1	US-08-371-121-9
20	35.8	9.2	2249	3	US-08-814-052-19
21	35.8	9.2	2300	3	US-08-814-052-18
22	35.8	9.2	3183	2	US-08-939-218A-1
23	35.8	9.2	3187	5	PCT-US95-06815-1
24	35.8	9.2	3192	1	US-08-706-037-26
25	35.8	9.2	3192	1	US-08-940-661A-1
26	35.8	9.2	3192	2	US-09-083-485-1
27	35.8	9.2	3192	2	US-09-005-397-26

28	34.4	8.8	1322	4	US-09-128-450-27	Sequence 27, Appl
29	34.4	8.8	1521	1	US-08-496-855A-3	Sequence 3, Appl
30	34.4	8.8	1521	2	US-07-938-154-9	Sequence 9, Appl
31	34.4	8.8	1521	5	PCT-US91-02311-9	Sequence 9, Appl
32	34.4	8.8	2450	2	US-08-466-589-9	Sequence 9, Appl
33	34.4	8.8	2450	2	US-08-700-636-9	Sequence 9, Appl
34	34.4	8.8	2450	3	US-08-467-574-9	Sequence 9, Appl
35	33.2	8.5	2712	3	US-09-025-691-4	Sequence 4, Appl
36	32.4	8.3	720	4	US-09-094-359-3	Sequence 3, Appl
37	32.4	8.3	720	4	US-09-094-359-7	Sequence 7, Appl
38	32.4	8.3	720	4	US-09-172-063-11	Sequence 11, Appl
39	32.4	8.3	720	4	US-09-172-063-13	Sequence 13, Appl
40	32.4	8.3	762	1	US-08-532-390-40	Sequence 40, Appl
41	32.4	8.3	762	4	US-08-717-294-40	Sequence 11, Appl
42	32.4	8.3	768	4	US-09-094-359-11	Sequence 11, Appl
43	32.4	8.3	850	4	US-09-062-102-2	Sequence 2, Appl
44	32.4	8.3	972	4	US-09-172-063-27	Sequence 27, Appl
45	32.4	8.3	972	4	US-09-172-063-29	Sequence 29, Appl

ALIGNMENTS

RESULT 1
US-08-012-543-1
: Sequence 1, Application US/08012543
: Patent No. 5596072
: GENERAL INFORMATION:
: APPLICANT: Culpepper, Janice
: APPLICANT: McKenzie, Andrew
: APPLICANT: Dang, Warren
: APPLICANT: de Waal Malefyt, Rene
: APPLICANT: Heath, Andrew
: APPLICANT: Aversa, Gregorio
: APPLICANT: Briere, Francine
: APPLICANT: Banchereau, Jacques
: APPLICANT: de Vries, Jan
: APPLICANT: Zurawski, Gerard
: TITLE OF INVENTION: Human Interleukin-13
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: DNAX Research Institute
: STREET: 901 California Avenue
: CITY: Palo Alto
: STATE: California
: COUNTRY: USA
: ZIP: 94304-1104
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Floppy disk
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: Patentin Release #1.0, Version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/012.543
: FILING DATE: 01-FEB-1993
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/933,416
: FILING DATE: 21-AUG-1992
: ATTORNEY/AGENT INFORMATION:
: NAME: Ching, Edwin P.
: REGISTRATION NUMBER: 34,090
: REFERENCE/DOCKET NUMBER: DX0302K1
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 415-852-9196
: TELEFAX: 415-496-1200
: INFORMATION FOR SEQ ID NO: 1:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1290 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: cDNA

FEATURE:
NAME/KEY: CDS
LOCATION: 45...443
US-08-012-543-1

Query Match 59.2%; Score 230.8; DB 1; Length 1290;
Best Local Similarity 77.7%; Pred. No. 6.8e-62;
Matches 306; Conservative 0; Mismatches 82; Indels 5; Gaps 2;
Qy 1 atggcgctctgttgactgtgttcattgtctcactgcctgcctggtgcttgcctccccc 60
Db 45 ATGGCGCTTTTGTGACACGGTCAATTGCTCTCACTTGGCTTGGCGGCTTGGCTCCCCA 104
Qy 61 agcctgtgactccctcccccaccctcaaggagctcattgaggagctgtgcaaatcacc 120
Db 105 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAACATCAC 164
Qy 121 cagaatc---aggatccctctgaacgcgcagcgtgtgagcgtcaaacctgaccgc 177
Db 165 CAGAACCAAGAGCTCCCTCTGCAATGGCAGCATGGTATGAGGAGCTCAACCTGACAGCT 224
Qy 178 ggcattgactgcgcagctctagaatctctgtatcaatgtctcgcagctgcagcgcctccaa 237
Db 225 GGCATGTACTGTGCAGCCCTGGATCCCTGATCAAGTCTCAGGCTGCAGTGCCTCGAG 284
Qy 238 aggacccagagatgctgaaagcactgtctctcctcaaaagccgcgcagc---gatttcc 294
Db 285 AAGACCCAGAGATGCTGAGCGGATCTGCCCGCACAAAGTCTCAGCTGGGCGAGTTTCC 344
Qy 295 agtgaacgcagcagacacacaaattgaagtgtatccagttgtgaaacacgtctcacc 354
Db 345 AGCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCGACAGTTTGTAAAGACCTGCTCTTA 404
Qy 355 tatgtaaggaggatttcgcgcattgcaatttca 388
Db 405 CATTTAAGAAACTTTTTCGCGAGGACGGTTCA 438

RESULT 2
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match 59.2%; Score 230.8; DB 5; Length 1290;

Best Local Similarity 77.7%; Pred. No. 6.8e-62;
Matches 306; Conservative 0; Mismatches 82; Indels 6; Gaps 2;
Qy 1 atggcgctctgttgactgtgttcattgtctcactgcctgcctggtgcttgcctccccc 60
Db 45 ATGGCGCTTTTGTGACACGGTCAATTGCTCTCACTTGGCTTGGCGGCTTGGCTCCCCA 104
Qy 61 accctgtgactccctcccccaccctcaaggagctcattgaggagctgtgcaaatcacc 120
Db 105 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAACATCAC 164
Qy 121 cagaatc---aggatccctctgaacgcgcagcgtgtgagcgtcaaacctgaccgc 177
Db 165 CAGAACCAAGAGCTCCCTCTGCAATGGCAGCATGGTATGAGGAGCTCAACCTGACAGCT 224
Qy 178 ggcattgactgcgcagctctagaatctctgtatcaatgtctcgcagctgcagcgcctccaa 237
Db 225 GGCATGTACTGTGCAGCCCTGGATCCCTGATCAAGTCTCAGGCTGCAGTGCCTCGAG 284
Qy 238 aggacccagagatgctgaaagcactgtctctcctcaaaagccgcgcagc---gatttcc 294
Db 285 AAGACCCAGAGATGCTGAGCGGATCTGCCCGCACAAAGTCTCAGCTGGGCGAGTTTCC 344
Qy 295 agtgaacgcagcagacacacaaattgaagtgtatccagttgtgaaacacgtctcacc 354
Db 345 AGCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCGACAGTTTGTAAAGACCTGCTCTTA 404
Qy 355 tatgtaaggaggatttcgcgcattgcaatttca 388
Db 405 CATTTAAGAAACTTTTTCGCGAGGACGGTTCA 438

RESULT 3
PCT-US93-07645-1
; Sequence 1, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
PCT-US93-07645-1

Query Match 59.2%; Score 230.8; DB 5; Length 1290;
Best Local Similarity 77.7%; Pred. No. 6.8e-62;
Matches 306; Conservative 0; Mismatches 82; Indels 6; Gaps 2;
Qy 1 atggcgctctgttgactgtgttcattgtctcactgcctgcctggtgcttgcctccccc 60
Db 45 ATGGCGCTTTTGTGACACGGTCAATTGCTCTCACTTGGCTTGGCGGCTTGGCTCCCCA 104

CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/371.121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 07/938,161
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
APPLICATION NUMBER: FR 91 03904
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 17:
SEQUENCE CHARACTERISTICS:
LENGTH: 384 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match 48.2%; Score 188; DB 1; Length 384;
Best Local Similarity 76.2%; Pred. No. 6.3e-49;
Matches 259; Conservative 0; Mismatches 75; Indels 6; Gaps 2;
QY 55 tccccgagccctgtgactccctcccccaacctcaaggagctcattgaggagctgtgctcaac 114
DB 16 TCCCCAGGCCCTGTGCCCTCCCTCTACGCCCTCAGGGAGCTCATTGAGGAGCTGTCAAC 75
QY 115 atcaccagaaac---aggcatccctctgcaacgagcagctggtgtgagcgctcaacctg 171
DB 76 ATCACCAGAACCCAGAGAGCTCCGCTGTGCAATGCGAGCTGATGAGGATCAACCTG 135
QY 172 acgcgcggcgtgactgcgagctctagaaatctctgtatcaatgtctcgcagctgcagcgcc 231
DB 136 ACAGCTGACATGTACTGTGAGCGCTGGAATCCCTGTATCAACGTGTGAGGCTGAGTGCC 195
QY 232 atccaaaggaccagagatgactgaaagcactgtgctctcaaaagcccgagcagg---g 288
DB 196 ATCAGAGAACCCAGAGATGCTGAGCGGATCTGCCCGCACAGGCTCTACCTGGGCGAG 255
QY 289 atttccagtgcaacgagcgcgagacaccaaattgagtgatccagtgtggtgaaacctg 348
DB 256 TTTTCCAGCTTGATGTCCGAGACACCAAAATCGAGGTGGCCCACTTTGTAAAGACCTG 315
QY 349 ctacacctatgtaagggggagtttatgcgcattggaatttca 388
DB 316 CTCTTACATTTAAAGAACTTTTTCGCGGAGGACGGTTCA 355
RESULT 6
US-08-371-121-24

Sequence 24, Application US/083711121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTEILLER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA: US/08/371.121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA: US 07/938,161
FILING DATE: 30-NOV-1992
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA: FR 91 00137
FILING DATE: 08-JAN-1992
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match 48.1%; Score 187.4; DB 1; Length 336;
Best Local Similarity 76.9%; Pred. No. 9.2e-49;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
QY 62 gccctgtgactccctcccaacctcaaggagctcattgaggagctggtaacatcaccc 121
DB 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 61
QY 122 agaatac---aggcatccctctgcaacgagcagcatggtgtggaagcgtcaacctgacgcgcg 178
DB 62 AGAACGAGAGGCTCGCTCTGCAATGGGAGCATGATGATGGAGCATCAACCTGACAGCTG 121
QY 179 gcattgtactgcgagctctatgaatctctgtatcaatgtctccgactgcagcgccatccaaa 238

Db 122 GCATGTACTGTGAGCCCTGGATCCTGATCAACGTGTGAGGTGAGTGCAGTGCATCGA 181
QY 239 ggaaccagaggaactgtgaagcactgtgtctctcaaaagcccgagg---gatttcca 295
Db 182 AGACCCAGAGGATGCTGAGCGGATCTGCCGACAAAGGTCTCAGCTGGGAGTTTCCA 241
QY 296 gtgaacgagcagcagacacaaatgaagtgtatccagttgggtgaaaaaacctgctcaact 355
Db 242 GCTTGATGTCGAGACACAAATCGAGGTGCCAGATTGTGTAAGGACCTGCTCTTAC 301
QY 356 atgaagggaggattatcgccatggaaattcca 388
Db 302 ATTAAAGAACTTTTCGCGAGGACGGTTCA 334
RESULT 7
US-08-594-469-4
; Sequence 4, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-4
Query Match 47.7%; Score 186.2; DB 1; Length 425;
Best Local Similarity 75.5%; Pred. No. 2.4e-48;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;
QY 52 gctctcccgagccctgtgactccctcccaaccctcaagagctcattgaggactgctc 111
Db 55 GCCTTCGCTGGCCCTGTGCGCTCCAGTACACCTCAGGAGGCTCATGTGAGGACTGGTC 114
QY 112 aacatcaccagaaac---aggcatccctctgcaacggcagcatgggtgtgagcgctcaac 168

Db 115 AACATCACCAGACCAAGGCTCCGTCTGCAATGGCAGCATGGTATGGAGCATCAAC 174
QY 169 ctgaccgcccgaactgtactgtcgcagctcttagaatactctgataatgtctctccgactgcagc 228
Db 175 CTGACAGCTGGCATGTACTGTGTCAGCCCTGGAAATCCCTGATCAACGTGTGAGGCTGCACT 234
QY 229 gccatccaaaaggaccacagagatgctgaaagcactgtctctcaaaaagcccgagcag- 287
Db 235 GCCATCGAGAAAGACAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGGTCTCAGCTGGG 294
QY 288 -gatttccagtgaacgcagccgacacacaaatgaagtgtatccagttgtgaaaaaac 345
Db 295 CAGTTTTCCAGCTTCATGTCGAGACACACAAATCGAGGTGCCAGTTGTAAAGGAC 354
QY 346 ctgctcacctatgtaaggggagtttatcgccatggaaattcca 388
Db 355 CTGCTCTTACATTTAAGAAACTTTTTCGCGAGGACGGTTCA 397
RESULT 8
US-08-906-957-4
; Sequence 4, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-4
Query Match 47.7%; Score 186.2; DB 2; Length 425;
Best Local Similarity 75.5%; Pred. No. 2.4e-48;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

Query Match	47.7%;	Score 186.2;	DB 1;	Length 4410;	
Best Local Similarity	75.5%;	Pred. No. 5.6e-48;			
Matches 259;	Conservative	0;	Mismatches 78;	Indels 6;	Gaps

QY	52	gcctcccccagccctctgactccctccccaacccctcaagagagctattgaggagctggctc	111
Db	392	GCCTTCGCCTGGCCCTGTGCTCCCATGATGCCCTCAGGAGGCTCAATTGAGAGCTGGTC	451
QY	112	aacatcacccagaatc--aggcatccctctcgaacggcagcatggtgtggagcgtcaac	168
Db	452	ACATCACCAGACACCAAGAGCTCCGCTCTGCAATGGCAGCATGTATGGAGCATCAAC	511
QY	169	ctgacgcgcggcgtactgtcgcgcagctctagaaatctctgatcaatgtctccgactgcagc	228
Db	512	CTCACAGCTGGCATGTACTGTGTGCAGGCCCTGGAATCCCTGATCAACGTGTCAAGCTCAGT	571
QY	229	gccatccaagaagaccagagatgctgaaagcactgtgctctcaaaagccccgcggcagg-	287
Db	572	GCCATCGAAGAAGACCCAGAGGATGCTGAGCGGATTTCGCCGCACAAAGTCTCAGCTGGG	631
QY	288	--gatttcagtgaaacgcgcgcgcgcagacacccaaaattgaagtgtatccagttggtgaaaaac	345
Db	632	CAGTTTTCCAGCTTGATGCTCCGAGACACCAAAATCGAGTGGCCCGAGTTTGTAAAGGAC	691
QY	346	ctgctcacctatgtaaggaggatgttatcccatggaaaattcoa	388
Db	692	CTGCTCTTACATTTAAAGAAACTTTTTTCGCGAGGACGGTTCA	734

RESULT 10
US-08-906-957-1
Sequence 1, Application US/08906957
Patent No. 5856142
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSER: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
Zip: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/906,957
FILING DATE: 06-AUG-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/594,469
FILING DATE:
APPLICATION NUMBER: FR 95 01083
FILING DATE: 31-JAN-1995
ATTORNEY/AGENT INFORMATION:
NAME: FICHTER, Richard E
REGISTRATION NUMBER: 26,382
REFERENCE/DOCKET NUMBER: REF/LEGOUX
TELECOMMUNICATION INFORMATION:
TELEPHONE: (703) 683-0500
TELEFAX: (703) 683-1080
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4410 base pairs

```
;
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-1

Query Match          47.7%; Score 186.2; DB 2; Length 4410;
Best Local Similarity 75.5%; Pred. No. 5.6e-48;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

Qy 52 gctcccccagccctgactccctcccaaacctcaagagctcattgaggagctgctc 111
Db 392 GCCTTCGCTGGCCCTGCTCCAGTACTGCTCCCTCAGGAGCTCATTTGAGGAGCTGCTC 451

Qy 112 aacatcccccagaatc---aggctccctctgcaagcgcagctggtgtgagcgtcaac 168
Db 452 AACATCACCAGAACCCAGAGAGGCTCCGCTCTGCAATGGCAGCATGTTGATGAGCATCAAC 511

Qy 169 ctgaccgcggcagctgactgagcagctctagaatctctgatatcctccgactgcagc 228
Db 512 CTCACAGCTGGCATGTACTGTGAGAGCCCTGGAAATCCCTGATCAACGTGTCCAGGCTGCAGT 571

Qy 229 gccatccaaagaccagaggtgctgaaagcactgtgctctcaaaagccgcgcagg- 287
Db 572 GCATCGAAGAACCCAGAGAGTGTGAGCGGATTTCTGCCGACAAAGGTTCTACGCTGGG 631

Qy 288 --gatttcagtgaaagcgcgcagacacccaaattgaagtgtccagttggtgaaaaac 345
Db 632 CAGTTTTCAGCTTGATGCTCCGAGACACCAAAATCAGGTGGCCCACTTTGTTAAAGGAC 691

Qy 346 ctgctcaccatgtatgaaggagtttatgcccatggaatttca 388
Db 692 CTGCTCTTACATTAAAGAAACTTTTTCGCGAGGACGGTTCA 734

RESULT 11
US-08-371-121-2
; Sequence 2, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
```

```
;
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match          47.6%; Score 185.8; DB 1; Length 336;
Best Local Similarity 76.6%; Pred. No. 2.9e-48;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

Qy 62 gccctgtgactccctcccaaacctcaagagctcattgagagctggtcaacatcaacc 121
Db 2 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTGAGAGGCTGGTCAACATCACCC 61

Qy 122 agaatc---aggcatccctctgcaacgcagcagctggtggagcgtcaacctgacgcgcg 178
Db 62 AGAACAGAGAGCTCCGCTCTGCAATGGCAGCATGTTGAGAGCATCAACCTGACAGCTG 121

Qy 179 gcattgactgcgcagctctagaatctctgataatgtctccgactgcagcgcacatccaa 238
Db 122 ACATGTACTGTGCAGCCCTCGGAATCCCTGATCAACGTGTGACGCTGCAGTGCATCGAGA 181

Qy 239 ggaccagagagatgctgaaagcactgtgctctcaaaagccgcgcgcagc---gatttcca 295
Db 182 AGACCCAGAGAGTGTGAGCGGATTTCTGCCGACAAAGGTCTCAGCTGGCAGATTTCOA 241

Qy 296 gtgaacgcagcgcagacacccaaattgaagtgtatccagttggtgaaaacctgctcaact 355
Db 242 GCTTGATGTCCGAGACACCAAAATCGAGGTGGCCCGCTTTGTAAAGGACCTGCTCTTAC 301

Qy 356 atgtaagsgggagtttatcgccatggaatttca 388
Db 302 ATTTAAAGAAACTTTTTCGCCGAGGACGGTTCA 334

RESULT 12
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
```


STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 26:
SEQUENCE CHARACTERISTICS:
LENGTH: 447 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cdna
US-08-371-121-26

Query Match	43.2%	Score 168.6	DB 1	Length 447
Best Local Similarity	68.2%	Pred. No. 6.2e-43		
Matches	272	Conservative	0	Mismatches 109
				Indels 18
				Gaps 2

QY	1	atggcgctcgttgactgtggtcattgctctcaacctgcctcgttgccctgcctccccg	60
DB	49	ATGGCGCTCTGGGTGACTGCAGTCCCTGCCTTCTGCTTGCCTTGGTGTCTCGCCGCCCA	108
QY	61	agcc-----ctgtagctccctccccaacctcaaggagctcattgagagctg	108
DB	109	GGGCGGTGCCAAGATCTGTGTCCTCTGACCTTAAGGAGCTATTGAGGAGCTG	168
QY	109	gtcaacatcacccagaatcaggcatccctctgcacgcagcatggtgtgagcgtcaac	168
DB	169	AGCAACATCACACAAGACCAGACTCCCTGTGTGCAACGGCAGCATGGTATGAGTGTGGAC	228
QY	169	ctgaaccgcggcatgtactgcgagctctagaatctctgatcaatgtctcgcgaactgagc	228
DB	229	CTGGCCGCTGGCGGGTCTGTGTAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAAT	288
QY	229	gcattcaaaaggaccagagatgctaaaacactgtctctcaaaagccgcgcgaggg	288
DB	289	CCCATCTACAGGACCCAGAGGATATTGCATGGCCCTCTTAACCGCAGGCCCCACATACG	348
QY	289	atttcagtgaaacgcagcgcgagacaccaaaattgaagtgtaccagttggtgaaaaacctg	348
DB	349	GTCTCCA-----GCCTCCCGGATACCAAAATCGAAGTAGCCCACTTATTAAACAAACTG	402
QY	349	ctcaacctatgaaggggagtttatcgccatggaatttc	387

```

1
2
3
4
5
6
7
8
9
10
11
12
13
14
15
16
17
18
19
20
21
22
23
24
25
26
27
28
29
30
31
32
33
34
35
36
37
38
39
40
41
42
43
44
45
46
47
48
49
50
51
52
53
54
55
56
57
58
59
60
61
62
63
64
65
66
67
68
69
70
71
72
73
74
75
76
77
78
79
80
81
82
83
84
85
86
87
88
89
90
91
92
93
94
95
96
97
98
99
100
101
102
103
104
105
106
107
108
109
110
111
112
113
114
115
116
117
118
119
120
121
122
123
124
125
126
127
128
129
130
131
132
133
134
135
136
137
138
139
140
141
142
143
144
145
146
147
148
149
150
151
152
153
154
155
156
157
158
159
160
161
162
163
164
165
166
167
168
169
170
171
172
173
174
175
176
177
178
179
180
181
182
183
184
185
186
187
188
189
190
191
192
193
194
195
196
197
198
199
200
201
202
203
204
205
206
207
208
209
210
211
212
213
214
215
216
217
218
219
220
221
222
223
224
225
226
227
228
229
230
231
232
233
234
235
236
237
238
239
240
241
242
243
244
245
246
247
248
249
250
251
252
253
254
255
256
257
258
259
260
261
262
263
264
265
266
267
268
269
270
271
272
273
274
275
276
277
278
279
280
281
282
283
284
285
286
287
288
289
290
291
292
293
294
295
296
297
298
299
300
301
302
303
304
305
306
307
308
309
310
311
312
313
314
315
316
317
318
319
320
321
322
323
324
325
326
327
328
329
330
331
332
333
334
335
336
337
338
339
340
341
342
343
344
345
346
347
348
349
350
351
352
353
354
355
356
357
358
359
360
361
362
363
364
365
366
367
368
369
370
371
372
373
374
375
376
377
378
379
380
381
382
383
384
385
386
387
388
389
390
391
392
393
394
395
396
397
398
399
400
401
402
403
404
405
406
407
408
409
410
411
412
413
414
415
416
417
418
419
420
421
422
423
424
425
426
427
428
429
430
431
432
433
434
435
436
437
438
439
440
441
442
443
444
445
446
447
448
449
450
451
452
453
454
455
456
457
458
459
460
461
462
463
464
465
466
467
468
469
470
471
472
473
474
475
476
477
478
479
480
481
482
483
484
485
486
487
488
489
490
491
492
493
494
495
496
497
498
499
500
501
502
503
504
505
506
507
508
509
510
511
512
513
514
515
516
517
518
519
520
521
522
523
524
525
526
527
528
529
530
531
532
533
534
535
536
537
538
539
540
541
542
543
544
545
546
547
548
549
550
551
552
553
554
555
556
557
558
559
560
561
562
563
564
565
566
567
568
569
570
571
572
573
574
575
576
577
578
579
580
581
582
583
584
585
586
587
588
589
590
591
592
593
594
595
596
597
598
599
600
601
602
603
604
605
606
607
608
609
610
611
612
613
614
615
616
617
618
619
620
621
622
623
624
625
626
627
628
629
630
631
632
633
634
635
636
637
638
639
640
641
642
643
644
645
646
647
648
649
650
651
652
653
654
655
656
657
658
659
660
661
662
663
664
665
666
667
668
669
670
671
672
673
674
675
676
677
678
679
680
681
682
683
684
685
686
687
688
689
690
691
692
693
694
695
696
697
698
699
700
701
702
703
704
705
706
707
708
709
710
711
712
713
714
715
716
717
718
719
720
721
722
723
724
725
726
727
728
729
730
731
732
733
734
735
736
737
738
739
740
741
742
743
744
745
746
747
748
749
750
751
752
753
754
755
756
757
758
759
760
761
762
763
764
765
766
767
768
769
770
771
772
773
774
775
776
777
778
779
780
781
782
783
784
785
786
787
788
789
790
791
792
793
794
795
796
797
798
799
800
801
802
803
804
805
806
807
808
809
810
811
812
813
814
815
816
817
818
819
820
821
822
823
824
825
826
827
828
829
830
831
832
833
834
835
836
837
838
839
840
841
842
843
844
845
846
847
848
849
850
851
852
853
854
855
856
857
858
859
860
861
862
863
864
865
866
867
868
869
870
871
872
873
874
875
876
877
878
879
880
881
882
883
884
885
886
887
888
889
890
891
892
893
894
895
896
897
898
899
900
901
902
903
904
905
906
907
908
909
910
911
912
913
914
915
916
917
918
919
920
921
922
923
924
925
926
927
928
929
930
931
932
933
934
935
936
937
938
939
940
941
942
943
944
945
946
947
948
949
950
951
952
953
954
955
956
957
958
959
960
961
962
963
964
965
966
967
968
969
970
971
972
973
974
975
976
977
978
979
980
981
982
983
984
985
986
987
988
989
990
991
992
993
994
995
996
997
998
999
1000
1001
1002
1003
1004
1005
1006
1007
1008
1009
1010
1011
1012
1013
1014
1015
1016
1017
1018
1019
1020
1021
1022
1023
1024
1025
1026
1027
1028
1029
1030
1031
1032
1033
1034
1035
1036
1037
1038
1039
1040

```

[illegible]

Db 190 AGCAACATCACAAAGACCAGACTCCCTCTGCAACGGCAGCATGGTATGGAGTGTGAC 249
Qy 169 ctgacccgcggcgtactgtcagctctcagctctcagctctcagctcagc 228
Db 250 CTGGCCGCTGGCGGCTGTCTGTAGCCCTGGATTCCTGACCAACATCTCCAATTGCAAT 309
Qy 229 gccatccaaagaccagcagagatgctgaaagcactgctcctcaaaagccgcgaggg 288
Db 310 GCATCTACAGGACCCAGAGGATATTGATGGCTCTGTAAACCGCAGGCCCCCAGCTACG 369
Qy 289 atttcagtgaaacgagcagcagacacacaaattgaagtgcagttggtgaaaaacctg 348
Db 370 GTCTCCA-----GCCTCCCGCATACCAAAATCGAAGTAGCCCACTTTTATAACAAACTG 423
Qy 349 ctcacctatgtaaggagggtttatgcacatggaatttc 387
Db 424 CTCAGCTACAAAGCAACTGTTTCCGCCACGGCCCTTC 462

RESULT 14

PCT-US93-07645A-3

; Sequence 3, Application PC/TUS9307645A

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Human Interleukin-13

; NUMBER OF SEQUENCES: 6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 6.0.5

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/07645A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/012543

; FILING DATE: 01-FEB-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/010977

; FILING DATE: 29-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/933416

; FILING DATE: 21-AUG-1992

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1212 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

PCT-US93-07645A-3

Query Match 43.2%; Score 168.6; DB 5; Length 1212;
Best Local Similarity 68.2%; Pred. No. 9.1e-43;
Matches 272; Conservative 0; Mismatches 109; Indels 18; Gaps 2;

Qy 1 atggcgctctgttactgtggtgctcctcactgcctcgttgcctgcctcccg 60
Db 70 ATGGCGCTCTGGTGACTGCAGTCTCTGGCTCTTGTGCTTGGTGTCTCGCCGCCCA 129
Qy 61 agcc-----ctgtgactccctcccaacctcaaggagctcattgagagctg 108
Db 130 GGCGCGGTGCAAGATCTGTGTCTCTCCCTCTGACCCTTAAGGAGCTTATTGAGGAGCTG 189
Qy 109 gtcaacatcaccagatacagatccctctgcaacggcagcagctggtgagcgtcaac 168
Db 190 AGCAACATCACAAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGAC 249
Qy 169 ctgacccgcggcgtactgtcagctctcagctctcagctctcagctcagc 228
Db 250 CTGGCCGCTGGCGGCTGTCTGTAGCCCTGGATTCCTGACCAACATCTCCAATTGCAAT 309
Qy 229 gccatccaaagaccagagagatgctgaaagcactgtgctcctcaaaagccgcgaggg 288

Db 310 GCCATCTACAGGACCCAGAGGATATTGATGGCTCTGTAAACGGCAGGCCCCCACTACG 369
Qy 289 atttcagtgaaacgagcagcagacacacaaattgaagtgcagttggtgaaaaacctg 348
Db 370 GTCTCCA-----GCCTCCCGCATACCAAAATCGAAGTAGCCCACTTTTATAACAAACTG 423
Qy 349 ctcacctatgtaaggagggtttatgcacatggaatttc 387
Db 424 CTCAGCTACAAAGCAACTGTTTCCGCCACGGCCCTTC 462

RESULT 15

PCT-US93-07645-3

; Sequence 3, Application PC/TUS9307645

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Human Interleukin-13

; NUMBER OF SEQUENCES: 6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 6.0.5

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/07645

; FILING DATE: 19930818

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/012543

; FILING DATE: 01-FEB-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/010977

; FILING DATE: 29-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/933416

; FILING DATE: 21-AUG-1992

; INFORMATION FOR SEQ ID NO: 3:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 1212 base pairs

; TYPE: nucleic acid

; STRANDEDNESS: double

; TOPOLOGY: linear

PCT-US93-07645-3

Query Match 43.2%; Score 168.6; DB 5; Length 1212;
Best Local Similarity 68.2%; Pred. No. 9.1e-43;
Matches 272; Conservative 0; Mismatches 109; Indels 18; Gaps 2;

Qy 1 atggcgctctgttactgtggtgctcctcactgcctcgttgcctgcctcccg 60
Db 70 ATGGCGCTCTGGTGACTGCAGTCTCTGGCTCTTGTGCTTGGTGTCTCGCCGCCCA 129
Qy 61 agcc-----ctgtgactccctcccaacctcaaggagctcattgagagctg 108
Db 130 GGCGCGGTGCAAGATCTGTGTCTCTCCCTCTGACCCTTAAGGAGCTTATTGAGGAGCTG 189
Qy 109 gtcaacatcaccagatacagatccctctgcaacggcagcagctggtgagcgtcaac 168
Db 190 AGCAACATCACAAAGACCAGACTCCCTGTGCAACGGCAGCATGGTATGGAGTGTGAC 249
Qy 169 ctgacccgcggcgtactgtcagctctcagctctcagctctcagctcagc 228
Db 250 CTGGCCGCTGGCGGCTGTCTGTAGCCCTGGATTCCTGACCAACATCTCCAATTGCAAT 309
Qy 229 gccatccaaagaccagagagatgctgaaagcactgtgctcctcaaaagccgcgaggg 288
Db 310 GCATCTACAGGACCCAGAGGATATTGATGGCTCTGTAAACGGCAGGCCCCCACTACG 369
Qy 289 atttcagtgaaacgagcagcagacacacaaattgaagtgcagttggtgaaaaacctg 348
Db 370 GTCTCCA-----GCCTCCCGCATACCAAAATCGAAGTAGCCCACTTTTATAACAAACTG 423

Qy 349 cccacctatgtaaaggggagtttatgcccatggaatttc 387
||||| || | | | | | | |
Dd 424 CTCAGTACACAAGAAGCAACTGTTTCGCCACGGCCCCCTC 462

Search completed: May 13, 2001, 14:21:44
Job time: 17855 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:38 ; Search time 5997.24 Seconds
(without alignments)
568.108 Million cell updates/sec

Title: US-09-451-527-102
Perfect score: 390
Sequence: 1 atggcgctctggtgactgt.....atgcgcattggaatttcaga 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues
Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est33:*
26: gb_est34:*
27: gb_est35:*
28: gb_est36:*
29: gb_est37:*
30: gb_est38:*
31: gb_est39:*
32: gb_est40:*
33: em_estba:*
34: em_estfun:*
35: em_esthum1:*
36: em_esthum2:*
37: em_esthum3:*
38: em_esthum4:*
39: em_esthum5:*
40: em_esthum6:*
41: em_esthum7:*
42: em_esthum8:*
43: em_esthum9:*
44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estin5:*
68: em_estomi:*
69: em_estom2:*
70: em_estov1:*
71: em_estov2:*
72: em_estpl1:*
73: em_estpl2:*
74: em_estpl3:*
75: em_estpl4:*
76: em_estpl5:*
77: em_estpl6:*
78: em_estpl7:*
79: em_estpl8:*
80: em_estpl9:*
81: em_estpl10:*
82: em_estro1:*
83: em_estro2:*
84: em_estro3:*
85: em_estro4:*
86: em_estro5:*
87: em_estro6:*
88: em_estro7:*
89: em_estro8:*
90: em_estro9:*
91: em_estro10:*
92: em_estro11:*
93: em_estro12:*
94: em_estro13:*
95: em_estro14:*
96: em_estro15:*
97: em_estro16:*
98: em_estro17:*
99: em_estro18:*
100: em_estro19:*
101: em_estro20:*
102: gb_est25:*
103: gb_est26:*
104: gb_est27:*
105: gb_est28:*
106: gb_est29:*
107: gb_est30:*
108: gb_est31:*
109: gb_est32:*
110: gb_est41:*
111: gb_est42:*
112: gb_est43:*
113: gb_est44:*
114: gb_est45:*
115: gb_est46:*
116: gb_est47:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB	ID	Description
1	43.4	11.1	581	219	AZ305110	IM0005P05
2	40	10.3	463	24	A1712497	A1712497 UI-R-AFL-
3	39	10.0	477	218	AZ261971	AZ261971 RPCI-23-1
4	39	10.0	521	215	AZ027551	AZ027551 RPCI-23-3
5	37.8	9.7	994	231	CNS0402X	AL300678 Tetraodon
6	36.8	9.4	576	141	BE907816	BE907816 601501924
7	36.6	9.4	329	146	BF292210	BF292210 WHE2208_A
8	36.4	9.3	277	137	BE593226	BE593226 WSL_99_B0
9	36.4	9.3	411	201	AQ001086	AQ001086 CIT-HSP-2
10	36.4	9.3	537	166	BE357229	BE357229 DGL_147_B
11	35.6	9.1	230	167	BE498968	BE498968 WHE0969_G
12	35.6	9.1	537	29	AV387571	AV387571 AV387571
13	35.6	9.1	1070	136	BE536034	BE536034 601062471
14	35.2	9.0	177	103	A1909438	A1909438 IL-BT208-
15	35.2	9.0	570	24	A1746678	A1746678 u106505_Y
16	35.2	9.0	757	174	BG260311	BG260311 602371427
17	35	9.0	359	17	AI209519	AI209519 B0E07al.f
18	34.8	8.9	507	138	BE705147	BE705147 SC02_08f0

```
c 19 34.6 8.9 965 217 AZ201624
20 34.4 8.8 462 143 BF039993
21 34.4 8.8 544 13 AR880435
22 34.4 8.8 553 106 AU075583
23 34.4 8.8 700 113 AW318852
24 34.4 8.8 712 115 AW475303
25 34.4 8.8 1056 144 BF143984
26 34.2 8.8 477 151 BF625277
27 34.2 8.8 535 161 BF032541
28 34.2 8.8 546 161 BF032543
29 34.2 8.8 616 106 AU066538
30 34.2 8.8 691 150 BF620464
31 34.2 8.8 2275 14 AF034173
32 34 8.7 341 163 BE127683
33 34 8.7 370 166 BE363650
34 34 8.7 562 166 BE361027
35 34 8.7 704 230 CNS02PBO
36 34 8.7 1122 141 BE889888
37 33.8 8.7 498 150 BF606532
38 33.6 8.6 487 138 BE704828
39 33.6 8.6 577 166 BE402120
40 33.6 8.6 714 166 BE414190
41 33.6 8.6 727 164 BE216356
42 33.6 8.6 891 151 BF685554
43 33.6 8.6 902 106 AL522415
44 33.4 8.6 619 173 BG112663
45 33.4 8.6 669 211 AQ780112
```

ALIGNMENTS

```
RESULT 1
AZ305110 581 bp DNA GSS 29-SEP-2000
LOCUS AZ305110
DEFINITION LM0005P05R Mouse 10kb plasmid UUGC1M library Mus musculus genomic
clone UUGC1M0005P05 R, DNA sequence.
ACCESSION AZ305110
VERSION AZ305110.1 GI:10341800
KEYWORDS house mouse,
SOURCE Mus musculus
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 581)
AUTHORS Dunn,D., Aoyagi,A., Barber,M., Beacorn,T., Duval,B., Hamil,C.,
Islam,H., Longacre,S., Mahmoud,M., Meenen,E., Pedersen,T., Reilly
M., Rose,M., Rose,R., Stokes,R., Tingey,A., von Niederhausern,A.,
and Wright,D., Weiss,R.
TITLE Mouse whole genome scaffolding with paired end reads from 10kb
plasmid inserts
JOURNAL Unpublished (2000)
COMMENT Contact: Robert B. Weiss
University of Utah Genome Center
University of Utah
Rm. 308, Biomedical Polymers Research Bldg., 20 S. 2030 E., SLC, UT
84112, USA
Tel: 801 585 5606
Fax: 801 585 7177
Email: ddunn@genetics.utah.edu
Insert Length: 10000 Std Error: 0.00
Plate: 0005 row: P column: 05
Seq primer: CACACAGGAACAGCTATGACC
Class: plasmid ends
High quality sequence stop: 581.
```

FEATURES

```
source
1..581
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="UUGC1M0005P05"
/clone_lib="Mouse 10kb plasmid UUGC1M library"
/sex="Male"
```

```
/lab_host="E. Coli strain XL10-Gold, T1-resistant, F-"
/notice="Vector: PWD42nv; Purified genomic DNA from M.
musculus C57BL/6J (male) was obtained from the Jackson
Laboratory Mouse DNA Resource
(http://www.jax.org/resources/documents/dnares/). The DNA
was hydrodynamically sheared by repeated passage through a
0.005 inch orifice at constant velocity. The sheared DNA
was blunt end-repaired with T4 DNA polymerase and T4
polynucleotide kinase. Adaptor oligonucleotides were
ligated to the blunt ends in high molar excess. The
adaptored DNA was purified and size-selected for a 9.5 to
10.5 kb range using preparative agarose gel
electrophoresis. Vector DNA was prepared from a derivative
of pWD42 (gi14732114|gbAF129072.1), a copy-number
inducible derivative of plasmid R1. The vector was ligated
with adaptors complementary to the insert adaptors and
purified. The sheared, adaptored mouse DNA was annealed to
adaptored vector DNA, and transformed into
chemically-competent E. coli XL10-Gold (Stratagene) cells
and selected for ampicillin resistance."
```

```
BASE COUNT 169 a 139 c 153 g 120 t
ORIGIN
```

```
Query Match 11.1%; Score 43.4; DB 219; Length 581;
Best Local Similarity 76.8%; Pred. No. 0.098;
Matches 53; Conservative 0; Mismatches 16; Indels 0; Gaps 0;
```

```
Qy 1 atggcgctggtgacgtggtcattgctcaccgtgctgggtggcttgcctcccg 60
|||||
Db 513 atggcgctggtggtgacgtgctcaccgtgctgggtggcttgcctcccg 572
|||||
Qy 61 agccctgtg 69
|||||
Db 573 ggccgggtg 581
```

```
RESULT 2
AZ1712497 463 bp mRNA EST 08-JUN-1999
LOCUS AZ1712497
DEFINITION UI-R-AFL-aap-b-12-0-UI.s1 UI-R-AFL Rattus norvegicus cDNA clone
UI-R-AFL-aap-b-12-0-UI 3', mRNA sequence.
ACCESSION AZ1712497
VERSION AZ1712497.1 GI:5016297
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
```

```
REFERENCE 1 (bases 1 to 463)
AUTHORS Ronaldo,M.F., Lennon,G. and Soares,M.B.
TITLE Normalization and subtraction: two approaches to facilitate gene
discovery
JOURNAL Genome Res. 6 (9), 791-806 (1996)
MEDLINE 97044477
COMMENT Contact: Soares, MB
Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
```

```
Oligo-dT track not found, Not I site shown in beginning of sequence
is likely internal to the message. cDNA Library Preparation: M.B.
Soares Lab Clone distribution: clones will be available through
Research Genetics (www.resgen.com)
Seq primer: M13 Forward
POLYA-No. Location/Qualifiers
1..463
/organism="Rattus norvegicus"
/strain="Sprague-Dawley"
```

```

/db_xref="taxon:10116"
/clone="UI-R-AFL-aap-b-12-0-UI"
/clone_lib="UI-R-AFL"
/dev_stage="adult"
/lab_host="DH10B (Life Technologies)"
/notes="Vector: pT730-Pac (Pharmacia) with a modified
polylinker; Site.1: Not I; Site.2: Eco RI; The UI-R-AFL
library is a normalized library constructed from 15 dpc
rat atrioventricular (AV) canal. The tag is a string of 5
nucleotides present between the Not I site and the
oligo-dr track. The library was constructed as described
by Bonaldo, Lennon and Soares, Genome Research 6: 791-806
, 1996. Tissue provided by Jim Lin, Department of Biology,
University of Iowa.
TAG_LIB=UI-R-AFL
TAG_TISSUE=AV canal at 15 dpc
TAG_SEQ=GAAGG"

```

```

BASE COUNT 97 a 130 c 92 g 144 t
ORIGIN

```

```

Query Match 10.3%; Score 40; DB 24; Length 463;
Best Local Similarity 58.3%; Pred. No. 0.83;
Matches 70; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Qy 23 tcattgctcaactgcctcgtggtgctcctcccccagagccctgtgactcctccccc 82
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 255 TGATTGCTGCCACACCCCTCTTTCTGACCTTCATGATCCCTATGACTTCTCCCTGC 314
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 83 ccctcaagagctcattagagctgggtcaacatcaccagcagcagcagcagcagcagc 142
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 315 CCCTTAGTTCACCTGATGATCTGGGCTCAGAACACAAATATTGGCCCTGGGGCTACA 374
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 3

```

AZ261971 A2261971 477 bp DNA GSS 26-JUL-2000
LOCUS RPCI-23-123P23.TJ RPCI-23 Mus musculus genomic clone RPCI-23-123P23
DEFINITION , DNA sequence.
ACCESSION AZ261971
VERSION AZ261971.1 GI:9470858
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 477)
REFERENCE Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Other.GSSs: RPCI-23-123P23.TJ
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pletter@jeng.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 123 row: P column: 23
Seq primer: T7
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..477
/organism="Mus musculus"
/strain="C57BL/6J"

```

```

/db_xref="taxon:10090"
/clone="RPCI-23-123P23"
/clone_lib="RPCI-23"
/sex="female"
/lab_host="DH10B"
/notes="Organ: Kidney/Brain; Vector: pBACE3.6; Site.1:
ECORI; Site.2: EcorI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcorI and EcorI Methyase. Size
selected DNA was cloned into the pBACE3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT 129 a 121 c 113 g 114 t
ORIGIN

```

```

Query Match 10.0%; Score 39; DB 218; Length 477;
Best Local Similarity 52.1%; Pred. No. 1.6;
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

Qy 155 tgtggagcgtcaacctgaccgcggcgtactgtcgcagctctagaatctctgatcaatg 214
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 273 TGGCTAGCTTCAGTCACATGCTCAGACTGGACTGAGGTGATTGGATCATCTGAATAAAT 332
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 215 tctccactgacgcgcaccatccaaaggaccagagaggtgctgaaagcactgtgctctcaaa 274
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 333 ATGGCAGCTGGAGCGTACTGGGATAGACAGTGGGACAACTGAGAACAACCTGGGTACAAA 392
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Qy 275 agcccgcgccgagcagattccagtgaaacgcagcgcgcgcgcgcgcgcgcgcgcgc 321
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 393 AGCTAGCAGTCTGCTTGCCTGAGATGGCAGCTGTCATATCCTGATT 439
| | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |

```

RESULT 4

```

AZ027551 521 bp DNA GSS 25-FEB-2000
LOCUS RPCI-23-343M24.TJ RPCI-23 Mus musculus genomic clone RPCI-23-343M24
DEFINITION , DNA sequence.
ACCESSION AZ027551
VERSION AZ027551.1 GI:7102935
KEYWORDS GSS.
SOURCE house mouse.
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 521)
REFERENCE Zhao, S., Nierman, W., Feldblyum, T., Malek, J., Shatsman, S., Akinret
, B., Levins, M., McGann, S., Tsegaye, G., Geer, K., Krol, M., de Jong, P.
and Fraser, C.M.
Mouse BAC End Sequences from Library RPCI-23
Unpublished (1999)
Contact: Shaying Zhao
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: szhao@tigr.org
Clones are derived from the mouse BAC library RPCI-23. For BAC
library availability, please contact Pieter de Jong
(pletter@jeng.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/orderingframe.htm)
or from Resea ch Genetics (info@resgen.com). BAC end page:
http://www.tigr.org/tdb/bac_ends/mouse/bac_end_intro.html
Plate: 343 row: M column: 24
Seq primer: SP6
Class: BAC ends.
FEATURES
source Location/Qualifiers
1..521
/organism="Mus musculus"
/strain="C57BL/6J"
/db_xref="taxon:10090"
/clone="RPCI-23-343M24"

```

```

/clone_lib="RPC1-23"
/sex="Female"
/lab_host="DH10B"
/Note="Organ: Kidney/Brain; Vector: pBACE3.6; Site_1:
ECORI; Site_2: EcoRI; Female C57BL/6J mouse kidney and/or
brain genomic DNA was isolated and partially digested
with a combination of EcoRI and EcoRI Methylase. Size
selected DNA was cloned into the pBACE3.6 vector at the
ECORI sites. The ligation products were transformed into
DH10B electrocompetent cells (BRL Life Technologies)."
BASE COUNT      135 a 136 c 124 g 124 t      2 others
ORIGIN

Query Match      10.0%; Score 39; DB 215; Length 521;
Best Local Similarity 52.1%; Pred. No. 1.6;
Matches 87; Conservative 0; Mismatches 80; Indels 0; Gaps 0;

QY 155 tttgagagtcacactgacgcggcgatgtactgagcagctctagatctctgataatg 214
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 277 TGGTAGCTTACATGCATGGTCAGACTGGACTGGAGTGATTGGATCATTTCTGAATAAAT 336
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 215 tctcgactgcagcccatccaaagaccagagaggtgctgaaagcactgtctctcaaa 274
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 337 ATGGCAGCTGGAGCGTACTGGGATACACAGTGGGACAACTGAGAACACTGTGTACAAA 396
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 275 agccgcgagcagggtattccagtgaacgcagccgagacacacaaaatt 321
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 397 AGCTAGCAGTCTGTCTGTGCTGAGATGGCAGTCTGCATATCCTGATT 443
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
CNS0402X/c      994 bp      DNA      GSS      25-MAY-2000
LOCUS
DEFINITION      Tetraodon nigroviridis genome survey sequence T7 end of clone
                  125F09 of library G from Tetraodon nigroviridis, genomic survey
                  sequence.
ACCESSION      AL300678
VERSION      AL300678.1 GI:8177652
KEYWORDS      GSS; genome survey sequence.
SOURCE      Tetraodon nigroviridis.
ORGANISM      Tetraodon nigroviridis
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
                  Eurypterygii; Ctenosquamata; Acanthomorpha; Euacanthomorpha;
                  Holacanthopterygii; Acanthopterygii; Percormorpha;
                  Tetraodontiformes; Tetraodontidae; Tetraodontidae; Tetraodon.
REFERENCE      1 (bases 1 to 994)
AUTHORS      Roest-Crollius,H., Jaillon,O., Dasilva,C., Fizames,C., Fisher,C.,
                  Bouneau,L., Billault,A., Quetier,F., Saurin,W., Bernot,A. and
                  Weissenbach,J.
TITLE      Characterization and repeat analysis of the compact genome of the
                  freshwater pufferfish Tetraodon nigroviridis
JOURNAL      Unpublished
REFERENCE      2 (bases 1 to 994)
AUTHORS      Roest-Crollius,H., Jaillon,O., Dasilva,C., Bouneau,L., Fisher,C.,
                  Bernot,A., Fizames,C., Wincker,P., Brottier,P., Quetier,F.,
                  Saurin,W. and Weissenbach,J.
TITLE      Human gene number estimate provided by genome wide analysis using
                  Tetraodon nigroviridis DNA sequence
JOURNAL      Unpublished
REFERENCE      3 (bases 1 to 994)
AUTHORS      Genoscope.
TITLE      Direct Submission
JOURNAL      Submitted (12-APR-2000) to the EMBL/GenBank/DBJ databases
REFERENCE      This sequence is a single read and was generated as part of a large
                  scale clone-end sequencing project of the Tetraodon nigroviridis
                  genome. For more information, please take a look at
                  http://www.genoscope.cns.fr/Tetraodon.
FEATURES      Location/Qualifiers
                  1..994
                  /organism="Tetraodon nigroviridis"
                  /db_xref="taxon:99883"

/clone="125F09"
/clone_lib="G"
/Note="Genoscope sequence ID : C08CL25CC05Lp1-end : T7"
BASE COUNT      198 a 295 c 325 g 174 t      2 others
ORIGIN

Query Match      9.7%; Score 37.8; DB 231; Length 994;
Best Local Similarity 51.5%; Pred. No. 4.2;
Matches 87; Conservative 0; Mismatches 82; Indels 0; Gaps 0;

QY 14 tgaactgtgctatgctctcaactgctcggtggtggtgctgctcccgagccctgtgactc 73
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 244 TGGCTGTGCTCTTTCTTCATCGGGACAAACAGAGCGCTTCGCTGCCCTCTCTCACGCCGACC 185
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 74 cctcccaacacctcaaggagctcattgaggagctggtgcaacatcaccacagaatcaggcat 133
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 184 TCGGGGCAAGTCTTCAGGAGTCTGTAGAGGACCTTGACACATCTGTCTATCTCCAGCTGC 125
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 134 ccctctgcaacggcagcatggtgtgagcgtcaacactgaccgccggcat 182
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 124 TCTGCTGTGTCAGCGCCTTGTCAAGATCACCGAGCAGAGCCAGGAAAT 76
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 6
BE907816      576 bp      mRNA      EST      20-OCT-2000
LOCUS
DEFINITION      601501924F1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903965 5',
                  mRNA sequence.
ACCESSION      BE907816
VERSION      BE907816.1 GI:10401759
KEYWORDS      EST.
SOURCE      human.
ORGANISM      Homo sapiens
                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
                  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE      1 (bases 1 to 576)
AUTHORS      NIH-MGC http://mgi.nci.nih.gov/.
TITLE      National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL      Unpublished (1999)
COMMENT      Contact: Robert Strausberg, Ph.D.
                  Tel: (301) 496-1550
                  Email: Robert_Strausberg@nih.gov
                  Tissue Procurement: ATCC
                  cDNA Library Preparation: Life Technologies, Inc.
                  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
                  DNA Sequencing by: Incyte Genomics, Inc.
                  Clone distribution: MGC clone distribution information can be
                  found through the I.M.A.G.E. Consortium/LLNL at:
                  http://image.llnl.gov
                  Plate: LHAM9708 row: o column: 06
                  High quality sequence stop: 571.
FEATURES      Location/Qualifiers
                  1..576
                  /organism="Homo sapiens"
                  /db_xref="taxon:9606"
                  /clone="IMAGE:3903965"
                  /clone_lib="NIH_MGC_70"
                  /tissue_type="epithelioid carcinoma"
                  /lab_host="DH10B (phage-resistant)"
                  /note="Organ: pancreas; Vector: pCMV-SPORT6; Site_1: NotI;
                  Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
                  Average insert size 1.1 kb. Library constructed by Life
                  Technologies."
BASE COUNT      108 a 174 c 147 g 147 t
ORIGIN

Query Match      9.4%; Score 36.8; DB 141; Length 576;
Best Local Similarity 48.1%; Pred. No. 6.9;
Matches 104; Conservative 0; Mismatches 112; Indels 0; Gaps 0;

QY 38 gcttcggtggccttgcctcccccgagccctgtgactccctcccccaacctcaaggagctca 97

```



```
Db 82 CGACGCCCGAGTGGTCAACGCCAGGTCATCCGGCCCAACGGCGCTACGTGTGATG 141
Qy 204 tctgatcaatgtctccgactgc 225
||||| | | | | |
Db 142 TCTGATCTTTAGCTTCTACAGC 163

RESULT 9
A0001086/c 411 bp DNA GSS 26-JUN-1998
LOCUS CIT-HSP-2288N10.TR CIT-HSP Homo sapiens genomic clone 2288N10, DNA
DEFINITION sequence.
ACCESSION A0001086
VERSION A0001086.1 GI:3028525
KEYWORDS GSS.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 411)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K.,
Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., Shizuya,H.,
Simon,M. and Venter,J.C.
TITLE Use of a random BAC End Sequence Database for Sequence-Ready Map
Building (1998)
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html
Seq primer: M13 Reverse
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..411
/organism="Homo sapiens"
/db_xref="GDB:7150045"
/clone_xref="taxon:9606"
/clone="2288N10"
/clone_lib="CIT-HSP"
/sex="Male"
/cell_type="Sperm"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

BASE COUNT 120 a 100 c 101 g .90 t
ORIGIN

Query Match 9.3%; Score 36.4; DB 201; Length 411;
Best Local Similarity 48.5%; Pred. No. 8.3;
Matches 100; Conservative 0; Mismatches 106; Indels 0; Gaps 0;

Qy 29 ctctacactgctcggtggtgcttgcctcccgagccgtgtaactccctcccaaccctca 88
||||| | | | | | | | | | | | | | | | | | | | | |
Db 287 CCTCGCCTGCTGTCATGCAAGCCACCCGAGCCAGTGCCCTTGTACCGCCCTCT 228
||||| | | | | | | | | | | | | | | | | | | | | |
Qy 89 aggagctcattgaggctggtcaacatcccccaggaatcagcctcctctgcaacgca 148
||||| | | | | | | | | | | | | | | | | | | | | |
Db 227 CCACACTGGGTCTGGTGGGGTGGGGCCACATGGGGTCTGAAAGGGCAGGCGTG 168
||||| | | | | | | | | | | | | | | | | | | | | |
Qy 149 gcatggtgtagcgctcaacccgacccgagcgtactgtagcagctctagaatctctga 208
||||| | | | | | | | | | | | | | | | | | | | | |
Db 167 GTGCTCAGGGGTCTGTCATGATCACGTCCCGCCTCTCTTTTCTGCTCACTAATCTCACA 108
||||| | | | | | | | | | | | | | | | | | | | | |
Qy 209 tcaatgtctccgactcagcgcattc 234
||||| | | | | | | | | | | | | | | | | | | | | |
Db 107 TCAGCTTTTAAAGAAATCCACTTC 82
||||| | | | | | | | | | | | | | | | | | | | | |
```

```
RESULT 10
BE357229 537 bp mRNA EST 20-JUL-2000
LOCUS DGI_147_B02.g1_A002 Dark Grown 1 (DGI) Sorghum bicolor cDNA, mRNA
DEFINITION sequence.
ACCESSION BE357229
VERSION BE357229.1 GI:9298786
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
; Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 537)
AUTHORS Cordonnier-Pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt
,L.H.
TITLE An EST database from Sorghum: dark-grown seedlings
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu
Sequences have been trimmed to exclude PolyA, vector and regions
below Phred quality 16. The threshold for highest quality sequence
is 20.
Seq primer: PolyTMix
High quality sequence start: 31
High quality sequence stop: 514
POLYA-No. Location/Qualifiers
1..537
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGI)"
/note="Organ: 5-day-old dark-grown seedlings; Vector:
Lambda Zap; Site_1: XhoI; Site_2: EcoRI; The library was
made from poly-A RNA in the cloning vector lambda ZAP II.
Clones to be sequenced were prepared by mass excision."

BASE COUNT 89 a 160 c 176 g 112 t
ORIGIN

Query Match 9.3%; Score 36.4; DB 166; Length 537;
Best Local Similarity 53.5%; Pred. No. 8.8;
Matches 76; Conservative 0; Mismatches 66; Indels 0; Gaps 0;

Qy 84 cctcaaggagctcattgaggagctgtcaacatcaccccaagaatcaggcatccctctgcaa 143
||||| | | | | | | | | | | | | | | | | | | | | |
Db 249 CCCCATGGAGAGGCTCGGGGAGCCCGCGGACATCGCGGGTGGTGGGTCTCTTGCAC 308
||||| | | | | | | | | | | | | | | | | | | | | |
Qy 144 cggcagcatggtgtgagcgtcaacctgacccgagcgtactgtagcgcagctctagaatc 203
||||| | | | | | | | | | | | | | | | | | | | | |
Db 309 .CGACGCCCGCAGTGGGTCAACGGCCAGGTCTATCCGCGCCACAGCGGCTACGTGTGATG 368
||||| | | | | | | | | | | | | | | | | | | | | |
Qy 204 tctgatcaatgtctccgactgc 225
||||| | | | | | | | | | | | | | | | | | | | | |
Db 369 TCTGATCTTTAGCTTCTACAGC 390
||||| | | | | | | | | | | | | | | | | | | | | |

RESULT 11
BE498968 230 bp mRNA EST 04-AUG-2000
LOCUS WHE0969_G06_N112S Wheat pre-anthesis spike cDNA library Triticum
DEFINITION aestivum cDNA clone WHE0969_G06_N11, mRNA sequence.
ACCESSION BE498968
VERSION BE498968.1 GI:9697585
KEYWORDS EST.
SOURCE bread wheat.
ORGANISM Triticum aestivum
```

Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Triticeae; Triticum.

REFERENCE 1 (bases 1 to 230)

AUTHORS Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han,P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

TITLE The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library

JOURNAL Unpublished (2000)

COMMENT Contact: Olin Anderson
US Department of Agriculture, Agriculture Research Service, Pacific West Area, Western Regional Research Center
800 Buchanan Street, Albany, CA 94710, USA
Tel: 5105595773
Fax: 5105595818
Email: andersn@pw.usda.gov
Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20
Seq primer: Stratagene SK primer.

FEATURES

source
1..230
/organism="Triticum aestivum"
/cultivar="Chinese Spring"
/db_xref="taxon:4565"
/clone="WHE0969_G06_N11"
/clone_lib="Wheat pre-anthesis spike cDNA library"
/tissue_type="Spike before anthesis"
/dev_stage="Adult plant"
/lab_host="E. coli SOLR"
/note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: EcoRI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, green and yellow anther were collected and total RNA, and poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give phagescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
BASE COUNT 42 a 69 c 74 g 45 t
ORIGIN

Query Match 9.1%; Score 35.6; DB 167; Length 230;
Best Local Similarity 50.6%; Pred. No. 12;
Matches 86; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

QY 20 tggcattgctctcacctgctcgtggtggtgcttgcctcccgagccctgtgactccctccc 79
DB 61 TCGCCATCTCTCTCCCTTCCTCCAGAGATCATCGCCGAGATTTTCGGGACCTACTTCC 120
QY 80 caaccctcaaggagctcattgagcgtcgttcaacatcacccagaatcaggcatccctct 139
DB 121 TGATCTTCGGGGGTGGCGCGGTGACCATCACAGAGAAATGGGAGATCAGCTTCC 180
QY 140 gcaaccgagcagctggttgagcgtcacctgacccgctgactgtactgc 189
DB 181 CCGCGGTGGCATCGTGTGGGGCTCACCGTGATGGTGATGGTGACTTCC 230

RESULT 12
AV387571/C 537 bp mRNA EST 29-SEP-2000
LOCUS AV387571 Chlamydomonas reinhardtii C9 Chlamydomonas reinhardtii
DEFINITION CDNA clone CM026e03_r, mRNA sequence.

ACCESSION AV387571.1 GI:6541787
VERSION AV387571
KEYWORDS EST.
SOURCE Chlamydomonas reinhardtii.
ORGANISM Chlamydomonas reinhardtii.
Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales; Chlamydomonadaeae; Chlamydomonas.

REFERENCE

AUTHORS Asanizu,E., Nakamura,Y., Sato,S., Fukuzawa,H. and Tabata,S.
TITLE A large scale structural analysis of cDNAs in a unicellular green alga, Chlamydomonas reinhardtii. I. Generation of 3433 non-redundant expressed sequence tags

JOURNAL

MEDLINE DNA Res. 6 (6), 369-373 (1999)
COMMENT Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan.
Email: ynakamu@kazusa.or.jp, URL: http://www.kazusa.or.jp/en/plant/.

FEATURES

source
1..537
/organism="Chlamydomonas reinhardtii"
/strain="C9"
/db_xref="taxon:3055"
/clone="CM026e03_r"
/clone_lib="Chlamydomonas reinhardtii C9"
/dev_stage="photoautotrophic growth"
/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2: XhoI"
BASE COUNT 62 a 220 c 166 g 89 t
ORIGIN

Query Match 9.1%; Score 35.6; DB 29; Length 537;
Best Local Similarity 47.0%; Pred. No. 15;
Matches 110; Conservative 0; Mismatches 124; Indels 0; Gaps 0;

QY 47 gccttgctcccgagccctgtgactccctcccccacccctcaaggagctcattgagagc 106
DB 497 GCAGGACATCACCCCTGCAGACACATTATCCGCAAGTTGAAGGTCTGAAGCGCCCA 438
QY 107 tggtaacatcacccagaatcaggctccctctgcaacggcagcagctgtgtgagcgctca 166
DB 437 AGTTGCATCATCACCAGCTCATGGAGGTGACGCGTACTACACGAGGAGGTGGGCCCA 378
QY 167 acctgacccgctgactgctgcgagctctagaatctctgatcaatgtctccgactgca 226
DB 377 AGATCAGCG 318

QY 227 gcgcattccaaaggaccagagagatgctgaaagcactgtgctctcaaaagcccg 280
DB 317 GCAGCGGTACCGCTCCGCGGAGGAGGAGAAATCGCTGCGCTGTGGGAATCCG 264

RESULT

13
BE536034/C 1070 bp mRNA EST 09-AUG-2000
LOCUS 601062471F1 NTH_MGC_10 Homo sapiens CDNA clone IMAGE:3448912 5',
DEFINITION mRNA sequence.

ACCESSION BE536034
VERSION BE536034.1 GI:9764679
KEYWORDS EST.
SOURCE human.

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov

Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov

CONTACT: Sampson A.J.O.
Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-SP,
Brazil
Tel: +55-11-2704922
Fax: +55-11-2707001
Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(<http://www.ludwig.org.br/seq/gethtml.pl?t1=IL&t2=IL-BT208-007.html&t3=080499&t4=1>)
Seq primer: puc 18 forward.
Location/Qualifiers
1. .177

```

/dev_stage="adult"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pME18S-FL3; Site_1: DraIII
(CACTGTGTG); Site_2: DraIII (CACCATGTG); 1st strand cDNA
was primed with an oligo(dT) primer
(ATGTGGCCTTTTITTTTTTTT); double-stranded cDNA was
ligated to a DraIII adaptor [TGTGGCCTACTGG], digested
and cloned into distinct DraIII sites of the pME18S-FL3
vector (5' site CACTGTGTG, 3' site CACCATGTG). XhoI should
be used to isolate the cDNA insert. Size selection was
performed to exclude fragments <1.5kb. Library
constructed by Dr. Sumio Sugano (University of Tokyo
Institute of Medical Science). Custom primers for
sequencing: 5' end primer CTTCTGCTCTAAAGCTGGG and 3' end
primer CGACCTCAGCTCGAGACA."
BASE COUNT 140 a 153 c 190 g 79 t 8 others
ORIGIN

```

```

Query Match          9.0%; Score 35.2; DB 24; Length 570;
Best Local Similarity 50.3%; Pred. No. 19;
Matches 85; Conservative 0; Mismatches 84; Indels 0; Gaps 0;

Qy 28 gctctcaccctgctggtggccttcctcccgagccctgtgactccctccccaaccctc 87
   || || || || || || || || || || || || || || || || || || || ||
Db 323 GCCATGACGAGCCCATGATCCAACTGTACTACAGGCCAGTGGATCAGTACAGCACAC 382

Qy 88 aaggagctcattgaggagctggtcaacatcacccagagaatcaggcatccctctgcaacggc 147
   || || || || || || || || || || || || || || || || || || || ||
Db 383 AACAACTTCGTGCAGGACTGCGTCAATATCACCATCAAGCAGCACACGCGTACACCACCACC 442

Qy 148 agcatggtgtgagcgtcaacctgaccgcccggcatgtactgcgcagctc 196
   || || || || || || || || || || || || || || || || || || || ||
Db 443 ACCAAAGGGGAGAACTTCACCGAGACCGCATGTGAAGAATGATGNAGCGC 491

```

Search completed: May 13, 2001, 11:40:52
Job time: 16527 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:25:11 ; Search time 9342.78 Seconds
(without alignments)
615.627 Million cell updates/sec

Title: US-09-451-527-102
Perfect score: 390
Sequence: 1 atggcgctctgttgactgt.....atgcgcattggaatttcaga 390

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues 2566470

Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*

- 1: gb_ba1:*
- 2: gb_ba2:*
- 3: gb_ba3:*
- 4: gb_in1:*
- 5: gb_in2:*
- 6: gb_in3:*
- 7: gb_om:*
- 8: gb_ov:*
- 9: gb_pat1:*
- 10: gb_pat2:*
- 11: gb_ph:*
- 12: gb_pi1:*
- 13: gb_pi2:*
- 14: gb_pi3:*
- 15: gb_pi4:*
- 16: em_bal:*
- 17: em_ba2:*
- 18: em_fun:*
- 19: em_htgo_hum:*
- 20: em_htgo_inv:*
- 21: em_htgo_rod:*
- 22: em_htg_hum1:*
- 23: em_htg_hum2:*
- 24: em_htg_hum3:*
- 25: em_htg_hum4:*
- 26: em_htg_hum5:*
- 27: em_htg_hum6:*
- 28: em_htg_hum7:*
- 29: em_htg_hum8:*
- 30: em_htg_inv1:*
- 31: em_htg_inv2:*
- 32: em_htg_other:*
- 33: em_htg_rod:*
- 34: em_hum1:*
- 35: em_hum2:*
- 36: em_hum3:*
- 37: em_hum4:*
- 38: em_hum5:*
- 39: em_hum6:*
- 40: em_hum7:*
- 41: em_in:*
- 42: em_om:*
- 43: em_or:*

- 44: em_ov:*
- 45: em_pat:*
- 46: em_ph:*
- 47: em_pi:*
- 48: em_ro:*
- 49: em_sts:*
- 50: em_sy:*
- 51: em_un:*
- 52: em_vi:*
- 53: gb_sts1:*
- 54: gb_sts2:*
- 55: gb_sts3:*
- 56: gb_sy:*
- 57: gb_un:*
- 58: gb_vil:*
- 59: gb_v12:*
- 60: gb_v12:*
- 61: gb_v12:*
- 62: gb_v12:*
- 63: gb_v12:*
- 64: gb_v12:*
- 65: gb_v12:*
- 66: gb_v12:*
- 67: gb_v12:*
- 68: gb_v12:*
- 69: gb_v12:*
- 70: gb_v12:*
- 71: gb_v12:*
- 72: gb_v12:*
- 73: gb_v12:*
- 74: gb_v12:*
- 75: gb_v12:*
- 76: gb_v12:*
- 77: gb_v12:*
- 78: gb_v12:*
- 79: gb_v12:*
- 80: gb_v12:*
- 81: gb_v12:*
- 82: gb_v12:*
- 83: gb_v12:*
- 84: gb_v12:*
- 85: gb_v12:*
- 86: gb_v12:*
- 87: gb_v12:*
- 88: gb_v12:*
- 89: gb_v12:*
- 90: gb_v12:*
- 91: gb_v12:*
- 92: gb_v12:*
- 93: gb_v12:*
- 94: gb_v12:*
- 95: gb_v12:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	377	96.7	1302	7 AF244915	AF244915 Canis fam
2	230.8	59.2	1270	93 HUMILI3A	L06801 Homo sapien
3	230.8	59.2	1282	92 HSNCS30	X69079 H.sapiens 1
4	230.8	59.2	1290	10 I34548	I34548 Sequence 1
5	229.2	58.8	417	88 AF043334	AF043334 Homo sapi
6	229.2	58.8	1297	9 A29948	A29948 Coding sequ
7	229.2	58.8	1297	10 I58488	I58488 Sequence 15
8	203.8	52.3	343	7 AF072807	AF072807 Bos tauru
9	188	48.2	384	9 A29950	A29950 Nucleic aci
10	188	48.2	384	10 I58489	I58489 Sequence 17
11	187.4	48.1	336	9 A29931	A29931 Sequence co

12 187.4 48.1 336 10 158494
13 186.2 47.7 425 9 AR027065
14 186.2 47.7 425 10 186198
15 186.2 47.7 4410 9 A52326
16 186.2 47.7 4410 9 AR027062
17 186.2 47.7 4410 10 186195
18 185.8 47.6 336 9 A29930
19 185.8 47.6 336 10 158481
20 186.6 43.2 447 10 158495
21 168.6 43.2 1207 94 MUSTRCP
22 168.6 43.2 1212 10 134549
23 163.2 41.8 443 94 RATIL13A
24 130.8 33.5 213343 78 AF276990
25 101.8 26.1 3714 93 HUM11DC99Z
26 101.8 26.1 4600 93 HUM11L13B
27 101.8 26.1 4740 93 HSU10307
28 101.8 26.1 5670 93 HSU31120
29 101.8 26.1 50282 85 AC004039
30 101.8 26.1 78469 75 AC074127
31 101.8 26.1 78469 75 AC074127
32 92.2 23.6 3520 7 BTA132441
33 71 18.2 3395 93 HUM11DC98Z
34 61.6 15.8 4376 94 MUSIL13A
35 61.6 15.8 142732 88 AC084392
36 61.6 15.8 159500 94 AC005742
37 61.6 15.8 237823 66 AC020886
38 44.6 11.4 60 9 A29941
39 44.6 11.4 60 10 158485
40 44.6 11.4 102 9 A29939
41 44.6 11.4 102 10 158483
42 40.8 10.5 1008 94 RATNACHR85
43 40.8 10.5 2461 95 RNU42976
44 40.8 10.5 38390 3 SC2H12
45 39.6 10.2 54 9 A29940

ALIGNMENTS

RESULT 1
AF244915
LOCUS AF244915 1302 bp mRNA MAM 16-OCT-2000
DEFINITION Canis familiaris interleukin-13 mRNA, complete cds.
ACCESSION AF244915
VERSION AF244915.1 GI:7528273
KEYWORDS
SOURCE dog.
ORGANISM
Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE
1 (bases 1 to 1302)
Yang, S., Borroughs, K.L. and McDermott, M.J.
Canine interleukin-13: molecular cloning of full-length cDNA and
expression of biologically active recombinant protein
J. Interferon Cytokine Res. 20 (9), 779-785 (2000)
JOURNAL
MEDLINE
PUBMED
20485146
11032397
REFERENCE
2 (bases 1 to 1302)
Yang, S.
Direct Submission
Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation,
1613 Prospect Parkway, Fort Collins, CO 80525, USA
JOURNAL
FEATURES
Location/Qualifiers
source
1. .1302
/organism="Canis familiaris"
/db_xref="taxon:9615"
1. .51
52. .447
/codon_start=1
/product="interleukin-13"
/protein_id="AAF63204.1"
/db_xref="GI:7528274"
/translation="MALWLTGVIALTCIGGLASPPVPTPLKELIEELVNITQNAQ

SLGSMWWSVNLTAGMYCALESILNVSDCAIQRTQRMKALCSOKPAGQISSER
SRDTKEIVQLVNLNLLTYRGVVRHGNFR"
448. .1302
3'UTR 337 a 318 c 340 g 307 t
BASE COUNT
ORIGIN
Query Match 96.7%; Score 377; DB 7; Length 1302;
Best Local Similarity 99.2%; Pred. No. 3.4e-86;
Matches 390; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 atggcgtctggttgactggtgctatgctctaccctgcctcggctggtgcttgcctcccg 60
|||||
Db 52 ATGGCGCTCTGGTTGACTGTGGTCTACCTCGCTCGGTGGCTTGGCTCCCGC 111
QY 61 agccctgtgactcctcccaaccctcaagagctcattgaggagctggtgcaacatcacc 120
|||||
Db 112 AGCCTGTGACTCCCTCCCAACCTCAAGAGAGCTCATTGAGGAGCTGGTCAACATCACC 171
QY 121 cagaatcaggcatcctctctgcaaggcagcatggtgagcgtcaacctgaccgcggc 180
|||||
Db 172 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGCTGTGGAGCGTCAACCTGACCGCGC 231
QY 181 atgtactgcagctctagaaatctctgataatctctccgactcagcgcctccaaagg 240
|||||
Db 232 ATGTACTGCGCAGCTCTAGAAATCTCTGATCAATCTCTCCGACTCGAGCGCATCAAGG 291
QY 241 acccaggaggtgctggaagcaactgctctctcaaaagcccgcgagg--gattccagt 297
|||||
Db 292 ACCGAGAGTGTGGAAGCACTGTGCTCTCAAAGCCGCGGCGGAGGAGATTTCCAGT 351
QY 298 gaacgcagccgagacacacaaattgaagtgcattggtgaaacacctgctcacctat 357
|||||
Db 352 GAACGCAGCCGAGACACCAAAATTTGAAGTATCCAGTTGGTGAATAACCTCTCACCTAT 411
QY 358 gtaagggaggttatcccatggaatttcaga 390
|||||
Db 412 GTAAGGGAGGTTTATGCCCATGGAATTTTCAGA 444
RESULT 2
HUMIL13A
LOCUS HUMIL13A 1270 bp mRNA PRI 22-JUL-1993
DEFINITION Homo sapiens interleukin 13 mRNA, complete cds.
ACCESSION L06801
VERSION L06801.1 GI:186275
KEYWORDS cytokine; growth factor; interleukin 13; regulatory protein.
SOURCE Homo sapiens
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE
1 (bases 1 to 1270)
McKenzie, A.N.J., Culpepper, J.A., de Waal Malefyt, R., Briere, F.,
Funenion, J., Aversa, G., Sato, A., Dang, W., Cocks, B.G., Menon, S., de
Vries, J.E., Banchereau, J., and Zurawski, G.R.
Interleukin-13, a T cell-derived cytokine that regulates human
monocyte and B cell function
Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)
JOURNAL
MEDLINE
93234572
FEATURES
Location/Qualifiers
source
1. .1270
/organism="Homo sapiens"
/db_xref="taxon:9606"
45. .443
/codon_start=1
/product="interleukin 13"
/protein_id="AAA36107.1"
/db_xref="GI:186276"
/translation="MALLLTVTVALTCLOGFASPGVPVPSTALRELIEELVNITQNAQ
APLCNGSMWSVNLTAGMYCALESILNVSDCAIQRTQRMKALCSOKPAGQISSER
HVRDTKEIVAQFVKDILLHLKLFREGFN"
1270
polya_site 288 a 335 c 336 g 311 t
BASE COUNT


```
Qy 355 tatgtgaagggagttatcgccatgaaatttca 388
|||||
Db 417 CATTTAAAGAACTTTTCCGCGAGGACGGTTCA 450

RESULT 4
I34548
LOCUS I34548 1290 bp DNA PAT 06-FEB-1997
DEFINITION Sequence 1 from patent US 5596072.
ACCESSION I34548
VERSION I34548.1 GI:1825339
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1290)
AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
TITLE Method of refolding human IL-13
JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
FEATURES
    source
        1..1290
            /organism="unknown"
BASE COUNT 308 a 335 c 336 g 311 t
ORIGIN

Query Match 59.2%; Score 230.8; DB 10; Length 1290;
Best Local Similarity 77.7%; Pred. No. 7.9e-49;
Matches 306; Conservative 0; Mismatches 82; Indels 6; Gaps 2;

Qy 1 atgggctctggttgactggttgctctcactgctcggtagccttgcctcccg 60
|||||
Db 45 ATGGCGCTTTTGTGACCAACGGTCAATTGCTCTCACTTGGCTTGGCGGCTTGCCTCCCA 104

Qy 61 agccttgactccctcccaaccccaagagctcattgagagctggtgacacatcacc 120
|||||
Db 105 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGAGCTGTCAACATCACC 164

Qy 121 cagaatc---aggcatccctctgcaacggcagctggtgtgagcgtcaacctgaccgcc 177
|||||
Db 165 CAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCT 224

Qy 178 ggcattgactgcagagctctcagaatctcgtatcattgctcgcactgagcgcacatccaa 237
|||||
Db 225 GGCATGTACTGTGACGCTCGAATCCCTGATCAACGCTGTACAGGCTGACGCTGCCATCGAG 284

Qy 238 agaccagagatgtgaaagcactgtgctcctcaaaagccgcgcag---gatttcc 294
|||||
Db 285 AAGACCCAGAGATGCTGAGCGGATCTGCGCGCACAGGCTCAGCTGGGAGTTTCC 344

Qy 295 agtgaacgcagccgagacacacaaattgagtgatccagttggtgaaacacctgctcacc 354
|||||
Db 345 AGCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTA 404

Qy 355 tatgtgaagggagttatcgccatgaaatttca 388
|||||
Db 405 CATTTAAAGAACTTTTTCGCGAGGACGGTTCA 438

RESULT 5
AF043334
LOCUS AF043334 417 bp mRNA PRI 21-FEB-1998
DEFINITION Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.
ACCESSION AF043334
VERSION AF043334.1 GI:2905619
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 417)
AUTHORS Jiang,J.S. and Kim,B.E.
TITLE Direct Submission

JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of
Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong,
Sosa-gu, Bucheon 422-231, Korea
COMMENT
    Nested PCR:
    1) first PCR :
        forward primer (5'-ctcaatccctctcctgttgca-3')
        reverse primer (5'-tagtcaggctccgtgtctctgc-3')
    2) second PCR :
        forward primer (5'-ctcatgagcgctttttgtgaccacg-3')
        reverse primer (5'-gtcgttcgaggtttcagttgaa-3').
FEATURES
    Location/Qualifiers
        1..417
            /organism="Homo sapiens"
            /db_xref="taxon:9606"
            /cell_type="PHA-treated peripheral blood leukocyte"
        1..417
            /gene="IL13"
        1..24
            /gene="IL13"
            /note="second PCR"
            /PCR_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles;
            DeltaCycler II from Ericomp"
        4..402
            /gene="IL13"
            /codon_start=1
            /product="interleukin 13 precursor"
            /protein_id="AAC03535.1"
            /db_xref="GI:2905620"
            /translation="MALLTTVIALVCLGGFASPGVPSTALRELIELLVNITONOK
            APLCNGSWMVSNLTAGMYCALESILNVSGCSATEKTMGLGGFCPHKVSAGQFSSL
            HVRDKIEVAQFVKDLLHLKLLFREGFN"
        4..63
            /gene="IL13"
        64..399
            /gene="IL13"
            /product="interleukin 13"
            /complement(394..417)
            /note="second PCR"
BASE COUNT 91 a 121 c 108 g 97 t
ORIGIN

Query Match 58.8%; Score 229.2; DB 88; Length 417;
Best Local Similarity 77.4%; Pred. No. 2.2e-48;
Matches 305; Conservative 0; Mismatches 83; Indels 6; Gaps 2;

Qy 1 atggccttggttgactggttgctcactgctcactgctggtgctgctcccg 60
|||||
Db 4 ATGGCGCTTTTGTGACCAACGGTCAATTGCTCTCACTTGGCTTGGCGGCTTGCCTCCCA 63

Qy 61 agccttgactccctcccaaccccaagagctcattgagagctggtgacacatcacc 120
|||||
Db 64 GGCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGAGCTGTCAACATCACC 123

Qy 121 cagaatc---aggcatccctctgcaacggcagcagctggtgtgagcgtcaacctgaccgcc 177
|||||
Db 124 CAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATTGGAGCATCAACCTGACAGCT 183

Qy 178 ggcattgactgcagcactctagaatctcgtatcattgctcgcactgagcgcacatccaa 237
|||||
Db 184 GGCATGTACTGTGACGCTCGAATCCCTGATCAACGCTGACGCTGACGCTGCCATCGAG 243

Qy 238 agaccagagatgtgaaagcactgtgctcctcaaaagccgcgcag---gatttcc 294
|||||
Db 244 AAGACCCAGAGATGCTGGCGGATTTCTGCCCGCACAGGCTCTCAGCTGGGAGTTTCC 303

Qy 295 agtgaacgcagccgagacacacaaattgagtgatccagttggtgaaacacctgctcacc 354
|||||
Db 304 AGCTTGCAATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTA 363

Qy 355 tatgtgaagggagttatcgccatgaaatttca 388
|||||
Db 364 CATTTAAAGAACTTTTTCGCGAGGACGGTTCA 397
```

```
RESULT 6
A29948 LOCUS 1297 bp DNA PAT 23-JUN-1995
DEFINITION Coding sequence for protein with cytokine like activity.
ACCESSION A29948
VERSION A29948.1 GI:1249028
KEYWORDS
SOURCE synthetic construct.
ORGANISM synthetic construct
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
Boutellier,C., Lepiatols,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 21 30-SEP-1992;
ELF SANOFI
FEATURES
source Location/Qualifiers
1..1297
/organism="synthetic construct"
/db_xref="taxon:32630"
CDS
15..455
/codon_start=1
/transl_table=11
/product="protein with cytokine like activity"
/protein_id="CAA01982.1"
/db_xref="GI:1249029"
/translation="MHPLNPLLLALGLMALLTTVIALTCILGGFASPGVPPSTALR
ELIELVNQKAPLNCNSHWSINLTADMYCALESILNVGSGSAIEKQRMLSG
FCPIKVSAGQFSSLRVDTKIEVAFVFDLLHLKLFREGFN"
BASE COUNT 309 a 341 c 336 g 311 t
ORIGIN
Query Match 58.8%; Score 229.2; DB 9; Length 1297;
Best Local Similarity 77.4%; Pred. No. 2e-48;
Matches 305; Conservative 0; Mismatches 83; Indels 6; Gaps 2;
Qy 1 atggcgctgtgaactgtgattgtctcattgtctcactgctgctggtgctgctcccg 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 ATGGCGCTTTTGTGACACGGTCAITGCTCTCATTGCTTGGCGGCTTGGCTCCCA 116
Qy 61 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcac 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 GSCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCAC 176
Qy 121 cagaatc---aggcatccctctgcaacgagcagcatggtgagcgtcaaacctgaccgc 177
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 CAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGATGGAGCATCAACCTGACAGCT 236
Qy 178 ggcattgactgcagctctagaatctctgataatgtctcagctgagcagcgcacacaa 237
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 GACATGTACTGTCCGACCCCTGGAATCCCTGATCAACGCTGTCAGGCTGACATCGAG 296
Qy 238 agaccagagagatgctgaagcactgtgctctcaaaagccgcgcgcagc---gatttcc 294
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 AGACCCAGAGAGTCTGAGCGGATCTGCCGCCACAGGCTCAGCTGGGCGAGTTTCC 356
Qy 295 agtgaacgagccgagacacacaaattgaagtatccagttggtgaaacacctgctcac 354
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 AGCTTGCATGTCGAGACACCAAAATCGAGGTGGCCCGAGTTTCTAAAGGACCTGCTCTTA 416
Qy 355 tatgtaaggggagtttatgcgcattggaataattca 388
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 CATTTAAGAAACTTTTTCGCGAGGACGGTTCA 450

RESULT 7
I58488 LOCUS 1297 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 15 from patent US 5652123.
ACCESSION I58488
VERSION I58488.1 GI:2477726
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 1297)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le
Boutellier,C., Lepiatols,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 15 29-JUL-1997;
FEATURES
source Location/Qualifiers
1..1297
/organism="unknown"
BASE COUNT 309 a 341 c 336 g 311 t
ORIGIN
Query Match 58.8%; Score 229.2; DB 10; Length 1297;
Best Local Similarity 77.4%; Pred. No. 2e-48;
Matches 305; Conservative 0; Mismatches 83; Indels 6; Gaps 2;
Qy 1 atggcgctgtgactgtgattgtgctcattgtctcactgctgctggtgctgctcccg 60
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 57 ATGGCGCTTTTGTGACACACGGTCAITGCTCTCATTGCTTGGCGGCTTGGCTCCCA 116
Qy 61 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcac 120
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 117 GSCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCAC 176
Qy 121 cagaatc---aggcatccctctgcaacgagcagcatggtgagcgtcaaacctgaccgc 177
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 177 CAGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGATGGAGCATCAACCTGACAGCT 236
Qy 178 ggcattgactgcagctctagaatctctgataatgtctcagctgagcagcgcacacaa 237
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 237 GACATGTACTGTCCGACCCCTGGAATCCCTGATCAACGCTGTCAGGCTGACATCGAG 296
Qy 238 agaccagagagatgctgaagcactgtgctctcaaaagccgcgcgcagc---gatttcc 294
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 297 AGACCCAGAGAGTCTGAGCGGATCTGCCGCCACAGGCTCAGCTGGGCGAGTTTCC 356
Qy 295 agtgaacgagccgagacacacaaattgaagtatccagttggtgaaacacctgctcac 354
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 357 AGCTTGCATGTCGAGACACCAAAATCGAGGTGGCCCGAGTTTCTAAAGGACCTGCTCTTA 416
Qy 355 tatgtaaggggagtttatgcgcattggaataattca 388
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 417 CATTTAAGAAACTTTTTCGCGAGGACGGTTCA 450

RESULT 8
AF072807 LOCUS 343 bp mRNA MAM 21-JAN-2000
DEFINITION Bos taurus interleukin-13 precursor (IL-13) mRNA, partial cds.
ACCESSION AF072807
VERSION AF072807.1 GI:4558813
KEYWORDS
SOURCE Cow.
ORGANISM Bos taurus
REFERENCE 1 (bases 1 to 343)
AUTHORS Trigona,W.L., Brown,W.C. and Estes,D.M.
TITLE Functional implications for signaling via the IL4R/IL13R complex on
bovine cells
JOURNAL Vet. Immunol. Immunopathol. 72 (1-2), 73-79 (1999)
MEDLINE 20080132
PUBMED 10614495
REFERENCE 2 (bases 1 to 343)
AUTHORS Trigona,W.T., Hirano,A. and Estes,D.M.
```

TITLE Direct Submission
JOURNAL Submitted (16-JUN-1998) Veterinary Pathobiology, University of Missouri-Columbia, W213 Veterinary Medicine Building, Columbia, MO 65211, USA

FEATURES
source Location/Qualifiers
1. .343
/organism="Bos taurus"
/db_xref="taxon:9913"
/cell_type="activated peripheral T lymphocytes"
1. .>343
/gene="IL-13"
1. .>343
/gene="IL-13"
/codon_start=1
/product="interleukin-13 precursor"
/protein_id="AAD22748.1"
/db_xref="GI:4558814"
/translation="MAULLTAVIVLFCFGLTSPVPSATALKELBELVNITONOK
VPLCGSMVMSLNLTSMYCAALDSLISNCSVIQTKRMLNALCPKPKSAKQVSE
YVRDTKIEVAQF"

BASE COUNT 78 a 101 c 85 g 79 t
ORIGIN

Query Match 52.3%; Score 203.8; DB 7; Length 343;
Best Local Similarity 78.7%; Pred. No. 6.9e-42; Indels 6; Gaps 2;
Matches 270; Conservative 0; Mismatches 67;

Qy 1 atgcccgtctgtgactgtgctcattcctcaccctgcctcctggtggtcctcctccccc 60
Db 1 ATGGCGCTCTTATTGACCGCGCTCATTTCTTATCTGCTTGGTGGCTCACCTCCCA 60
Qy 61 agccctgtactcctcccccaccctcaagagctcatttgaggagctggtcaaccacc 120
Db 61 AGCCCTGTGCTTCTGTACAGCCCTCAAGGAGCTCATTTGAAGAGCTGGTTAATATCAC 120
Qy 121 cagaatc---aggcatcctctgaacgcagcagcagcagcagcagcagcagcagc 177
Db 121 CAGAACCAAGAGGATGCTGAATGCACTCTGTCTCTCAAGCCCTCAGCTAAGCAGTTTCC 180
Qy 178 ggcattgactgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 237
Db 181 AGCATGTACTGTGAGCCCTGGACTCCCTGATCAGCATCTCCAACTGCTCATCCAA 240
Qy 238 agaccagagagatgctgaagcagcagcagcagcagcagcagcagcagcagcagc 294
Db 241 AGGACCAAGAGGATGCTGAATGCACTCTGTCTCTCAAGCCCTCAGCTAAGCAGTTTCC 300
Qy 295 agtgaacgcagcagcagcagcagcagcagcagcagcagcagcagcagcagc 337
Db 301 AGTGAGTACGTCGAGACACCAAAATCGAGTGGCCAGTTTG 343

RESULT 9
LOCUS A29950 384 bp DNA PAT 23-JUN-1995
DEFINITION Nucleic acid fragment B.
ACCESSION A29950
VERSION A29950.1 GI:1249030
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM
REFERENCE 1 (bases 1 to 384)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms
JOURNAL Patent: Ep 0506574-A 23 30-SEP-1992;
ELF SANOFI
FEATURES
source Location/Qualifiers
1. .384
/organism="synthetic construct"

BASE COUNT 97 a 104 c 99 g 84 t
ORIGIN

Query Match 48.2%; Score 188; DB 9; Length 384;
Best Local Similarity 76.2%; Pred. No. 7.4e-38;
Matches 259; Conservative 0; Mismatches 75; Indels 6; Gaps 2;

Qy 55 tccccgagccctgtgactcctcccccaccctcaagagctcatttgaggagctggtcaac 114
Db 16 TCCCCAGGCCCTGTGCTTCCCTCTACGGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAAC 75
Qy 115 atacaccagaatc---aggcatcctctgcaacgagcagcagcagcagcagcagc 171
Db 76 ATACCCAGAACCAAGAGGCTCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135
Qy 172 accgcgcgctgactgctcagcagcagcagcagcagcagcagcagcagcagcagc 231
Db 136 ACAGCTGACATGTACTGTGCGCCCTGGAATCCCTCATCAACGTGTACAGCTGCAGTGCC 195
Qy 232 atccaaaggaccagagatgctgaaagcactgtgctctcaaaagcccgagg---g 288
Db 196 ATCGAGAAGACCCAGAGGATGCTGAGCGATTCTGCCCGCACAAAGTCTCAGCTGGGCG 255
Qy 289 atttcagtgaaagc 348
Db 256 TTTCAGGCTTGCATGTCCGAGACACCAAAATCGAGTGGCCAGTTTGTAAAGAGCTG 315
Qy 349 ctacacctatgaaggaggtttatccgccatggaattcca 388
Db 316 CTCCTTACATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 355

RESULT 10
LOCUS I58489 384 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 17 from patent US 5652123.
ACCESSION I58489
VERSION I58489.1 GI:2477727
KEYWORDS Unknown.
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 384)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Bouteiller,C., Leplatols,P., Magazin,M. and Minty,A.
TITLE Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 17 29-JUL-1997;
FEATURES Location/Qualifiers
1. .384
/organism="unknown"

BASE COUNT 97 a 104 c 99 g 84 t
ORIGIN

Query Match 48.2%; Score 188; DB 10; Length 384;
Best Local Similarity 76.2%; Pred. No. 7.4e-38;
Matches 259; Conservative 0; Mismatches 75; Indels 6; Gaps 2;

Qy 55 tccccgagccctgtgactcctcccccaccctcaagagctcatttgaggagctggtcaac 114
Db 16 TCCCCAGGCCCTGTGCTTCCCTCTACGGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAAC 75
Qy 115 atacaccagaatc---aggcatcctctgcaacgagcagcagcagcagcagcagc 171
Db 76 ATACCCAGAACCAAGGCTCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTG 135
Qy 172 accgcgcgctgactgctcagcagcagcagcagcagcagcagcagcagcagcagc 231
Db 136 ACAGCTGACATGTACTGTGCGCCCTGGAATCCCTCATCAACGTGTACAGCTGCAGTGCC 195

Qy 232 atccaaagaccagagagatgctgaagcaactgtgtctctcaaaagccgcgcagcagg---g 288
 Db 196 ATTCGAGAAGACGACAGAGATGCTGAGCGGATTTCTCCCGCACCAAGGCTCTCAGCTGGCAG 255
 Qy 289 attccactgaacgcagcgcagacacacaaaattgaagtgatccagtttgtgtaaaaaacctg 348
 Db 256 TTTTCCAGCTTGCAATGCTCCGAGACACCAAAATPCGAGAGTGGCCAGTTTGTAAAGGACCTG 315
 Qy 349 ctccactatgaaggsgagtttatcgccatggaatttca 388
 Db 316 CTCCTACATTTAAGAAACTTTTTCGCCGAGGACGGTTCA 355

RESULT 11
 A29931
 LOCUS 336 bp DNA PAT 23-JUN-1995
 DEFINITION Sequence coding for the mature cytokine like protein.
 ACCESSION A29931
 VERSION A29931.1 GI:1249019
 KEYWORDS
 SOURCE synthetic construct.
 ORGANISM
 1 (bases 1 to 336)
 Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
 Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
 Protein having cytokin type activity, recombinant DNA coding for
 this protein, transformed cells and microorganisms
 JOURNAL Patent: EP 0506574-A 3 30-SEP-1992;
 Euf SANOFI

FEATURES
 source Location/Qualifiers
 1..336
 /organism="synthetic construct"
 /db_xref="taxon:32630"
 80..a 95 c 90 g 71 t

BASE COUNT 80 a 95 c 90 g 71 t
 ORIGIN

Query Match 48.1%; Score 187.4; DB 9; Length 336;
 Best Local Similarity 76.9%; Pred. No. 1.le-37;
 Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps

Qy 62 gccctgtgactccctccccaaacctcaaggagctcataggagctggtcaacatcaccc 121
 Db 2 GCCCTGTGCCCTCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGCTCAACATCACCC 61
 Qy 122 agaatc---aggcatccctctgcaacgcagcagctggtgagagctcaacctgaccgcg 178
 Db 62 AGAACCAAGAGAGCTCCGCTCTGCAATGGACGATGGTATGGAGCATCAACCTGACAGCTG 121
 Qy 179 gcattgactgcgcagctagaattctgtatcaatgtctccgactgcagcgcattccaaa 238
 Db 122 CCATGTAATGTGCAGCCCTGGAATCCCTGATCAACGCTGTACAGCTGCAGTGCCTATCGAGA 181
 Qy 239 ggaccagagagatgctgaagcaactgtgtctctcaaaagccgcgcagcagg---gatttcca 295
 Db 182 AGACCCAGAGATGCTGAGCGGATTTCTCCCGCACCAAGGCTCTCAGCTGGCAGTTTTCCTCA 241
 Qy 296 gtgaacgcagccgcagacacaaaattgaagtgatccagtttgtgtaaaaaacctgtcacct 355
 Db 242 GCTTGCAATGCTCCGAGACACCAAAATPCGAGAGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301
 Qy 356 atgcaaggggagtttatcgccatggaatttca 388
 Db 302 ATTTAAGAAACTTTTTCGCCGAGGACGGTTCA 334

RESULT 12
 158494
 LOCUS 336 bp DNA PAT 07-OCT-1997
 DEFINITION Sequence 24 from patent US 5652123.
 ACCESSION 158494
 VERSION 158494.1 GI:2477732

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 336)
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-te Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms
JOURNAL	Patent: US 5652123-A 24 29-JUL-1997;
FEATURES	Location/Qualifiers 1..336
BASE COUNT	80 a 95 c 90 g 71 t
ORIGIN	/organism="unknown"
Query Match	48.1%; Score 187.4; DB 10; Length 336;
Best Local Similarity	76.9%; Pred. No. 1.1e-37;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2	
QY 62	gcctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcaccc 121
DB	2 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGTCACATCACCC 61
QY 122	agaatc---agcgcacctctcaacgcgcagcatggtgagcgtcaacctgaccgcg 178
DB	62 AGAACCAAGAGGCTCGGCTCTGCATGGCAGCATGGTATGGAGCATCAACCTGCACAGCTG 121
QY 179	gcattgactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaa 238
DB	122 GCATGTACTGTGCAGCCCTGGAAATCCCTGATCAACGTGTCAGGCTGCAGTGCATCGAGA 181
QY 239	ggaccagagatgctgaaagcaactgtctctcaaaagcccgccgagg--gatttcca 295
DB	182 AGACCCAGAGGATGTGTGACGGGATTCTGCCCGCACAAAGTCTCAGCTGGGCAGTTTCCA 241
QY 296	gtgaacgcagccgcagacaccaaattgaagtgtatcagttggtgaaacacctgctcacct 355
DB	242 GCTTGCATCTCCGACACACCAAAATCGAGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 301
QY 356	atgtaagggaggtttatcgccatgaaatttca 388
DB	302 ATTTAAGAAACTTTTTCGCGAGGAGCGGTTCA 334
RESULT 13	
LOCUS	AR027065
DEFINITION	AR027065 425 bp DNA PAT 29-SEP-1999
ACCESSION	Sequence 4 from patent US 5856142.
VERSION	AR027065.1 GI:5937905
KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unclassified.
REFERENCE	1 (bases 1 to 425)
AUTHORS	Legoux,R., Maldonado,P. and Salome,M.
TITLE	Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine
JOURNAL	Patent: US 5856142-A 4 05-JAN-1999;
FEATURES	Location/Qualifiers 1..425
BASE COUNT	100 a 116 c 110 g 99 t
ORIGIN	/organism="unknown"
Query Match	47.7%; Score 186.2; DB 9; Length 425;
Best Local Similarity	75.5%; Pred. No. 2.1e-37;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2	
QY 52	gcctcccgagccctgtactccctcccaaccctcaaggagctcattgaagagctgattc 111

```

Db 55 GCCTTCGCTGGCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCATTTAGGAGCTGGTC 114
Qy 112 aacatcacccagaatc---aggcatccctctgcaacgagcagatggtgtgagcgtcaac 168
Db 115 AACATCACCCAGAACACAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGGACATCAAC 174
Qy 169 ctgaccgcgcgcgtactgctgcgcagctctagaaatctctgataatctctccgactcagc 228
Db 175 CTGACAGCTGGCATGTACTGTGTCAGGCCCTGGAAATCCCTGATCAACGTGTACAGCTCAGT 234
Qy 229 gccatccaaagaccagagaggtgctgaaagcactgtctctcaaaagcccgcgagcagg- 287
Db 235 GCCATCGAGAACACCCAGAGGATGCTGACGGATTCTGCCCGCACAAAGTCTCAGCTGGG 294
Qy 288 --gatttcacagtgaacgcagcagcagacacacaaaattgaagtgtatccagttggtgaaaaac 345
Db 295 CAGTTTTCAGCTTGCATGTCTCCGAGACACCAAAATCCAGGTGGCCAGTTTGTAAAGGAC 354
Qy 346 ctgctcacctatgaaggaggtttatcgccatggaatttca 388
Db 355 CTGCTTTACATTTAAGAAACTTTTTCGAGGAGCGGTTC 397

RESULT 14
LOCUS 186198 425 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5700665.
ACCESSION 186198
VERSION 186198.1 GI:3205916
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 425)
Legoux,R., Maldonado,P. and Salome,M.
METHOD for the extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
PATENT: US 5700665-A 4 23-DEC-1997;
JOURNAL Location/Qualifiers
FEATURES
source
1..425
/organism="unknown"
BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 47.7%; Score 186.2; DB 10; Length 425;
Best Local Similarity 75.5%; Pred. No. 2.1e-37;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

Qy 52 gctctcccgagccctgtgactccctcccaacccctcaagagctcattgagagctggtc 111
Db 55 GCCTTCGCTGGCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCATTTAGGAGCTGGTC 114
Qy 112 aacatcacccagaatc---aggcatccctctgcaacgagcagcagatggtgtgagcgtcaac 168
Db 115 AACATCACCCAGAACACAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGGACATCAAC 174
Qy 169 ctgaccgcgcgcgtactgctgcgcagctctagaaatctctgataatctctccgactcagc 228
Db 175 CTGACAGCTGGCATGTACTGTGTCAGGCCCTGGAAATCCCTGATCAACGTGTACAGCTCAGT 234
Qy 229 gccatccaaagaccagagaggtgctgaaagcactgtctctcaaaagcccgcgagcagg- 287
Db 235 GCCATCGAGAACACCCAGAGGATGCTGACGGATTCTGCCCGCACAAAGTCTCAGCTGGG 294
Qy 288 --gatttcacagtgaacgcagcagcagacacacaaaattgaagtgtatccagttggtgaaaaac 345
Db 295 CAGTTTTCAGCTTGCATGTCTCCGAGACACCAAAATCCAGGTGGCCAGTTTGTAAAGGAC 354
Qy 346 ctgctcacctatgaaggaggtttatcgccatggaatttca 388
Db 355 CTGCTTTACATTTAAGAAACTTTTTCGAGGAGCGGTTC 397
```

```

RESULT 15
LOCUS A52326 4410 bp DNA PAT 12-DEC-1997
DEFINITION Sequence 1 from Patent EP0725140.
ACCESSION A52326
VERSION A52326.1 GI:2851987
KEYWORDS
SOURCE unidentified.
ORGANISM unidentified.
REFERENCE
1 (bases 1 to 4410)
Legoux,R., Maldonado,P. and Salome,M.
METHOD for extraction of periplasmic proteins from prokaryotic
microorganisms in the presence of arginine
PATENT: EP 0725140-A 1 07-AUG-1996;
JOURNAL Location/Qualifiers
COMMENT SANOFI SA (PR)
Other publication SK 10696 960904
Other publication CZ 960290 960814
Other publication JP 8242879 960924
Other publication FI 960427 960801
Other publication PL 312543 960805
Other publication NO 960396 960801
Other publication FR 2729972 960802
Other publication CA 2168382 960801
Other publication AU 4224496 960808.

FEATURES
source
1..4410
/organism="unidentified"
/db_xref="taxon:32644"
promoter
5'UTR 283..337
misc_RNA
338..762
/note="SEQUENCE DE LA REGION 5' NON TRADUITE DU MESSAGE"
terminator
763..812
/note="SEQUENCE CODANT POUR LE PRECURSEUR DE L'IL-13"
terminator
813..1012
/note="TERMINATEUR DU GENE 10 DU PHAGE T7"
terminator
1013..1253
/note="TERMINATEUR DU PHAGE FD"
misc_RNA
1254..2505
/note="GENE CODANT POUR LE REPRESSEUR DE L'OPERON LACTOSE"
misc_RNA
2506..4410
/note="SEQUENCE DE PBR 327"
BASE COUNT 1078 a 1142 c 1096 g 1094 t
ORIGIN

Query Match 47.7%; Score 186.2; DB 9; Length 4410;
Best Local Similarity 75.5%; Pred. No. 1.8e-37;
Matches 259; Conservative 0; Mismatches 78; Indels 6; Gaps 2;

Qy 52 gctctcccgagccctgtgactccctcccaacccctcaagagctcattgagagctggtc 111
Db 392 GCCTTCGCTGGCCCTGTGCTCCAGTACTGCCCTCAGGAGCTCATTTAGGAGCTGGTC 451
Qy 112 aacatcacccagaatc---aggcatccctctgcaacgagcagcagatggtgtgagcgtcaac 168
Db 452 AACATCACCCAGAACACAGAGGCTCCGCTCTGCAATGGCAGCATGTTATGGAGCATCAAC 511
Qy 169 ctgaccgcgcgcgtactgctgcgcagctctagaaatctctgataatctctccgactcagc 228
Db 512 CTGACAGCTGGCATGTACTGTGTCAGGCCCTGGAAATCCCTGATCAACGTGTACAGCTGAGT 571
Qy 229 gccatccaaagaccagagaggtgctgaaagcactgtctctcaaaagcccgcgagcagg- 287
Db 572 GCCATCGAGAACACCCAGAGGATGCTGAGCGGATTTGCCCGCACAAAGTCTCAGCTGGG 631
Qy 288 --gatttcacagtgaacgcagcagcagacacacaaaattgaagtgtatccagttggtgaaaaac 345
Db 632 CAGTTTTCAGCTTGCATGTCTCCGAGACACCAAAATCCAGGTGGCCAGTTTGTAAAGGAC 691
```

Qy 346 ctgctcacctaagttaaggagggttttatcgcccatggaaatttca 388
||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 692 CTGCTCTTACATTTAAGAAACTTTTTTCGCGAGGACGGTTCA 734

Search completed: May 13, 2001, 14:25:18
Job time: 19398 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:25:18 ; Search time 9342.78 Seconds
(without alignments)
520.915 Million cell updates/sec

Title: US-09-451-527-104
Perfect score: 330
Sequence: 1 agccctgtactccctcccc.....atcgccatggaatttcaga 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 1283235 seqs, 7373929652 residues 2566470
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_om.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
14: gb_pl3.*
15: gb_pl4.*
16: gb_ba1.*
17: em_ba2.*
18: em_fun.*
19: em_htgo_hum.*
20: em_htgo_inv.*
21: em_htgo_rod.*
22: em_htg_hum1.*
23: em_htg_hum2.*
24: em_htg_hum3.*
25: em_htg_hum4.*
26: em_htg_hum5.*
27: em_htg_hum6.*
28: em_htg_hum7.*
29: em_htg_hum8.*
30: em_htg_inv1.*
31: em_htg_inv2.*
32: em_htg_other.*
33: em_htg_rod.*
34: em_hum1.*
35: em_hum2.*
36: em_hum3.*
37: em_hum4.*
38: em_hum5.*
39: em_hum6.*
40: em_hum7.*
41: em_in.*
42: em_om.*
43: em_or.*

44: em_ov.*
45: em_pat.*
46: em_ph.*
47: em_pl.*
48: em_ro.*
49: em_sts.*
50: em_sy.*
51: em_un.*
52: em_vi.*
53: gb_sts1.*
54: gb_sts2.*
55: gb_sts3.*
56: gb_sy.*
57: gb_un.*
58: gb_vil.*
59: gb_vil2.*
60: gb_vil3.*
61: gb_vil4.*
62: gb_vil5.*
63: gb_vil6.*
64: gb_vil7.*
65: gb_vil8.*
66: gb_vil9.*
67: gb_vil10.*
68: gb_vil11.*
69: gb_vil12.*
70: gb_vil13.*
71: gb_vil14.*
72: gb_vil15.*
73: gb_vil16.*
74: gb_vil17.*
75: gb_vil18.*
76: gb_vil19.*
77: gb_vil20.*
78: gb_vil21.*
79: gb_vil22.*
80: gb_vil23.*
81: gb_vil24.*
82: gb_vil25.*
83: gb_vil26.*
84: gb_vil27.*
85: gb_vil28.*
86: gb_vil29.*
87: gb_vil30.*
88: gb_vil31.*
89: gb_vil32.*
90: gb_vil33.*
91: gb_vil34.*
92: gb_vil35.*
93: gb_vil36.*
94: gb_vil37.*
95: gb_vil38.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	317	96.1	1302	7	AF244915	AF244915 Canis fam
2	187.4	56.8	336	9	A29931	A29931 Sequence co
3	187.4	56.8	336	10	I58494	I58494 Sequence 24
4	187.4	56.8	1270	93	HUMIL13A	L06801 Homo sapien
5	187.4	56.8	1282	92	HSNC30	X69079 H.sapiens i
6	187.4	56.8	1290	10	I34548	I34548 Sequence 1
7	185.8	56.3	336	9	A29930	A29930 Sequence co
8	185.8	56.3	336	10	I58481	I58481 Sequence 2
9	185.8	56.3	417	88	AF043334	AF043334 Homo sapi
10	185.8	56.3	1297	9	A29948	A29948 Coding sequ
11	185.8	56.3	1297	10	I58488	I58488 Sequence 15

```
12 184.2 55.8 384 9 A29950
13 184.2 55.8 384 10 I58489
14 182.6 55.3 425 9 AR027065
15 182.6 55.3 425 10 I86198
16 182.6 55.3 4410 9 A52326
17 182.6 55.3 4410 9 AR027062
18 182.6 55.3 4410 10 I86195
19 163 49.4 343 7 AF072807
20 151.4 45.9 447 10 I58495
21 151.4 45.9 1207 94 M0557CPE
22 151.4 45.9 1212 10 I34549
23 140.8 42.7 443 94 RATIL13A
24 106.4 32.2 213343 78 AF276990
25 71.4 21.6 3714 93 HUM11DC92Z
26 71.4 21.6 4600 93 HUM11L3B
27 71.4 21.6 4740 93 HSU10307
28 71.4 21.6 5670 93 HSU31120
29 71.4 21.6 50282 85 AC004039
30 71.4 21.6 78469 75 AC074127
31 71 21.5 3395 93 HUM11DC98Z
32 70 21.2 3520 7 BTA132441
33 58.4 17.7 78469 75 AC074127
34 51.6 15.6 4376 94 MUSIL13A
35 49.4 15.0 142732 88 AC084392
36 49.4 15.0 159500 94 AC005742
37 49.4 15.0 237823 66 AC020886
38 40.8 12.4 38390 3 SC2H12
39 39 11.8 13684 94 MUGSABAT
40 37 11.2 39739 3 SCD16A
41 36.8 11.2 185300 2 AP000063
42 36.6 11.1 51440 12 AB025632
43 36.4 11.0 2437 3 SRAJ3310
44 36.4 11.0 2437 3 SAU77894
45 36.2 11.0 3073 94 AF195788
```

ALIGNMENTS

```
RESULT 1
AF244915 AF244915 1302 bp mRNA MAM 16-OCT-2000
LOCUS Canis familiaris interleukin-13 mRNA, complete cds.
DEFINITION Canis familiaris interleukin-13 mRNA, complete cds.
ACCESSION AF244915
VERSION AF244915.1 GI:7528273
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1302)
AUTHORS Yang, S., Boroughs, K.L. and McBernott, M.J.
TITLE Canine interleukin-13: molecular cloning of full-length cDNA and
expression of biologically active recombinant protein
JOURNAL J.. Interferon Cytokine Res. 20 (9), 779-785 (2000)
MEDLINE 20485146
PUBMED 11032397
REFERENCE 2 (bases 1 to 1302)
AUTHORS Yang, S.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation,
1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES
source
1. .1302
Location/Qualifiers
/db_xref="taxon:9615"
/organism="Canis familiaris"
/codon_start=1
/product="interleukin-13"
/protein_id="AAF63204.1"
/db_xref="GI:7528274"
/translation="MALWLVVIALTCGLGLASPVPVPTSLKELIELVNIQNAQ
```

```
SLCNGSMVWSVNLTAGMYCAALESLINVDCAIQTQRMKALCSQKPAAGQISSER
SDTKTEVLIOLYKNLLTYRGVYRHGNER"
448..1302
3'UTR 337 a 318 c 340 g 307 t
BASE COUNT
ORIGIN
Query Match 96.1%; Score 317; DB 7; Length 1302;
Best Local Similarity 99.1%; Pred. No. 1.1e-72;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 agccctgtgactccctcccaaccctcaagagctcattgagagctggtcaacatcaccc 60
|||||
Db 112 AGCCCTGTGACTCCCTCCCAACCCTCAAGAGCTCATTGAGGAGCTGGTCAACATCACCC 171
QY 61 cagaatcaggcatccctctgtcgaaggcagcagatggtgaggcgtcaacctgaccgcggc 120
|||||
Db 172 CAGAATCAGGCATCCCTCTCTGCAAGCGCAGCATGCTGTGGAGCGTCAACCTGACCGCGGC 231
QY 121 atgtactgcagctcttagaatctctgatactctcgaactgcagcgcacatccaaagg 180
|||||
Db 232 ATGTACTGCCAGCTCTAGAAATCTCTGATCAATGCTCTCCGACTGCAGCGCATCAAAAGG 291
QY 181 acccagagtgctgaaagcactgtctctcaaaagccgcgcagcagg---gatttcagtg 237
|||||
Db 292 ACCCAGAGTAGTGTGAAGGACACTGTGCTCTCAAAGCCCGCGGAGGCAATTCAGT 351
QY 238 gaacgcagcgcagacacacaaattgaagtgcagtgatccagttggtgaaacacctgctcacctat 297
|||||
Db 352 GAACGCAGCGCGAGACACCAAAATGAAGTGAATGATCAGTTGGTGAACCACTGCTCACCTAT 411
QY 298 gtaagggagttatgcgcattgaaatttcaga 330
|||||
Db 412 GTAAGGGAGTTTATCGCCATGGAATTTTCAGA 444
```

RESULT 2

```
A29931 A29931 336 bp DNA PAT 23-JUN-1995
LOCUS Sequence coding for the mature cytokine like protein.
ACCESSION A29931
VERSION A29931.1 GI:1249019
KEYWORDS synthetic construct.
SOURCE synthetic construct
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput, D., Ferrara, P., Guilleminot, J.C., Kaghad, M., Labit-le
Bouteiller, C., Lepiatols, P., Magazin, M. and Minty, A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 3 30-SEP-1992;
ELF SANOFI
FEATURES
source
1. .336
Location/Qualifiers
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN
Query Match 56.8%; Score 187.4; DB 9; Length 336;
Best Local Similarity 76.9%; Pred. No. 9.3e-39;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
QY 2 gccctgtgactccctcccaaccctcaagagctcattgagagctggtcaacatcaccc 61
|||||
Db 2 GCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61
QY 62 agaatac---aggatccctctgcaacggcagcagatggtgtgagcgtcaacctgaccgcgg 118
|||||
Db 62 AGAACCAAGAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121
```


QY 119 gcatgtactgagcagctctagaaatctctgatcaatgtctcgcagctgagcgccatccaaa 178
Db 122 GCATGTACTGTGAGCCCTGGATCCCTGATCAACGTGTGAGCTGAGTGCCTATCCGAGA 181
QY 179 ggaaccagaggtgctgaaagcactgtgctctcaaaagccgcggcagg---gatttcca 235
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGACAAAGGTCCTCAGCTGGCAGTTTCCA 241
QY 236 gtgaacgcagcgcagagacacacaaatgaagtgtatccagttggtgaaacacgtctcacct 295
Db 242 GCTTGCATGTCGAGACACAAATCGAGTGGCCAGTTTGTAAAGAGCTGCTCTTAC 301
QY 296 atgtaaggaggagtttatcccatggaatttca 328
Db 302 ATTAAAGAACTTTTCGGAGGGACGGTTCA 334

RESULT 3
LOCUS 158494 336 bp DNA PAT 07-OCT-1997
DEFINITION Sequence 24 from patent US 5652123.
ACCESSION 158494
VERSION 158494.1 GI:2477732
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE protein having interleukin 13 activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: US 5652123-A 24 29-JUL-1997;
FEATURES
source Location/Qualifiers
BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN 1..336
/organism="unknown"

Query Match 56.8%; Score 187.4; DB 10; Length 336;
Best Local Similarity 76.9%; Pred. No. 9.3e-39;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGGTCAACATCACCC 61
QY 62 agaate---aggatccctctgcaacgcgcagcagatggtgtgagcgtcaacacctgaccgcg 118
Db 62 AGAACCCAGAAAGCTCGGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121
QY 119 gcatgtactgagcagctctagaaatctctgatcaatgtctcgcagctgagcgccatccaaa 178
Db 122 GCATGTACTGTGAGCCCTGGATCCCTGATCAACGTGTGAGCTGAGTGCCTATCCGAGA 181
QY 179 ggaaccagaggtgctgaaagcactgtgctctcaaaagccgcggcagg---gatttcca 235
Db 182 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGACAAAGGTCCTCAGCTGGCAGTTTCCA 241
QY 236 gtgaacgcagcgcagagacacacaaatgaagtgtatccagttggtgaaacacgtctcacct 295
Db 242 GCTTGCATGTCGAGACACAAATCGAGTGGCCAGTTTGTAAAGAGCTGCTCTTAC 301
QY 296 atgtaaggaggagtttatcccatggaatttca 328
Db 302 ATTAAAGAACTTTTCGGAGGGACGGTTCA 334

RESULT 4
LOCUS HUM113A 1270 bp mRNA PRI 22-JUL-1993
DEFINITION Homo sapiens interleukin 13 mRNA, complete cds.

ACCESSION L06801
VERSION L06801.1 GI:186275
KEYWORDS cytokine; growth factor; interleukin 13; regulatory protein.
SOURCE Homo sapiens cDNA to mRNA.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1270)
AUTHORS McKenzie,A.N.J., Culpepper,J.A., de Waal Malefyt,R., Briere,F.,
Punnonen,J., Aversa,G., Sato,A., Dang,W., Cocks,B.G., Menon,S., de
Vries,J.E., Banchereau,J. and Zurawski,G.R.
TITLE Interleukin-13, a T cell-derived cytokine that regulates human
monocyte and B cell function
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 90, 3735-3739 (1993)
MEDLINE 93234572
FEATURES
source Location/Qualifiers
BASE COUNT 288 a 335 c 336 g 311 t
ORIGIN 1..1270
/organism="Homo sapiens"
/db_xref="taxon:9606"
45..443
/codon_start=1
/product="interleukin 13"
/protein_id="AA36107.1"
/db_xref="GI:186276"
/translation="MALLTTVIALTCLGGFASPGVPVPPSTALRELIELBELVNITONQK
APLNGSMVMSINLTAGMYCALESILNVSCSAIEKTRMLSGFCHKVSAGQFSSL
HVRDTKIEVAQFVKDLLHLHLKLFREGFN"
polya_site 288 a 335 c 336 g 311 t
QY 2 gccctgtgactccctcccaacccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 106 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 165
QY 62 agaate---aggatccctctgcaacgcgcagcagatggtgtgagcgtcaacacctgaccgcg 118
Db 166 AGAACCCAGAAAGCTCGGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 225
QY 119 gcatgtactgagcagctctagaaatctctgatcaatgtctcgcagctgagcgccatccaaa 178
Db 226 GCATGTACTGTGAGCCCTGGATCCCTGATCAACGTGTGAGCTGAGTGCCTATCCGAGA 285
QY 179 ggaaccagaggtgctgaaagcactgtgctctcaaaagccgcggcagg---gatttcca 235
Db 286 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGACAAAGGTCCTCAGCTGGCAGTTTCCA 345
QY 236 gtgaacgcagcgcagagacacacaaatgaagtgtatccagttggtgaaacacgtctcacct 295
Db 346 GCTTGCATGTCGAGACACACAAATTCGAGGTGGCCAGTTTGTAAAGAGGACCTGCTCTTAC 405
QY 296 atgtaaggaggagtttatcccatggaatttca 328
Db 406 ATTAAAGAACTTTTCGGAGGGACGGTTCA 438

RESULT 5
LOCUS HSNC30 1282 bp mRNA PRI 17-FEB-1997
DEFINITION H.sapiens interleukin-13 mRNA.
ACCESSION X69079
VERSION X69079.1 GI:297787
KEYWORDS lymphokine.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Mammalia; Eutheria;
Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 1282)

AUTHORS Minty,A.J.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches, Labège Innopole, Voie 1, BP 137, 31676 Labège Cedex, FRANCE
 REFERENCE 2 (bases 1 to 1282)
 AUTHORS Minty,A.J., Chalon,P., Detocq,J.M., Dumont,X., Guillemot,J.C., Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C., Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and Caput,D.
 TITLE Interleukin-13 is a new human lymphokine regulating inflammatory and immune responses
 JOURNAL Nature 362 (6417), 248-250 (1993)
 MEDLINE 93211479
 FEATURES
 source Location/Qualifiers
 1..1282 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5q 23-31"
 /cell_type="peripheral blood lymphocytes"
 15..455 /gene="NC30"
 15..116 /gene="NC30"
 /product="NC30; alternative"
 15..455 /gene="NC30"
 /note="alternative; ATG at 15 is an alternative start codon"
 /codon_start=1
 /evidence=experimental
 /protein_id="CAA48823.1"
 /db_xref="GI:580330"
 /db_xref="SWISS-PROT:P35225"
 /translation="MHPLNPLLLALGLMALITTVIALTCIGGFASPGVPVPSTALR ELIELVNITONKAPICNGSMVWSINLTAGMYCAALESILNVSGCSALEKQRMLSG FLPHKVSAGQFSSLHVRDKIEVAQFVKDILLHLKLFREGFN"
 57..455 /gene="NC30"
 /note="alternative; ATG at 15 is an alternative start codon"
 /codon_start=1
 /evidence=experimental
 /protein_id="CAA48824.1"
 /db_xref="GI:673420"
 /db_xref="SWISS-PROT:P35225"
 /translation="MALITTVIALTCIGGFASPGVPVPSTALRELIELVNITONK APLCNGSMVWSINLTAGMYCAALESILNVSGCSALEKQRMLSGFCPHKVSAGQFSSL HVRDKIEVAQFVKDILLHLKLFREGFN"
 57..116 /gene="NC30"
 /product="NC30; alternative"
 117..452 /gene="NC30"
 /evidence=experimental
 238 /gene="NC30"
 /replace="a"
 856..860 /note="ATTTA motif"
 873..877 /note="ATTTA motif"
 1134..1138 /note="ATTTA motif"
 1153..1157 /note="ATTTA motif"
 1264..1269 /note="ATTTA motif"
 polyA_signal 293 a 341 c 337 g 311 t
 BASE COUNT 293 a 341 c 337 g 311 t
 ORIGIN
 Query Match 56.8%; Score 187.4; DB 92; Length 1282;
 Best Local Similarity 76.9%; Pred. No. 8.5e-39;
 Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaacctcaaggagctcattgaggagctggtcaacatcaccc 61
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 118 GCCTGTGCTCCTCTACAGCCCTCAGGAGCTCATTTGAGGAGCTGTTCAACATCACCC 177
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 62 agaate---aggcatcctctgcaacggcagcatggtgtgagcgctcaacactgacgcgcg 118
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 178 AGAACCAAGAAGGTCGCCCTCGCAATGGCAGCATGTTATGGAGCATCAACCTGACAGCTG 237
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 238 GCATGTACTGTGAGCCCTGGAATCCCTGATCAACGTTTCAGGCTGAGTCCCATCAGA 297
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 179 ggaccagagagatgctgaaagcaactgtgtctctcaaaagcccgcgagg---gatttcca 235
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 298 AGACCCAGAGGATGCTGAGCGGATTTCTGCCCGCACAAAGTCTCAGCTGGCAGTTTTCCA 357
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 236 gtgaacgcagccgagacacacaaatgaagtatccagttggtgaaaaacctgctcacct 295
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 358 GCTTGATGTCCGAGACACCAAAATCGAGTGGCCCAAGTTTGTAAAGGACCTGCTCTTAC 417
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 296 atgaaggggagtttatcgccatggaaatttca 328
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 418 ATTTAAAGAACTTTTTCGCGAGGACGGTTCA 450
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 6
 LOCUS I34548 1290 bp DNA PAT 06-FEB-1997
 DEFINITION Sequence 1 from patent US 5596072.
 ACCESSION I34548
 VERSION I34548.1 GI:1825339
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE 1 (bases 1 to 1290)
 AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
 TITLE Method of refoinding human IL-13
 JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
 FEATURES Location/Qualifiers
 source 1..1290
 BASE COUNT 308 a 335 c 336 g 311 t
 ORIGIN
 Query Match 56.8%; Score 187.4; DB 10; Length 1290;
 Best Local Similarity 76.9%; Pred. No. 8.5e-39;
 Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

FEATURES	source	Location/Qualifiers
BASE COUNT	81 a 95 c 89 g 71 t	
ORIGIN		
Query Match	56.3%; Score 185.8; DB 10; Length 336;	
Best Local Similarity	76.6%; Pred. No. 2.4e-38;	
Matches 255; Conservative	0; Mismatches 72; Indels 6; Gaps 2;	
Oy 2	gccctgtgactccctcccccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61	
Db 2	gccctgtgctccctctacagccctcaggagctcattgaggagctggtcaacatcaccc 61	
Oy 62	agaatc---aggaatccctctgaaacggcagcagctggtgtgagagctcaacctgaccgcg 118	
Db 62	agaaccagaagagctccgctcgcgaatggcagcattggtatggagcattcaacttgacagctg 121	
Oy 119	gcatgtactgcgcagctctagaatctctgtacaatgtctccagctgcagcgccatcaaa 178	
Db 122	acatgtactgtcagcccttgaaatccctgatcactgctcagctgcagtgccatcaga 181	
Oy 179	ggaccagagagatgctgaaagcactgtgctctcaaaacggcgccgagcagg---gatttcca 235	
Db 182	agaccagagagatgctgagcggattctgccgcgacaaagctctcagctggcgagctttcca 241	
Oy 236	gtgaacgcagcgcagacacaaaattgaattgctcagctggtgataaaacctgctcacct 295	
Db 242	gcttgcatgtccgagacacaaatcagagtgccgagcttggtaagagcctgctctttac 301	
Oy 296	atgtaaggggagttatccgccatgaaattcca 328	
Db 302	atttaagaaacttttccgcaggcagctttca 334	
RESULT 9		
LOCUS	AF043334 417 bp mRNA PRI 21-FEB-1998	
DEFINITION	Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.	
ACCESSION	AF043334	
VERSION	AF043334.1 GI:2905619	
KEYWORDS	human.	
SOURCE	human.	
ORGANISM	Homo sapiens	
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.	
AUTHORS	1 (bases 1 to 417)	
TITLE	Jang, J.S. and Kim, B.E.	
JOURNAL	Direct Submission	
COMMENT	Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon I-dong, Sosa-gu, Bucheon 422-231, Korea	
COMMENT	Nested PCR:	
COMMENT	1) first PCR :	
COMMENT	forward primer (5'-ctcaatcctctcctgttgca-3')	
COMMENT	reverse primer (5'-tagtcaggctctgtctcgc-3')	
COMMENT	2) second PCR :	
COMMENT	forward primer (5'-ctcatgagcgtctttgttgaccagc-3')	
COMMENT	reverse primer (5'-gatcttcgaagtticagtga-3').	
FEATURES	Location/Qualifiers	
source	1..417	
gene	/organism="Homo sapiens"	
primer_bind	/db_xref="taxon:9606"	
primer_bind	/cell_type="PHA-treated peripheral blood leukocyte"	
primer_bind	1..417	
primer_bind	/gene="IL13"	
primer_bind	1..24	
primer_bind	/gene="IL13"	
primer_bind	/note="second PCR"	
primer_bind	/PCR_conditions="94C-1min, 50C-1min, 72C-3min, 30 cycles; Deltacycler II from Ericomp"	
CDS	4..402	

Best Local Similarity 76.0%; Pred. No. 1.6e-37;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

```
Qy 2 gccctgtgactccctcccaaccctcaaggagctcataggagctgtgtcaacatcaccc 61
Db 65 GCCCTGTGCCCTCCAGTACTGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 124
Qy 62 agaatc---aggcatccctctgcaacgcagcatggtgtgagcgtcaacctgacgcgcg 118
Db 125 AGAACCAAGAGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 184
Qy 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacccaaa 178
Db 185 GCATGTACTGTGCACCCCTGGAAATCCCTGTATCAACGTGTCAAGCTGCAGTGCATCGAGA 244
Qy 179 ggaccagagatgctgaaagcactgtgtctctcaaaaagccgcgcgcagg---gatttcca 235
Db 245 AGACCCAGAGGATGCTGAGCGGATTCTCCCGCACAAAGTCTCAGCTGGGCAGTTTTTCCA 304
Qy 236 gtgaacgcagcgcagacacccaaaattgaagtgtatccagttggtgaaaaacctgtcacct 295
Db 305 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC 364
Qy 296 atgtaaggaggagtttatcgcccatgaaatttca 328
Db 365 ATTTAAGAAACTTTTCGCGAGGACGGTTCA 397
```

RESULT 15

```
186198          186198      425 bp      DNA          PAT      10-JUN-1998
LOCUS          Sequence 4 from patent US 5700665.
DEFINITION     186198
ACCESSION      186198
VERSION        186198.1 GI:3205916
KEYWORDS       Unknown.
SOURCE         Unknown.
ORGANISM       Unclassified.
REFERENCE      1 (bases 1 to 425)
AUTHORS       Legoux,R., Maldonado,P. and Salome,M.
TITLE         Method for the extraction of periplasmic proteins from prokaryotic
              microorganisms in the presence of arginine
JOURNAL       Patent: US 5700665-A 4/23-DEC-1997;
FEATURES       Location/Qualifiers
               source
               1..425
               /organism="unknown"
```

BASE COUNT 100 a 116 c 110 g 99 t

Query Match 55.3%; Score 182.6; DB 10; Length 425;

Best Local Similarity 76.0%; Pred. No. 1.6e-37;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

```
Qy 2 gccctgtgactccctcccaaccctcaaggagctcataggagctgtgtcaacatcaccc 61
Db 65 GCCCTGTGCCCTCCAGTACTGCCCTCAGGAGCTCAATTGAGGAGCTGGTCAACATCACCC 124
Qy 62 agaatc---aggcatccctctgcaacgcagcatggtgtgagcgtcaacctgacgcgcg 118
Db 125 AGAACCAAGAGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 184
Qy 119 gcatgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgcacccaaa 178
Db 185 GCATGTACTGTGCACCCCTGGAAATCCCTGTATCAACGTGTCAAGCTGCAGTGCATCGAGA 244
Qy 179 ggaccagagatgctgaaagcactgtgtctctcaaaaagccgcgcgcagg---gatttcca 235
Db 245 AGACCCAGAGGATGCTGAGCGGATTCTCCCGCACAAAGTCTCAGCTGGGCAGTTTTTCCA 304
Qy 236 gtgaacgcagcgcagacacccaaaattgaagtgtatccagttggtgaaaaacctgtcacct 295
Db 305 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCGAGTTGTAAAGGACCTGCTCTTAC 364
```

Qy 296 atgtaaggaggagtttatcgcccatggaatttca 328
Db 365 ATTTAAGAAACTTTTTCGCGAGGACGGTTCA 397

Search completed: May 13, 2001, 14:25:22
Job time: 19402 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:30:24 ; Search time 472.02 Seconds
(without alignments)
408.135 Million cell updates/sec

Title: US-09-451-527-104

Perfect score: 330

Sequence: 1 agccctgtactcctcccc.....atgccatggaatttcaga 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*

```

1: /cgnl_8/gcgdata/geneseq/geneseqn/NA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseqn/NA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseqn/NA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseqn/NA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseqn/NA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseqn/NA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseqn/NA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseqn/NA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseqn/NA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseqn/NA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseqn/NA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseqn/NA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseqn/NA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseqn/NA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseqn/NA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseqn/NA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseqn/NA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseqn/NA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseqn/NA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseqn/NA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseqn/NA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseqn/NA2001.DAT.*

```

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	ID	Description
1	330	100.0	330 21	Canine mature inte
2	330	100.0	330 21	Canine mature inte
3	330	100.0	330 21	Canine interleukin
4	330	100.0	390 21	Canine interleukin
5	330	100.0	1269 21	Canine interleukin
6	330	100.0	1269 21	Canine interleukin
7	317	96.1	333 21	Canine mature inte
8	317	96.1	333 21	Canine mature inte
9	317	96.1	393 21	Canine interleukin
10	317	96.1	393 21	Canine interleukin
11	317	96.1	1302 21	Canine interleukin

C	12	317	96.1	1302	21	255556	Canine interleukin
	13	240	72.7	272	21	255553	Canine interleukin
	14	218	66.1	278	21	255554	Canine interleukin
	15	187.4	56.8	336	13	Q28944	Gly41-Cytokine cod
	16	187.4	56.8	1270	21	F21334	Human low adenodin
	17	187.4	56.8	1270	21	A35212	Human adenosine re
	18	187.4	56.8	1282	21	F21332	Human low adenodin
	19	187.4	56.8	1282	21	A35210	Human adenosine re
	20	187.4	56.8	1290	15	Q56692	Sequence encoding
	21	187.4	56.8	6952	21	F21333	Human low adenodin
	22	187.4	56.8	6952	21	A35211	Human adenosine re
	23	187.4	56.8	14978	21	F21338	Human low adenodin
	24	187.4	56.8	14978	21	A35216	Human adenosine re
	25	185.8	56.3	336	13	Q28943	Asp41-Cytokine cod
	26	185.8	56.3	1297	13	Q28947	Cytokine NC30. Q
	27	151.4	45.9	1212	15	Q56693	Sequence encoding
	28	71.4	21.6	5670	21	F21331	Human low adenodin
	29	71.4	21.6	5670	21	F21337	Human low adenodin
	30	71.4	21.6	5670	21	A35209	Human adenosine re
	31	71.4	21.6	5670	21	A35215	Human adenosine re
	32	39	11.8	166	21	255552	Canine interleukin
	33	34	10.3	479	21	C38383	Zea mays DNA fragm
	34	34	10.3	1896	21	Z48297	S. coelicolor YesW
	35	33.8	10.2	2792	20	X78074	Rat DRDST cDNA. R
	36	33.4	10.1	66	20	Z32227	Human interleukin
	37	33.4	10.1	772	19	V48405	Dominant-negative
	38	32.4	9.8	717	21	A93373	Enhanced green flu
	39	32.4	9.8	717	21	A93374	Enhanced blue fluo
	40	32.4	9.8	717	21	A93375	Enhanced cyan fluo
	41	32.4	9.8	717	21	A27573	DNA encoding EGFP
	42	32.4	9.8	717	21	A27574	DNA encoding EBFP
	43	32.4	9.8	717	21	A27575	DNA encoding ECFP
	44	32.4	9.8	720	21	C62377	cDNA encoding a gr
	45	32.4	9.8	720	21	Z45644	DNA encoding the m

ALIGNMENTS

RESULT 1

ID Z55565 standard; cDNA; 330 BP.

AC Z55565;

DT 14-MAR-2000 (first entry)

DE Canine mature interleukin-13 (IL-13) clone 78 cDNA.

KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response; immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

OS Canis familiaris.

PN WO9961618-A2.

PD 02-DEC-1999.

PF 28-MAY-1999; 99WO-US11942.

PR 29-MAY-1998; 98US-0087306.

PA (HESK-) HESKA CORP.

PI SIm G, Yang S, Dreitz MJ, Wonderling RS;

DR WPI; 2000-072623/06.

DR P-PSDB; Y58224.

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs, useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim li.: Page 239-240; 264pp; English.

XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.3e-88;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaacccctcaaggagctcattgaggagctgtcaacatcacc 60
 DB 1 agccctgtgactccctcccaacccctcaaggagctcattgaggagctgtcaacatcacc 60

QY 61 cagaatcaggatccctctgcaacggcagcagctgtgtgagcgtcaacctgaccgccgc 120
 DB 61 cagaatcaggatccctctgcaacggcagcagctgtgtgagcgtcaacctgaccgccgc 120

QY 121 atgtactgcagctctgagaatctctgtatcattgtctccgactgagcgccatccaaagg 180
 DB 121 atgtactgcagctctgagaatctctgtatcattgtctccgactgagcgccatccaaagg 180

QY 181 accagagagatgctgaagcactgtgctcctcaaaagccgcggcaggatttccagttaa 240
 DB 181 accagagagatgctgaagcactgtgctcctcaaaagccgcggcaggatttccagttaa 240

QY 241 cgcagccgagacacacaaattgaaatgatccagttgggtgaaacacctgctaccctatgta 300
 DB 241 cgcagccgagacacacaaattgaaatgatccagttgggtgaaacacctgctaccctatgta 300

QY 301 agggaggttatcgccatggaaatttcaga 330
 DB 301 agggaggttatcgccatggaaatttcaga 330

RESULT 2
 Z55566/c
 ID Z55566 standard; cDNA: 330 BP.
 XX AC Z55566;
 XX AC Z55566;
 XX AC Z55566;
 DT 14-MAR-2000 (first entry)
 XX Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.
 DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX Canis familiaris.
 OS WO9961618-A2.
 PN 02-DEC-1999.
 XX

PF 28-MAY-1999; 99WO-US11942.
 XX 29-MAY-1998; 98US-0087306.
 PR (HESK-) HESKA CORP.
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 PI WPI: 2000-072623/06.
 XX P-PSDB; Y58224.
 DR Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX useful for treating or preventing e.g. tumors or autoimmune disease
 PT Claim 11; Page 241; 264pp; English.
 XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 330;
 Best Local Similarity 100.0%; Pred. No. 1.3e-88;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaacccctcaaggagctcattgaggagctgtcaacatcacc 60
 DB 330 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGGAGCTGGTCAACATCACC 271

QY 61 cagaatcaggatccctctgcaacggcagcagctgtgtgagcgtcaacctgaccgccgc 120
 DB 270 CAGAATCAGGCATCCCTCTGCAACGGCAGCATGCTGTGGAGCTCAACCTGACCGCGGC 211

QY 121 atgtactgcagctctgagaatctctgtatcattgtctccgactgagcgccatccaaagg 180
 DB 210 ATGTACTGCGAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCGAGCGCATCCAAAGG 151

QY 181 accagagagatgctgaagcactgtgctcctcaaaagccgcggcaggatttccagttaa 240
 DB 150 ACCCAGAGGATGCTGAAGCAGCTGTGCTCTCAAAAGCCCGCGGAGGATTTCAGTGAA 91

QY 241 cgcagccgagacacacaaattgaaatgatccagttgggtgaaacacctgctaccctatgta 300
 DB 90 CGCAGCCGAGACACCAAAATTTGAAGTGATCCAGTTGTTGTAACCACTGCTCACCTATGTA 31

QY 301 agggaggttatcgccatggaaatttcaga 330
 DB 30 AGGGAGGTTTATCGCCATGGAAATTCAGA 1

RESULT 3
 Z55563
 ID Z55563 standard; cDNA: 390 BP.
 XX

AC 255563;
 XX 14-MAR-2000 (first entry)
 DT Canine interleukin-13 (IL-13) clone 78 cDNA coding region.
 XX
 DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 KW
 XX Canis familiaris.
 OS
 XX WO9961618-A2.
 PN
 XX PD 02-DEC-1999.
 XX
 XX PF 28-MAY-1999; 99WO-US11942.
 XX
 XX PR 29-MAY-1998; 98US-0087306.
 XX
 XX PA (HESK-) HESKA CORP.
 XX
 XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 XX WPI; 2000-072623/06.
 DR P-PSDB; Y58223.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PT
 XX Claim 11; Page 238-239; 264pp; English.
 PS
 XX Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;
 SQ

Query Match 100.0%; Score 330; DB 21; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.4e-88;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 60
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 61 agccctgtgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 61 cagaatcagagcatccctctgcaacgacgacatggtggaagcgtcaacctgacgcggc 120
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 121 cagaaacagggcaacctctgcaacgacgacatggtggaagcgtcaacctgacgcggc 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 121 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaagg 180
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 181 atgtactgcgcagctctagaatctctgatcaatgtctccgactgcagcgccatccaagg 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 181 acccagagatgctgaagcactgtgctctcctcaaacgccccggaaggatttcagtga 240
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 241 acccagagatgctgaagcactgtgctctcctcaaacgccccggaaggatttcagtga 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 241 cgcagccgagacaccacaaattgaagtatccagttggtgaaacacctgtcactatgta 300
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 301 cgcagccgagacaccacaaattgaagtatccagttggtgaaacacctgtcactatgta 360
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 QY 301 aggggagttatcgccatggaatttcaga 330
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 DB 361 aggggagttatcgccatggaatttcaga 390
 ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

RESULT 4
 255564/C
 ID 255564 standard; cDNA; 390 BP.
 XX
 XX AC 255564;
 XX
 XX DT 14-MAR-2000 (first entry)
 XX
 XX DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.
 XX
 XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 XX OS Canis familiaris.
 XX
 XX WO9961618-A2.
 PN
 XX PD 02-DEC-1999.
 XX
 XX PF 28-MAY-1999; 99WO-US11942.
 XX
 XX PR 29-MAY-1998; 98US-0087306.
 XX
 XX PA (HESK-) HESKA CORP.
 XX
 XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 XX WPI; 2000-072623/06.
 DR P-PSDB; Y58223.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PT
 XX Claim 11; Page 239; 264pp; English.
 PS
 XX Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;
 SQ

Query Match 100.0%; Score 330; DB 21; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.4e-88;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agccctgtgactccctcccccaccctcaaggagctcattgagagctgtcaacatcacc 60
 |||||
 Db 330 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTTGAGAGCTGTCAACATCACC 271
 |||||
 Qy 61 cagaatcaggatccctctgcacgcgagcatggtgtgagcgctcaacctgaccgcggc 120
 |||||
 Db 270 CAGATCAGGCATCCCTCTGCAACGCGCAGCATGGTGTGGAGGCTCAACCTGACCGCCGCGC 211
 |||||
 Qy 121 atgtactgcgcagctctagaaatctctgtatcaatgtctcgcagctgcagcgccatccaaagg 180
 |||||
 Db 210 ATGTACTGCGAGCTCTAGAAATCTGTGATCAATGTCTCGACTGCGAGCGCCATCCAAAGG 151
 |||||
 Qy 181 acccagagatgctgaagcactgtgctctcaaaagccgcgcggcagggatttccagtgaa 240
 |||||
 Db 150 ACCCCAGAGATGCTGAAGACACTGTGCTCTCAAAAGCCCGCGCAGGGATTTCCAGTGAA 91
 |||||
 Qy 241 cgcagccgagacacacaaatgaagtgtccagttggtgaaagaaacctgtccacctatgta 300
 |||||
 Db 90 CGCAGCCGAGACACCAAAATGAAGTGATCCAGTGGTGGAAGAAACCTGCTCACCTATGTA 31
 |||||
 Qy 301 agggaggtttatcgccatggaaatttcaga 330
 |||||
 Db 30 AGGGAGTATTATCGCATGTGAATTTTCA 1
 |||||

RESULT 5

ID Z55561 standard; cDNA; 1269 BP.

XX AC Z55561;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-13 (IL-13) clone 78 cDNA.

XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX FH Key Location/Qualifiers
 XX FT CDS 57...449
 XX FT /*tag= a
 XX FT /product= "Canine IL-13 clone 78"

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US11942.

XX PR 29-MAY-1998; 98US-0087306.

XX PA (HESK-) HESKA CORP.

XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX DR WPI; 2000-072623/06.

XX DR P-PSDB; Y58223.

XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 XX PT useful for treating or preventing e.g. tumors or autoimmune disease

XX PS Claim 11; Page 235-236; 264pp; English.

XX CC Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA

XX CC sequences encoding canine interleukin-13 (IL-13) clones 80

XX CC and 78 respectively. The invention relates to canine

XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or

XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline

XX CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

XX CC colony-stimulating factor (GM-CSF), and nucleotides which encode these

CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX SQ Sequence 1269 BP; 302 A; 320 C; 340 G; 307 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 1269;
 Best Local Similarity 100.0%; Pred. No. 2.1e-88;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 agccctgtgactccctcccccaccctcaaggagctcattgagagctgtcaacatcacc 60
 |||||
 Db 117 agccctgtgactccctcccccaccctcaaggagctcattgagagctgtcaacatcacc 176
 |||||

Qy 61 cagaatcaggatccctctgcacgcgagcatggtgtgagcgctcaacctgaccgcggc 120
 |||||
 Db 177 cagaatcaggatccctctgcacgcgagcatggtgtgagcgctcaacctgaccgcggc 236
 |||||

Qy 121 atgtactgcgcagctctagaaatctctgtatcaatgtctcgcagctgcagcgccatccaaagg 180
 |||||
 Db 237 atgtactgcgcagctctagaaatctctgtatcaatgtctcgcagctgcagcgccatccaaagg 296
 |||||

Qy 181 acccagagatgctgaagcactgtgctctcaaaagccgcgcggcaggttccagtgaa 240
 |||||
 Db 297 acccagagatgctgaagcactgtgctctcaaaagccgcgcggcaggttccagtgaa 356
 |||||

Qy 241 cgcagccgagacacacaaatgaagtgtccagttggtgaaagaaacctgtccacctatgta 300
 |||||
 Db 357 cgcagccgagacacacaaatgaagtgtccagttggtgaaagaaacctgtccacctatgta 416
 |||||

Qy 301 agggaggtttatcgccatggaaatttcaga 330
 |||||
 Db 417 agggaggtttatcgccatggaaatttcaga 446
 |||||

RESULT 6

Z55562/C
 ID Z55562 standard; cDNA; 1269 BP.

XX AC Z55562;

XX DT 14-MAR-2000 (first entry)

XX DE Canine interleukin-13 (IL-13) clone 78 cDNA complement.

XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX OS Canis familiaris.

XX FH Key Location/Qualifiers
 XX FT CDS complement (821..1213)
 XX FT /*tag= a
 XX FT /product= "Canine IL-13 clone 78"

XX PN WO9961618-A2.

XX PD 02-DEC-1999.

XX PF 28-MAY-1999; 99WO-US11942.

XX PR 29-MAY-1998; 98US-0087306.

XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX KW WPI; 2000-072623/06.
XX DR P-PSDB; Y58223.
XX DR
XX PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX PS useful for treating or preventing e.g. tumors or autoimmune disease
XX PS Claim 11; Page 237-238; 264pp; English.
XX CC Sequences 255552-255560 and 255561-255566 represent cDNA
XX CC sequences encoding canine interleukin-13 (IL-13) clones 80
XX CC and 78 respectively. The invention relates to canine
XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX CC immunoregulatory proteins. The proteins, their associated
XX CC nucleic acids, specific antibodies and inhibitors may be used as
XX CC vaccines for therapeutic or prophylactic regulation of an immune
XX CC response in animals (particularly cats, dogs, horses and humans).
XX CC They may be used to treat autoimmune or infectious diseases including
XX CC allergies, tumours, inflammation and graft rejection, and to increase
XX CC the response from a co-administered antigen. The nucleotide sequences
XX CC can also be used for the recombinant production of a protein, while
XX CC nucleotide fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for
XX CC modulators of activity, while the antibodies may be used in detection,
XX CC and in drug targeting.
XX SQ Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 1269;
Best Local Similarity 100.0%; Pred. No. 2.1e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 agccctgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 60
DB 1153 AGCCCTGTGACTCCCTCCCAACCCCTCAAGAGCTCATTTGAGGAGCTTGGTCAACATCACC 1094

QY 61 cagaatcaggatccctctgcaacgcagcatggtgtgagcgtcaacctgacccggc 120
DB 1093 CAGAAATCAGCATCCCTCTCTCAACGCGCAGCATGCTGTGGAGCGGTCAACCTGACCGCGGC 1034

QY 121 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatccaagg 180
DB 1033 ATGTACTGCGAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGGCATCCAAAGG 974

QY 181 acccagagatgctgaaacactgtgtctcaaaagcccgaggatttcacgtgaa 240
DB 973 ACCCAGAGATGCTGAAAGACACGTGTCTCTCAAAAGCCCGCAGGAGTTTCCAGTGAA 914

QY 241 cgcagccgagacacaaattgaagtgtatccagttggtgaaacacctgtcacctatgta 300
DB 913 CGCAGCCGAGACACCAAAATTTGAAGTGTATCCAGTTGGTGTGAAACCTGTCTCACCTATGTA 854

QY 301 agggaggtttatgccatgaaatttcaga 330
DB 853 AGGGAGTTTATGCCCATGGAATTTTCAGA 824

RESULT 7
ID Z55559
XX Z55559 standard; cDNA; 333 BP.
AC Z55559;
XX
DT 14-MAR-2000 (first entry)

XX DE Canine mature interleukin-13 (IL-13) clone 80 cDNA.
XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX OS Canis familiaris.
XX PN WO9961618-A2.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US11942.
XX PR 29-MAY-1998; 98US-0087306.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX DR P-PSDB; Y58222.
XX CC Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX CC useful for treating or preventing e.g. tumors or autoimmune disease
XX CC Claim 11; Page 233-234; 264pp; English.
XX CC Sequences 255552-255560 and 255561-255566 represent cDNA
XX CC sequences encoding canine interleukin-13 (IL-13) clones 80
XX CC and 78 respectively. The invention relates to canine
XX CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX CC immunoregulatory proteins. The proteins, their associated
XX CC nucleic acids, specific antibodies and inhibitors may be used as
XX CC vaccines for therapeutic or prophylactic regulation of an immune
XX CC response in animals (particularly cats, dogs, horses and humans).
XX CC They may be used to treat autoimmune or infectious diseases including
XX CC allergies, tumours, inflammation and graft rejection, and to increase
XX CC the response from a co-administered antigen. The nucleotide sequences
XX CC can also be used for the recombinant production of a protein, while
XX CC nucleotide fragments are useful as probes, as amplification primers and
XX CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX CC The proteins may be used to raise antibodies and to screen for
XX CC modulators of activity, while the antibodies may be used in detection,
XX CC and in drug targeting.
XX SQ Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 333;
Best Local Similarity 99.1%; Pred. No. 9.2e-85;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

QY 1 agccctgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 60
DB 1 agccctgactccctcccaaccctcaaggagctcattgagagctggtcaacatcacc 60

QY 61 cagaatcaggatccctctgcaacgcagcatggtgtgagcgtcaacctgacccggc 120
DB 61 cagaatcaggatccctctgcaacgcagcatggtgtgagcgtcaacctgacccggc 120

QY 121 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatccaagg 180
DB 121 atgtactgcgagctctagaaatctctgatcaatgtctccgactgcagcgccatccaagg 180

QY 181 acccagagatgctgaaacactgtgtctcaaaagcccgaggatttcacgtgaa 237
DB 181 acccagagatgctgaaacactgtgtctcaaaagcccgaggatttcacgtgaa 240

QY 238 gaacgagccgagacacaaattgaagtgtatccagttggtgaaacacctgtctacat 297

```

Db 241 gaacgagcagacacaaattgaagtatccagttgtgtaaaacctgtcacctat 300
|||||
Qy 298 gtaagggagttatcgccatgaaatttcaga 330
|||||
Db 301 gtaagggagttatcgccatgaaatttcaga 333
|||||

RESULT 8
255360/c
ID 255560 standard; cDNA; 333 BP.
XX AC 255560;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 80 cDNA complement.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
WPI: 2000-072623/06.
XX
P-PSDB; Y58222.
XX
Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 235; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC modulators of activity, while the antibodies may be used in detection,
XX and in drug targeting.
XX
SQ Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 333;
Best Local Similarity 99.1%; Pred. No. 9.2e-85;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 agccctgtgactccctccacccctcaaggagctcattgaggagctgtcaacatcacc 60
|||||

```

```

Db 333 AGCCCTGTGACTCCCTCCCAACCCCTCAAGGAGCTCATTGAGGAGCTGGTCAACATCACC 274
Qy 61 cagaatcagggatccctctctgcaacgagcatggtgtggagcgtcaacctgacccgcgcgc 120
|||||
Db 273 CAGAATCAGGATCCCTCTGCAACGCGCAGCATGGTGTGGAGCGTCAACCTTGACCGCGGC 214
|||||
Qy 121 atgtactgagcagctctagaaatctctgataatgtctccgactgcagcgccatcccaagg 180
|||||
Db 213 ATGTACTGGCAGCTCTAGAAATCTCTGATCAATGTCTCCGACTGCAGCGCCATCCAAAGG 154
|||||
Qy 181 acccagaggtgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgcgc 237
|||||
Db 153 ACCCAGAGGATGCTGAAGCAGCTGTGCTCTCAAAAGCCCGCGCAGGCGCAGATTTCCAGT 94
|||||
Qy 238 gaacgagcagcagacacacaaattgaagtatccagttgtgtaaaacctgtcacctat 297
|||||
Db 93 GAACGCGCGCGAGACACCAAAATTTGAAGTGATCCAGTTGTTGAAACCTGTCTCACCTAT 34
|||||
Qy 298 gtaagggagttatcgccatgaaatttcaga 330
|||||
Db 33 GTAAGGGAGGTTTATCCCGCATGGAAATTTTCAGA 1
|||||

RESULT 9
255557
ID 255557 standard; cDNA; 393 BP.
XX AC 255557;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
WPI: 2000-072623/06.
XX
P-PSDB; Y58221.
XX
Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 232-233; 264pp; English.
XX
CC Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while

```


Db 1131 CAGAAATCAGGATCCCTCTGCAACGGCAGCATGGTGTGGAGCTCAACCTGACCGCGGC 1072
Qy 121 atgtactgcgagctcagaatctctgatcaatgtctccagctgcagcgcacatcaaaag 180
Db 1071 ATCTACTGGCAGCTCTAGAATCTCTGATCAATGTCTCCGACTGCAGCGCATCAAAAGG 1012
Qy 181 acccagagatgctgaagcactgtctctcaaaagcccgccgagcagg---gatttcag 237
Db 1011 ACCCAGAGATGCTGAAAGCAGCTGTCTCTCAAAAGCCCGCAGGCGAGATTTCAGT 952
Qy 238 gaacgcagcgcgagacacccaaattgaagtgcagctgtgtgtaaaacctgctcacctat 297
Db 951 GAACGAGCGGAGACACCAAAATTGAAGTGATCCAGTTGGTGAATAAACCTGCTCACCTAT 892
Qy 298 gtaaggggagttatcgccatggaatttcaga 330
Db 891 CTAAGGGGAGTTATCCCATGCAAAATTTTCAGA 859

RESULT 13
ID Z5553
XX Z5553 standard; cDNA; 272 BP.
AC Z5553;
XX
DT 14-MAR-2000 (first entry)
DE Canine interleukin-13 (IL-13) cDNA fragment nCaiL13-272.
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
OS Canis familiaris.
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 228; 264pp; English.
XX
CC Sequences Z5552-255560 and Z55561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,

CC and in drug targeting.
XX
SQ Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;

Query Match 72.7%; Score 240; DB 21; Length 272;
Best Local Similarity 98.8%; Pred. No. 5.7e-62;
Matches 253; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

Qy 1 agccctgtgactccctcccaacccctcaaggagctcattgagagctggtgacatcacc 60
Db 17 agccctgtgactccctcccaacccctcaaggagctcattgagagctggtgacatcacc 76
Qy 61 cagaatcaggcatccctctgcacagcgagcagctggtgtgagcgtcaacctgaccgcggc 120
Db 77 cagaatcaggcatccctctgcacagcgagcagctggtgtgagcgtcaacctgaccgcggc 136
Qy 121 atgtactgcgagctcagaatctctgatcaatgtctccagctgcagcgcacatcaaaag 180
Db 137 atgtactgcgagctcagaatctctgatcaatgtctccagctgcagcgcacatcaaaag 196
Qy 181 acccagagatgctgaagcactgtgtctcaaaagcccgccgagcagg---gatttcag 237
Db 197 acccagagatgctgaagcactgtgtctcaaaagcccgccgagcagg---gatttcag 256
Qy 238 gaacgcagcgcgagaca 253
Db 257 gaacgcagcgcgagaca 272

RESULT 14
ID Z5554
XX Z5554 standard; cDNA; 278 BP.
AC Z5554;
XX
DT 14-MAR-2000 (first entry)
DE Canine interleukin-13 (IL-13) cDNA probe.
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
OS Canis familiaris.
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 1i; Page 229; 264pp; English.
XX
CC Sequences Z5552-255560 and Z55561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:44 ; Search time 226.02 Seconds
(without alignments)
254.928 Million cell updates/sec

Title: US-09-451-527-104
Perfect score: 330
Sequence: 1 agccctgtactccctccc.....atgcgcattggaatttcaga 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_NA.*
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq.*
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq.*
3: /cgnl_7/ptodata/1/ina/6A_COMB.seq.*
4: /cgnl_7/ptodata/1/ina/6B_COMB.seq.*
5: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq.*
6: /cgnl_7/ptodata/1/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	187.4	56.8	336	1	US-08-371-121-24
2	187.4	56.8	1290	1	US-08-012-543-1
3	187.4	56.8	1290	5	PCT-US93-07645A-1
4	187.4	56.8	1290	5	PCT-US93-07645-1
5	185.8	56.3	336	1	US-08-371-121-2
6	185.8	56.3	1297	1	US-08-371-121-15
7	184.2	55.8	384	1	US-08-371-121-17
8	182.6	55.3	425	1	US-08-594-469-4
9	182.6	55.3	425	2	US-08-906-957-4
10	182.6	55.3	4410	1	US-08-594-469-1
11	182.6	55.3	4410	2	US-08-906-957-1
12	151.4	45.9	447	1	US-08-371-121-26
13	151.4	45.9	1212	1	US-08-012-543-3
14	151.4	45.9	1212	5	PCT-US93-07645A-3
15	151.4	45.9	1212	5	PCT-US93-07645-3
16	33.4	10.1	1322	4	US-09-128-450-27
17	32.4	9.8	720	4	US-09-094-359-3
18	32.4	9.8	720	4	US-09-094-359-7
19	32.4	9.8	720	4	US-09-172-063-11
20	32.4	9.8	720	4	US-09-172-063-13
21	32.4	9.8	762	1	US-08-532-390-40
22	32.4	9.8	762	4	US-08-717-294-40
23	32.4	9.8	768	4	US-09-094-359-11
24	32.4	9.8	850	4	US-09-062-102-2
25	32.4	9.8	972	4	US-09-172-063-27
26	32.4	9.8	972	4	US-09-172-063-29
27	32.4	9.8	1095	4	US-09-085-305-5

28	32.4	9.8	1929	2	US-08-818-253-1	Sequence 1, Appli
29	32.4	9.8	1929	2	US-08-818-253-5	Sequence 5, Appli
30	32.4	9.8	1929	4	US-08-818-252-1	Sequence 1, Appli
31	32.4	9.8	1929	4	US-08-818-252-5	Sequence 5, Appli
32	32.4	9.8	1959	2	US-08-818-253-3	Sequence 3, Appli
33	32.4	9.8	1959	4	US-08-818-252-3	Sequence 3, Appli
34	32.4	9.8	1971	2	US-08-818-253-7	Sequence 7, Appli
35	32.4	9.8	1971	4	US-08-818-252-7	Sequence 7, Appli
36	32.4	9.8	7938	4	US-09-331-581-14	Sequence 14, Appli
37	32	9.7	1926	2	US-08-978-182-2	Sequence 2, Appli
38	32	9.7	1926	2	US-09-205-681-2	Sequence 2, Appli
39	31.8	9.6	35081	2	US-08-752-760A-1	Sequence 1, Appli
40	31.4	9.5	398	4	US-09-080-756-630	Sequence 630, App
41	31.2	9.5	720	4	US-09-094-359-5	Sequence 5, Appli
42	31.2	9.5	720	4	US-09-094-359-9	Sequence 9, Appli
43	31.2	9.5	720	4	US-09-172-063-12	Sequence 12, Appli
44	31.2	9.5	720	4	US-09-172-063-14	Sequence 14, Appli
45	31.2	9.5	720	4	US-09-172-063-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-08-371-121-24

; Sequence 24, Application US/083711121

; Patent No. 5652123

; GENERAL INFORMATION:

; APPLICANT: CAPUT, Daniel

; APPLICANT: FERRARA, Pascual

; APPLICANT: GUILLEMET, Jean-Claude

; APPLICANT: LEPLATOIS, Pascal

; APPLICANT: MINTY, Adrian

; APPLICANT: KAGHAD, Mourad

; APPLICANT: LABIT-LE BOUTELLER, Christine

; APPLICANT: MAGAZIN, Marilyn

; TITLE OF INVENTION: Protein having a cytokine type

; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FOLEY & LARDNER

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington, D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/371,121

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/938,161

; FILING DATE: 30-NOV-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: PCT/FR92/00280

; FILING DATE: 27-MAR-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 00137

; FILING DATE: 08-JAN-1992

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: FR 91 03904

; FILING DATE: 29-MAR-1991

; ATTORNEY/AGENT INFORMATION:

; NAME: SAXE, Bernhard D.

; REGISTRATION NUMBER: 28,665

; REFERENCE/DOCKET NUMBER: 16781/383

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (202) 672-5300

; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 336 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
; US-08-371-121-24

Query Match 56.8%; Score 187.4; DB 1; Length 336;
Best Local Similarity 76.9%; Pred. No. 2.1e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaacccctcaaggagctcattgagagctggtgtaacatcacccc 61
DB 2 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 61

QY 62 agaatc---aggcatccctctgcaacgagcagcatggtgtggagcgtcaacctgaccgcg 118
DB 62 AGAACCAAGAGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 121

QY 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
DB 122 GCATGTACTGTGTCAGCCCTGGAATCCCTGATCAACGCTGTACAGCTGCAGTGCATCGAGA 181

QY 179 ggaccagagatgctgaaagcaactgtctctcaaaagccgcgagcag- -gatttcca 235
DB 182 AGACCAAGAGATGCTGAGCGGATTCGCCGCAACAGGCTCAGCTGGGAGTTTCCA 241

QY 236 gtgaacgcagcgcgagacaccacaaattgaagtgtatccagttgtgtaaaacctgctcaact 295
DB 242 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTCTAAAGGACCTGCTCTTAC 301

QY 296 atgtaagggaggatttatcgccatggaatttcca 328
DB 302 ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 334

RESULT 2
US-08-012-543-1
; Sequence 1, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchemau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012.543
; FILING DATE: 01-FEB-1993

; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1290 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: CDS
; LOCATION: 45..443
; US-08-012-543-1

Query Match 56.8%; Score 187.4; DB 1; Length 1290;
Best Local Similarity 76.9%; Pred. No. 3.5e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaacccctcaaggagctcattgagagctggtgtaacatcacccc 61
DB 106 GCCCTGTGCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGCTGGTCAACATCACCC 165

QY 62 agaatc---aggcatccctctgcaacgagcagcatggtgtggagcgtcaacctgaccgcg 118
DB 166 AGAACCAAGAGCTCCGCTCTGCAATGGCAGCATGGTATGAGCATCAACCTGACACCTG 225

QY 119 gcatgtactgcgagctctagaatctctgatcaatgtctccgactgcagcgccatccaaa 178
DB 226 GCATGTACTGTGCGAGCTGGAAATCCCTGATCAACGCTGTCAGGCTGCAGTGCATCGAGA 285

QY 179 ggaccagagatgctgaaagcaactgtctctcaaaagccgcgagcag- -gatttcca 235
DB 286 AGACCAAGAGATGCTGAGCGGATTCGCCGCAACAGGCTCAGCTGGGAGTTTCCA 345

QY 236 gtgaacgcagcgcgagacaccacaaattgaagtgtatccagttgtgtaaaacctgctcaact 295
DB 346 GCTTGCATGTCGAGACACCAAAATCGAGGTGGCCAGTTTGTAAAGGACCTGCTCTTAC 405

QY 296 atgtaagggaggatttatcgccatggaatttcca 328
DB 406 ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 438

RESULT 3
PCT-US93-07645A-1
; Sequence 1, Application PC/TUS9307645A
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645A
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977

APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match 56.3%; Score 185.8; DB 1; Length 336;
Best Local Similarity 76.6%; Pred. No. 6.7e-50;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctgtgtaacatcaccc 61
DB 2 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGTGTGTAACATCACCC 61
QY 62 agaatc---aggatccctctgcaacgcgcagcatggtgtgagcgtcaacctgacgcgcg 118
DB 62 AGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGCAGCTG 121
QY 119 gcatgtactgcgcagctcagaaatctctgataatctctcgcagctgcagcgcacccaaa 178
DB 122 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGCAGCTGCAGTGCATCGAGA 181
QY 179 gaaccagagatgctgaaagcactgtctctcctcaaaagccgcgcgcg---gatttcca 235
DB 182 AGACCCAGAGGATGCTGAGCGGATTCGCCGACAAAGTCTCAGCTGGCGAGTTTCCA 241
QY 236 gtgaacgcagcgcagacacacaaatgaagtgatccagtgtgtaaaacctgctcacct 295
DB 242 GCTTGCATGCTCCGAGACACCAAAATCGAGGTGGCCAGTTGTAAAGGACCTGCTCTTAC 301
QY 296 atgtaaggggagttatgccatggaatttca 328
DB 302 ATTTAAGAAACTTTTTCGCGAGGAGCGTTCA 334

RESULT 6
US-08-371-121-15
Sequence 15, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTILLIER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESS: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1297 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..452
NAME/KEY: mat_peptide
LOCATION: 117..452
US-08-371-121-15

Query Match 56.3%; Score 185.8; DB 1; Length 1297;
Best Local Similarity 76.6%; Pred. No. 1.1e-49;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 2 gccctgtgactccctcccaaccctcaaggagctcattgaggagctgtgtaacatcaccc 61
DB 118 GCCCTGTGCCCTCCCTCTACAGCCCTCAGGAGCTCATTGAGGAGTGTGTAACATCACCC 177
QY 62 agaatc---aggatccctctgcaacgcgcagcatggtgtgagcgtcaacctgacgcgcg 118
DB 178 AGAACCAGAAGGCTCCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGCAGCTG 237
QY 119 gcatgtactgcgcagctcagaaatctctgataatctctcgcagctgcagcgcacccaaa 178
DB 238 ACATGTACTGTGCAGCCCTGGAATCCCTGATCAACGTGTGCAGCTGCAGTGCATCGAGA 297
QY 179 gaaccagagagatgctgaaagcactgtctctcaaaagccgcgcgcg---gatttcca 235
DB 298 AGACCCAGAGGATGCTGAGCGGATTCGCCGACAAAGTCTCAGCTGGCGAGTTTCCA 357
QY 236 gtgaacgcagcgcagacacacaaatgaagtgatccagtgtgtaaaacctgctcacct 295
DB 358 GCTTGCATGCTCCGAGACACCAAAATCGAGGTGGCCAGTTGTAAAGGACCTGCTCTTAC 417
QY 296 atgtaaggggagttatgccatggaatttca 328
DB 418 ATTTAAGAAACTTTTTCGCGAGGAGCGTTCA 450

RESULT ' 7

```
US-08-371-121-17
; Sequence 17, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascal
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrien
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: Saxe, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 17:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 384 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-371-121-17

Query Match 55.8%; Score 184.2; DB 1; Length 384;
Best Local Similarity 76.3%; Pred. No. 2.3e-49;
Matches 254; Conservative 0; Mismatches 73; Indels 6; Gaps 2;

Qy 2 gccctgtactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 23 GCCCTGTGCTCCTCTACGGCCCTCAGGAGCTCATTGAGGAGCTGTCAACATCACCC 82

Qy 62 agaatac---aggatccctctgaacagcgagcagatggtgtgagcgtcaacctgaccgcg 118
Db 83 AGAACGAGAGGCTCGCTCTGCAATGGCAGCATGGTATGGAGCATCAACCTGACAGCTG 142

US-08-594-469-4
; Sequence 4, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E.
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-594-469-4

Query Match 55.3%; Score 182.6; DB 1; Length 425;
Best Local Similarity 76.0%; Pred. No. 7.5e-49;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

Qy 2 gccctgtactccctcccaaccctcaaggagctcattgaggagctggtcaacatcaccc 61
Db 65 GCCCTGTGCTCCTCCAGTACTGCCCTCAGGAGCTCATTGAGGAGCTGTCAACATCACCC 124
```

QY 62 agaatc---aggatccctctgaacgagcagcatggtgtggagctgaacacctgaccgccc 118
DB 125 AGACCAAGAGCTCGCTCTCATAGGCGAGCATGTATGGAGCATCAACCTGACAGCTG 184
QY 119 gcatgtactgcgagctctagaaatctctgataatctctccgactgagcagcgccatccaa 178
DB 185 GCATGTACTGTGCGCCCTTGGAAATCCCTGATCAACGTGTGAGCTGCATGCCATCGAGA 244
QY 179 ggaccagaagatgtgaaagcactgtctctcaaaagcccgccgagc---gatttcca 235
DB 245 AGACCCAGAGGATGTGAGCGGATTTCTGCCCGCACAAAGGCTCTCAGGTGGCGAGTTTCCA 304
QY 236 gtgaacgagcagcgagacacacaaattgaagtgtatccagttgtgtaaaacacctgctcacct 295
DB 305 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCGCAGTTGTAAAGGACCTGCTCTTAC 364
RESULT 9
US-08-906-957-4
; Sequence 4, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906.957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594.469
; FILING DATE:
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-4

Query Match 55.3%; Score 182.6; DB 2; Length 425;

Best Local Similarity 76.0%; Pred. No. 7.5e-49;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;
QY 2 gcccgtgactccctcccaacccctcaagagagctcattgaggagctggtcaacatcaccc 61
DB 65 GCCTGTGCTCCAGTACVTCCTCAGGAGCTCATTTGAGGAGCTGCTCAACATCACCC 124
QY 62 agaatc---aggatccctctgaacgagcagcatggtgtggagctgaacacctgaccgccc 118
DB 125 AGAACAGAAAGGTCCGCTCTGCAATGGCAGCATGTGATGGAGCATCAACCTGACAGCTG 184
QY 119 gcatgtactgcgagctctagaaatctctgataatctctccgactgagcagcgccatccaa 178
DB 185 GCATGTACTGTGAGCGCTTGGAAATCCCTGATCAACGTGTGAGCTGCATGCCATCGAGA 244
QY 179 ggaccagaagatgtgaaagcactgtctctcaaaagcccgccgagc---gatttcca 235
DB 245 AGACCCAGAGGATGTGAGCGGATTTCTGCCCGCACAAAGGCTCTCAGGTGGCGAGTTTCCA 304
QY 236 gtgaacgagcagcgagacacacaaattgaagtgtatccagttgtgtaaaacacctgctcacct 295
DB 305 GCTTGCATGTCCGAGACACCAAAATCGAGGTGGCCCGCAGTTGTAAAGGACCTGCTCTTAC 364
QY 296 atgtaaggggagtttatcgccatggaaattcca 328
DB 365 ATTTAAAGAAACTTTTTCGCGAGGACGGTTCA 397
RESULT 10
US-08-594-469-1
; Sequence 1, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594.469
; FILING DATE:
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)


```

;
; SEQUENCE CHARACTERISTICS:
;
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
;
; MOLECULE TYPE: DNA (genomic)
;
US-08-906-957-1

```

```

; free: nucleic acid
; ;
; STRANDEDNESS: single
; ;
; TOPOLOGY: linear
; ;
; MOLECULE TYPE: DNA (genomic)
; ;
US-08-906-957-1

Query Match.          55.3%; Score 182.6; DB 2; Length 4410;
Best Local Similarity 76.0%; Pred. No. 1.8e-48;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

QY      2  gccctgtgaactccctccccaaacctcaaggagctcattgaggagctggccaacatcaccc 61
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      402  GCCTGTGTGCTCCGACTCTGCCTCAGGAGAGCTCATGTAGGAGCTGGTCAACATCACCC 461
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      62  agaatc---aggcatccctctgaacggcgagcatggctgtgagcgctcaaacctgaccgcg 118
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      462  AGAACGAGAGAGGCTCCGCTCTGCATGCGCAGCATGGTATGGAGGAGCATCAACCTGACAGCTG 521
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      119  gcattgactgcgcagctctagaatactctgatcaatgtctccgcagctgcagcgccatccaaa 178
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      522  GCATGTACTTGCAGGCCCTGGAATCCCTGTATCAACGTGTCAGGCTGCAGTGCCATCGAGA 581
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      179  ggaccagagatgctgaaagcaactgtgctctcaaaaggccgcggcagg---gatttcca 235
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db      582  AGACCCAGAGAGGATGCTGAGCGGATTCGTGCCCGCACAGGCTCAAGCTGGGAGATTTTCCA 641
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY      236  gtaacacgacccagacaccaaaattgaatgattccagtttagtcaaaaacactgctcacct 295
          ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

```

042 GCTTCGACGTCCGGAGACACCAAAATCGAGGTGGGCCCTTTTGTAAAGACCCTGCCTTTAC 701

Qy 296 atgtaaggggagtttatcgccatggaatttca 328
| | | | | | | | | | |
Db 702 ATTTAAGAACAATTTTTTCGCGAGGACGGTTCA 734

RESULT 12
US-08-371-121-26
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992

;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR92/00280
;; FILING DATE: 27-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 91 00137
;; FILING DATE: 08-JAN-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 91 03904
;; FILING DATE: 29-MAR-1991
;; ATTORNEY/AGENT INFORMATION:
;; NAME: SAXE, Bernhard D.
;; REGISTRATION NUMBER: 28.665
;; REFERENCE/DOCKET NUMBER: 16781/383
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: (202) 672-5300
;; TELEFAX: (202) 672-5399
;; TELEX: 904136
;; INFORMATION FOR SEQ ID NO: 26:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 447 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
US-08-371-121-26

Query Match 45.9%; Score 151.4; DB 1; Length 447;
Best Local Similarity 68.8%; Pred. No. 5.8e-39;
Matches 225; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
Qy 1 agccctgtgactccctcccccaaccctcaaggagctcattgaggagctgtgtaacatcacc 60
Db 121 AGATCTGTCTCTCCCTCTGACCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 180
Qy 61 cagaatcaggcatccctctgcaacgcagcatggtgagcgtaacactgaccgcgcgc 120
Db 181 CAAGACAGACTCCCTCTGCAACGGCAGCATGGTATGGAGTGTGGACCTGGCCGCTGGC 240
Qy 121 atgtactgcgcagctctagaatctctgataatgtctccgactgcagcgccatccaaagg 180
Db 241 GGGTTCTGTGAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAATGCCATCTACAGG 300
Qy 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgc 240
Db 301 ACCCAGAGGATATTGCATGGCCCTCTGTAACCGAAGGCCCCCACTACGCTCTCCA----- 355
Qy 241 cgcagc 300
Db 356 -GCCTCCCGATACCAAAATCGAAGTAGCCCACTTTTATAACAAAATGCTCTAGCTACACA 414
Qy 301 aggggagtttatcgccatggaatttc 327
Db 415 AAGCAACTGTTTCGCCACGCGCCCTTC 441

RESULT 13
US-08-012-543-3
; Sequence 3, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culppepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchemreau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: DNAX Research Institute
;; STREET: 901 California Avenue
;; CITY: Palo Alto
;; STATE: California
;; COUNTRY: USA
;; ZIP: 94304-1104
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/012,543
;; FILING DATE: 01-FEB-1993
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/933,416
;; FILING DATE: 21-AUG-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Ching, Egwin P.
;; REGISTRATION NUMBER: 34,090
;; REFERENCE/DOCKET NUMBER: DX0302K1
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 415-852-9196
;; TELEFAX: 415-496-1200
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1212 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
;; MOLECULE TYPE: cDNA
;; FEATURE:
;; NAME/KEY: CDS
;; LOCATION: 70..465
US-08-012-543-3

Query Match 45.9%; Score 151.4; DB 1; Length 1212;
Best Local Similarity 68.8%; Pred. No. 8.5e-39;
Matches 225; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
Qy 1 agccctgtgactccctcccccaaccctcaaggagctcattgaggagctgtgtaacatcacc 60
Db 142 AGATCTGTCTCTCCCTCTGACCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 201
Qy 61 cagaatcaggcatccctctgcaacgcagcatggtgagcgtaacactgaccgcgcgcgcgcgc 120
Db 202 CAAGACAGACTCCCTCTGCAACGGCAGCATGGTATGGAGTGTGGACCTGGCCGCTGGC 261
Qy 121 atgtactgcgcagctctagaatctctgataatgtctccgactgcagcgccatccaaagg 180
Db 262 GGGTTCTGTGAGCCCTGGATTCCCTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321
Qy 181 acccagagatgctgaaagcactgtgctctcaaaagccgcgcgcgcgcgcgcgcgcgcgcgc 240
Db 322 ACCCAGAGGATATTGCATGGCCCTCTGTAACCGAAGGCCCCCACTACGCTCTCCA----- 376
Qy 241 cgcagc 300
Db 377 -GCCTCCCGATACCAAAATCGAAGTAGCCCACTTTTATAACAAAATGCTCTAGCTACACA 435
Qy 301 aggggagtttatcgccatggaatttc 327
Db 436 AAGCAACTGTTTCGCCACGCGCCCTTC 462
RESULT 14
PCT-US93-07645A-3
; Sequence 3, Application PC/TUS9307645A
; .GENERAL INFORMATION:
; APPLICANT:

;; TITLE OF INVENTION: Human Interleukin-13
;; NUMBER OF SEQUENCES: 6
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 6.0.5
;; SOFTWARE: Microsoft Word 5.1a
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/07645A
;; FILING DATE:
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/012543
;; FILING DATE: 01-FEB-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/010977
;; FILING DATE: 29-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/933416
;; FILING DATE: 21-AUG-1992
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1212 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
PCT-US93-07645A-3

Query Match 45.9%; Score 151.4; DB 5; Length 1212;
Best Local Similarity 68.8%; Pred. No. 8.5e-39;
Matches 225; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
QY 1 agccctgtgactccctcccaacccctcaaggagctcattgagagctggtgctcaacatcacc 60
Db 142 AGATCTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 201
QY 61 cagaatcaggatccctctgcaacgagcagcatggtgtgagcgtcaacctgaccgccgcgc 120
Db 202 CAAGACAGAGACTCCCTCTGCAACGGCAGCATGGTATGAGTGTGGACCTGGCCGCTGGC 261
QY 121 atgtactgcgagctctagaatctctgataatgtctccgactgcagcgcaatccaaagg 180
Db 262 GGGTCTGTGAGCCCTGGATTCCTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321
QY 181 acccagaggtgctgaaagcactgtctctcaaaagccgcgcgagggatttccagtga 240
Db 262 GGGTCTGTGAGCCCTGGATTCCTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321
QY 241 acccagaggtgctgaaagcactgtctctcaaaagccgcgcgagggatttccagtga 240
Db 322 ACCCAGAGGATTTGCGCTCTGTAAACCGAAGGCCCCCTACGGTCTCCA----- 376
QY 241 cgcagccgagacacacaaattgaagtgtccagttggtgaaacacctgctcacctatgta 300
Db 377 -GCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTATAACAAAACCTGCTCAGCTACACA 435
QY 301 agggagtttatcgccatggaatttc 327
Db 436 AAGCAACTGTTTCGCCACGGCCCCCTTC 462

RESULT 15
PCT-US93-07645-3
;; Sequence 3, Application PC/TUS9307645
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Human Interleukin-13
;; NUMBER OF SEQUENCES: 6
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 6.0.5
;; SOFTWARE: Microsoft Word 5.1a
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/07645
;; FILING DATE: 19930818
;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/012543
;; FILING DATE: 01-FEB-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/010977
;; FILING DATE: 29-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/933416
;; FILING DATE: 21-AUG-1992
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1212 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
PCT-US93-07645-3
Query Match 45.9%; Score 151.4; DB 5; Length 1212;
Best Local Similarity 68.8%; Pred. No. 8.5e-39;
Matches 225; Conservative 0; Mismatches 96; Indels 6; Gaps 1;
QY 1 agccctgtgactccctcccaacccctcaaggagctcattgagagctggtgctcaacatcacc 60
Db 142 AGATCTGTCTCTCCCTCTGACCCCTTAAGGAGCTTATTGAGGAGCTGAGCAACATCACA 201
QY 61 cagaatcaggatccctctgcaacgagcagcatggtgtgagcgtcaacctgaccgccgcgc 120
Db 202 CAAGACAGAGACTCCCTCTGCAACGGCAGCATGGTATGAGTGTGGACCTGGCCGCTGGC 261
QY 121 atgtactgcgagctctagaatctctgataatgtctccgactgcagcgcaatccaaagg 180
Db 262 GGGTCTGTGAGCCCTGGATTCCTGACCAACATCTCCAATTGCAATGCCATCTACAGG 321
QY 181 acccagaggtgctgaaagcactgtctctcaaaagccgcgcgagggatttccagtga 240
Db 322 ACCCAGAGGATTTGCGCTCTGTAAACCGAAGGCCCCCTACGGTCTCCA----- 376
QY 241 cgcagccgagacacacaaattgaagtgtccagttggtgaaacacctgctcacctatgta 300
Db 377 -GCCTCCCGGATACCAAAATCGAAGTAGCCCACTTTATAACAAAACCTGCTCAGCTACACA 435
QY 301 agggagtttatcgccatggaatttc 327
Db 436 AAGCAACTGTTTCGCCACGGCCCCCTTC 462

Search completed: May 13, 2001, 14:21:47
Job time: 17858 sec

GenCore version 4.5
Copyright (C) 1993 - 2000 CompuGen Ltd.

OM nucleic.- nucleic search, using sw model

Run on: May 13, 2001, 11:40:52 ; Search time 5997.24 Seconds
(without alignments)
480.707 Million cell updates/sec

Title: US-09-451-527-104
Perfect score: 330
Sequence: 1.agccctgtgactccctccccc.....atcgccatggaatttcaga 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , *Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_est3:*
4: gb_est4:*
5: gb_est5:*
6: gb_est6:*
7: gb_est7:*
8: gb_est8:*
9: gb_est9:*
10: gb_est10:*
11: gb_est11:*
12: gb_est12:*
13: gb_est13:*
14: gb_est14:*
15: gb_est15:*
16: gb_est16:*
17: gb_est17:*
18: gb_est18:*
19: gb_est19:*
20: gb_est20:*
21: gb_est21:*
22: gb_est22:*
23: gb_est23:*
24: gb_est24:*
25: gb_est33:*
26: gb_est34:*
27: gb_est35:*
28: gb_est36:*
29: gb_est37:*
30: gb_est38:*
31: gb_est39:*
32: gb_est40:*
33: em_estba:*
34: em_estfun:*
35: em_esthum1:*
36: em_esthum2:*
37: em_esthum3:*
38: em_esthum4:*
39: em_esthum5:*
40: em_esthum6:*
41: em_esthum7:*
42: em_esthum8:*
43: em_esthum9:*

44: em_esthum10:*
45: em_esthum11:*
46: em_esthum12:*
47: em_esthum13:*
48: em_esthum14:*
49: em_esthum15:*
50: em_esthum16:*
51: em_esthum17:*
52: em_esthum18:*
53: em_esthum19:*
54: em_esthum20:*
55: em_esthum21:*
56: em_esthum22:*
57: em_esthum23:*
58: em_esthum24:*
59: em_esthum25:*
60: em_esthum26:*
61: em_esthum27:*
62: em_esthum28:*
63: em_estin1:*
64: em_estin2:*
65: em_estin3:*
66: em_estin4:*
67: em_estin5:*
68: em_estomi:*
69: em_estom2:*
70: em_estov1:*
71: em_estov2:*
72: em_estpl1:*
73: em_estpl2:*
74: em_estpl3:*
75: em_estpl4:*
76: em_estpl5:*
77: em_estpl6:*
78: em_estpl7:*
79: em_estpl8:*
80: em_estpl9:*
81: em_estpl10:*
82: em_estro1:*
83: em_estro2:*
84: em_estro3:*
85: em_estro4:*
86: em_estro5:*
87: em_estro6:*
88: em_estro7:*
89: em_estro8:*
90: em_estro9:*
91: em_estro10:*
92: em_estro11:*
93: em_estro12:*
94: em_estro13:*
95: em_estro14:*
96: em_estro15:*
97: em_estro16:*
98: em_estro17:*
99: em_estro18:*
100: em_estro19:*
101: em_estro20:*
102: gb_est25:*
103: gb_est26:*
104: gb_est27:*
105: gb_est28:*
106: gb_est29:*
107: gb_est30:*
108: gb_est31:*
109: gb_est32:*
110: gb_est41:*
111: gb_est42:*
112: gb_est43:*
113: gb_est44:*
114: gb_est45:*
115: gb_est46:*
116: gb_est47:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Match	Query Length	DB ID	Description
1	39	11.8	477	218	AZ261971
2	39	11.8	521	215	AZ027551
3	36.4	11.0	277	137	BE593226
4	36.4	11.0	537	166	BE357229
5	35.2	10.7	757	174	BE260311
6	34.4	10.4	462	143	BF039993
7	34.4	10.4	507	138	BE705147
8	34.2	10.4	535	161	BE032541
9	34.2	10.4	546	161	BE032543
10	34.2	10.4	570	24	A1746678
11	34.2	10.4	965	217	AZ201624
12	34.2	10.4	2275	14	AF034173
13	34	10.3	370	166	BE363650
14	34	10.3	562	166	BE361027
15	33.8	10.2	341	163	BE127683
16	33.8	10.2	498	150	BF606532
17	33.6	10.2	577	166	BE402120
18	33.6	10.2	714	166	BE414190

FEATURES	Location/Qualifiers
source	1. .277
	/organism="Sorghum bicolor"
	/db_xref="taxon:4558"
	/clone_lib="water-stressed 1 (WS1)"
	/note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda Zap; Site.1: XhoI; Site.2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda Zap II. Clones to be sequenced were prepared by mass excision."
BASE COUNT	47 a 81 c 78 g 71 t

	Query Match	11.0%	Score 36.4	DB 166	Length 537
	Best Local Similarity	53.5%	Pred. No. 3.9		
	Matches	76	Conservative	0	Mismatches 66
					Indels 0
					Gaps 0
QY	24	ctcaaggagctcatgagagctggtcaacatcacccagaatacaggcatccctctgcaa	83		
DB	249	CCCATGGGAGGCTCGGGGAGCCGGCGACATCGGGCGCGGTGGTGGGTTCCTCTGCAC	308		
QY	84	cggcagcatggtgtggagcgtcaacctgacgcgcggcagctactctgcagctctagaatc	143		


```

Db 309 CGACGCCGCGAGTGGTCAACGCCAGGTCATCCGGCCACCGGCTACGTGTGATG 368
QY 144 tctgatcaaatgtctcgactgac 165
Db 369 TCTGATCTTTAGTCTTCTACAGC 390

RESULT 5
BG260311/c
LOCUS 602371427F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4479367 5',
DEFINITION mRNA sequence.
ACCESSION BG260311
VERSION BG260311.1 GI:12770127
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10311 row: f column: 08
High quality sequence stop: 736.
FEATURES
source
Location/Qualifiers
1..757
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4479367"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/notes="Organ: bladder; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by life technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 186 a 200 c 201 g 170 t
ORIGIN
Query Match 10.7%; Score 35.2; DB 174; Length 757;
Best Local Similarity 49.0%; Pred. No. 9.5;
Matches 94; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 137 tagaattctgatcaatgtctcgactgagcgccatccaaagaccagagagatgtga 196
Db 688 TGAAGCCCTCATAGTGGCGAGGCGCGCCGACCTTGTCCAGAGGGCCCAACGACTGGGGT 629
QY 197 aagcactgtctctcaaaagccgcgcagggatttccagtgaacgcagccgagacacca 256
Db 628 ATGTACTTTGACCCCAACAGCCATCTGGGATGAGCCGCTTTTTCAGCCACCATGCTTCAA 569
QY 257 aaattgaagtatccagttggtgtaaaaacctgtctcaacctatgtaaggggagtttatgcc 316
Db 568 ATTATCAGCATTTGAATTTGGTGAAGCCCACTTCTTTTGATGTGTGGATCTTCTGGCGGC 509
QY 317 atggaatttca 328
Db 508 CAGGAACCTTGA 497

```

RESULT 6

```

BF039993
LOCUS 462 bp mRNA EST 10-OCT-2000
DEFINITION BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA
clone BP250023B10D12 5', mRNA sequence.
ACCESSION BF039993
VERSION BF039993.1 GI:10757048
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 462)
AUTHORS Lewin,H.A., Soares,M.B., Rebeiz,M., Pardinas,J., Liu,L. and Larson
,J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector Trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR Primers
FORWARD: TAATACGACTCACTATAGGG
BACKWARD: ATTAACCCCTCACTAAAG
Insert Length: 462 Std Error: 0.00
Plate: BP250023B10 row: D column: 12
Seq primer: AGCGGATAACAATTTCACACAGGA
High quality sequence stop: 462.
FEATURES
source
Location/Qualifiers
1..462 ~
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250023B10D12"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/notes="Organ: placenta; Vector: pT7T3Pac; Site_1: EcoRI;
Site_2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 110 a 153 c 123 g 73 t 3 others
ORIGIN
Query Match 10.4%; Score 34.4; DB 143; Length 462;
Best Local Similarity 49.7%; Pred. No. 14;
Matches 86; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 25 ctcaagagctcattgagagctggtcaacatcacccagaaatccctctctgcaac 84
Db 113 CTGATGGAGTTTCAGTGAGCACCCTGCCCATCATCTCTGGAGGAGCAGCCGCTCCGACATCAGC 172
QY 85 ggcagcagtggtgagcgctcaacctgacccgcgcgcatgtactgcgagctctagaatct 144
Db 173 TCCACCTCGGCCAACACATCAACCAACACAGGAGCTGCTGCCCATCGAGCTGGACACC 232
QY 145 ctgatcaatgtctcgactgagcgccatccaaagaccagagagatgctgaa 197
Db 233 CTGGTGGCAAGGGCGCTTCCGCCGAGNTCTACAGGCCAAGCTGAAGCAGAA 285

```

```

RESULT 7
BE705147 LOCUS BE705147 507 bp mRNA EST 12-SEP-2000
DEFINITION Sc02_08f05_A Sc02_AAPC_ECORC_cold_stressed_winter_rye_seedlings
COMMENT Secale cereale cDNA clone Sc02_08f05, mRNA sequence.
ACCESSION BE705147
VERSION BE705147.1 GI:10093412
KEYWORDS EST.
SOURCE rye.
ORGANISM Secale cereale
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; Poideae; Triticeae;
Secale.
1 (bases 1 to 507)
Singh,J.A., Piche,C., Couroux,P., De Moors,A., Harris,L.J., Hattori
,J.I., Ouellet,T., Robert,L.S., Spratt,D. and Tinker,N.A.
Expressed Sequence Tags from Cold-Stressed Winter Rye Seedlings
Unpublished (2000)
Contact: Singh,J.A.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
960 Carling Avenue, Bldg. 20, Ottawa, Ontario, K1A 0C6, Canada
Tel: (613) 759-1662
Fax: (613) 759-1701
Email: singhja@em.agr.ca.
FEATURES
source
1..507
/organism="Secale cereale"
/cultivar="Puma (winter rye)"
/db_xref="taxon:4550"
/clone="Sc02_08f05"
/clone_lib="Sc02_AAPC_ECORC_cold_stressed_winter_rye_seedlings"
/tissue_type="leaf, crown"
/dev_stage="seedling three-leaf stage"
/note="Vector: Bluescript SK+/XhoI-EcoRI; Site_1: Eco RI; Site_2: Xho I; Sampled three-leaf seedlings treated for one week at 20C, 12 hrs light/day. Library made with Stratagene UNIZAP XR kit/(not packaged). cDNA is directly ligated into SK+/XhoI-EcoRI, then electroporated into TOP10 cells (Invitrogen)."
```

```

BASE COUNT 115 a 169 c 148 g 65 t 10 others
ORIGIN
Query Match 10.4%; Score 34.4; DB 138; Length 507;
Best Local Similarity 55.98; Pred. No. 15;
Matches 57; Conservative 4; Mismatches 41; Indels 0; Gaps 0;
QY 10 actccctcccaacccctcaaggagctcattgaggagctgtgtaacatcaccagaaatcag 69
DB 165 ACGCGTCCAGCACCRACARARCCCCACCGGAGGAGCGGACGACGAACAAACAC 224
QY 70 gcatccctctgcaacggcagcatgggtg9ggcg9tcaacctg 111
DB 225 GCGTCCCGCCGACTCCGGCGACCACTGGATGAAGAAGAHCA 266
RESULT 8
BE032541 LOCUS BE032541 535 bp mRNA EST 09-JUL-2000
DEFINITION 131940 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE032541
VERSION BE032541.1 GI:8327550
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 535)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
```

```

and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
FORWARD: AGGAACACGCTATGACCAT
BACKWARD: GTTTTCCAGTCACGACG
Plate: 63 row: E column: 8
Seq primer: ATTAGTGCACACTATAG.
FEATURES
source
1..535
/organism="Sus scrofa"
/db_xref="taxon:9823"
/clone_lib="MARC lPIG"
/tissue_type="pooled"
/lab_host="DHL08"
/note="Vector: pCMV SPORT6; Site_1: XbaI; Site_2: XhoI; Library made from pooled tissue from day 11, 13, 15, 20, and 30 embryos."
```

```

BASE COUNT 121 a 151 c 168 g 95 t
ORIGIN
Query Match 10.4%; Score 34.2; DB 161; Length 535;
Best Local Similarity 55.5%; Pred. No. 17;
Matches 66; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 4 cctgtgactccctcccaacccctcaaggagctcattgaggagctgtgtaacatcaccag 63
DB 227 CCTGTGACCACCCAGCGTCTACGATGACAAAGGCAATGAGAAGAGCATCACCGTGGCC 286
QY 64 atcaggcatccctctgcaacggcagcatgggtg9ggcg9tcaacctgaccgcgcgcat 122
DB 287 GATGAGGCGATCGGCCCAACACCCACCATGGAGGGCGCTGCCAACTGAAGCGTCTCT 345
RESULT 9
BE032543 LOCUS BE032543 546 bp mRNA EST 09-JUL-2000
DEFINITION 131942 MARC lPIG Sus scrofa cDNA 5', mRNA sequence.
ACCESSION BE032543
VERSION BE032543.1 GI:8327552
KEYWORDS EST.
SOURCE pig.
ORGANISM Sus scrofa
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
1 (bases 1 to 546)
Fahrenkrug,S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E.,
Stone,R.T., Heaton,M.P., Grosse,W.M., Bennett,G.A., Laegreid,W.W.
and Keele,J.W.
Design and use of two pooled tissue normalized cDNA libraries for
EST discovery in swine
Unpublished (2000)
Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
Tel: 402 762 4366
Fax: 402 762 4390
Email: smith@email.marc.usda.gov
Single pass sequencing. Bases called and alt_trimmed with phred
v0.980904.e. Vector identified by cross_match with the -minscore 18
and -minmatch 12 options.
PCR Primers
```


Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae
; Andropogoneae; Sorghum.

REFERENCE 1 (bases 1 to 562)
AUTHORS Cordonnier-Pratt, M.-M., Gingle, A., Marsala, C., Sudman, M. and Pratt, L.H.

TITLE An EST database from Sorghum: dark-grown seedlings

JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM

Department of Botany

The University of Georgia

Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA

Tel: 706 542 1860

Fax: 706 542 1805

Email: mmpratt@uga.edu

Sequences have been trimmed to exclude polyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.

Seq primer: JEN REV

High quality sequence stop: 560

POLYA=No.

FEATURES

source
1..562
Location/Qualifiers
/organism="Sorghum bicolor"
/db_xref="taxon:4558"
/clone_lib="Dark Grown 1 (DGL)"
/note="Organ: 5-day-old dark-grown seedlings; Vector: Lambda Zap; Site 1: XhoI; Site 2: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
130 a 174 c 187 g 71 t

BASE COUNT

ORIGIN
Query Match 10.3%; Score 34; DB 166; Length 562;
Best Local Similarity 56.1%; Pred. No. 20;
Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

QY 13 cctccccaacctcaggagctcattgagtggtgagcgtcaccatccacgaatcaggca 72
|||||
Db 171 CCTTCGGCGAGTCAAGGACGTCAAGACGCCGCTGGACAGTCCACGACGACCGC 230

QY 73 tccctctgaacggcagcattggtgagcgtcaccctgacccgcgcattac 126
|||||
Db 231 TCCTCGGCTTCGTCACCTTCCTTGTAGCGGAGGAGCGCGCGCTGCATGGAC 284

RESULT 15

BE127683
LOCUS DEPA1432 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5',
DEFINITION mRNA sequence.
ACCESSION BE127683
VERSION BE127683.1 GI:8550422
KEYWORDS EST.
SOURCE Norway rat.
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 341)
AUTHORS Sleeman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P., McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D.
TITLE Expressed sequence tags of cDNA clones from rat dermal papilla cells

JOURNAL Unpublished (2000)
COMMENT Contact: Sleeman MA
Biology
Genesis Research and Development Corporation Limited
P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand
Tel: 0064 9 373 5600
Fax: 0064 9 373 2189
Email: m.sleeman@genesis.co.nz
Seq primer: T3 forward

High quality sequence stop: 341.

source
1..341
Location/Qualifiers

/organism="Rattus norvegicus"

/strain="Dark-Agouti"

/db_xref="taxon:10116"

/clone_lib="Rat Lambda ZAP Express Library"

/tissue_type="vibrissae"

/cell_type="dermal papilla"

BASE COUNT 88 a 88 c 105 g 58 t 2 others

ORIGIN

Query Match 10.2%; Score 33.8; DB 163; Length 341;
Best Local Similarity 55.1%; Pred. No. 20;
Matches 65; Conservative 0; Mismatches 53; Indels 0; Gaps 0;
QY 1 agccctgtgactccctccccaacctcaggagctcattgaggagctggtcacaatcacc 60
|||||
Db 164 AGGCCGGTGGATCAGTACAGCAACCACTTCGTGCACGACTGTGTCAATATCACC 223
QY 61 cagaatcaggcatccctctgcaacggcagcagctggtgagcgtcaccctgacgcgcg 118
|||||
Db 224 ATCAAGCAGCATACAGTACCACCACCCAGGGGGGAGAACTTCACGGAGACCGNGC 281

Search completed: May 13, 2001, 11:40:59

Job time: 16534 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:25:22 ; Search time 9342.78 Seconds
(without alignments)
520.915 Million cell updates/sec

Title: US-09-451-527-106
Perfect score: 330
Sequence: 1 tctgaaattccatgcgcgat.....ggggaggaggtcacagggct 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 1283235 seqs, 7373929652 residues
Total number of hits satisfying chosen parameters: 2566470

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl.*
1: gb_ba1.*
2: gb_ba2.*
3: gb_ba3.*
4: gb_in1.*
5: gb_in2.*
6: gb_in3.*
7: gb_om.*
8: gb_ov.*
9: gb_pat1.*
10: gb_pat2.*
11: gb_ph.*
12: gb_pl1.*
13: gb_pl2.*
14: gb_pl3.*
15: gb_pl4.*
16: em_ba1.*
17: em_ba2.*
18: em_fun.*
19: em_htgo_hum.*
20: em_htgo_inv.*
21: em_htgo_rod.*
22: em_htg_hum1.*
23: em_htg_hum2.*
24: em_htg_hum3.*
25: em_htg_hum4.*
26: em_htg_hum5.*
27: em_htg_hum6.*
28: em_htg_hum7.*
29: em_htg_hum8.*
30: em_htg_inv1.*
31: em_htg_inv2.*
32: em_htg_other.*
33: em_htg_rod.*
34: em_hum1.*
35: em_hum2.*
36: em_hum3.*
37: em_hum4.*
38: em_hum5.*
39: em_hum6.*
40: em_hum7.*
41: em_in.*
42: em_om.*
43: em_or.*

44: em_ov.*
45: em_pat.*
46: em_ph.*
47: em_pl.*
48: em_ro.*
49: em_sts.*
50: em_sy.*
51: em_un.*
52: em_vi.*
53: gb_sts1.*
54: gb_sts2.*
55: gb_sts3.*
56: gb_sy.*
57: gb_un.*
58: gb_vil.*
59: gb_vil2.*
60: gb_vil3.*
61: gb_vil4.*
62: gb_vil5.*
63: gb_vil6.*
64: gb_vil7.*
65: gb_vil8.*
66: gb_vil9.*
67: gb_vil10.*
68: gb_vil11.*
69: gb_vil12.*
70: gb_vil13.*
71: gb_vil14.*
72: gb_vil15.*
73: gb_vil16.*
74: gb_vil17.*
75: gb_vil18.*
76: gb_vil19.*
77: gb_vil20.*
78: gb_vil21.*
79: gb_vil22.*
80: gb_vil23.*
81: gb_vil24.*
82: gb_vil25.*
83: gb_vil26.*
84: gb_vil27.*
85: gb_vil28.*
86: gb_vil29.*
87: gb_vil30.*
88: gb_vil31.*
89: gb_vil32.*
90: gb_vil33.*
91: gb_vil34.*
92: gb_vil35.*
93: gb_vil36.*
94: gb_vil37.*
95: gb_vil38.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
c 1	317	96.1	1302	7	AF244915
c 2	187.4	56.8	336	9	A29931
c 3	187.4	56.8	336	10	I58494
c 4	187.4	56.8	1270	93	HUMIL13A
c 5	187.4	56.8	1282	92	HSNC30
c 6	187.4	56.8	1290	10	I34548
c 7	185.8	56.3	336	9	A29930
c 8	185.8	56.3	336	10	I58481
c 9	185.8	56.3	417	88	AF043334
c 10	185.8	56.3	1297	9	A29948
c 11	185.8	56.3	1297	10	I58488

```
c 12 184.2 55.8 384 9 A29950
c 13 184.2 55.8 384 10 I58489
c 14 182.6 55.3 425 9 AR027065
c 15 182.6 55.3 425 9 AR027065
c 16 182.6 55.3 425 9 AR027065
c 17 182.6 55.3 425 9 AR027065
c 18 182.6 55.3 425 9 AR027065
c 19 163 49.4 343 7 AF072807
c 20 151.4 45.9 447 10 I58495
c 21 151.4 45.9 1207 94 MUSSTRPE
c 22 151.4 45.9 1212 10 I34549
c 23 140.8 42.7 443 94 RATIL13A
c 24 106.4 32.2 213343 78 AF276990
c 25 71.4 21.6 3714 93 HUM11DC9Z
c 26 71.4 21.6 4600 93 HUM11L13B
c 27 71.4 21.6 4740 93 HSU10307
c 28 71.4 21.6 5670 93 HSU31120
c 29 71.4 21.6 50282 85 AC004039
c 30 71.4 21.6 78469 75 AC074127
c 31 71 21.5 3395 73 HUM11DC98Z
c 32 70 21.2 3520 7 BTA132441
c 33 58.4 17.7 78469 75 AC074127
c 34 51.6 15.6 4376 94 MUS11L13A
c 35 49.4 15.0 142732 88 AC084392
c 36 49.4 15.0 159500 94 AC005742
c 37 49.4 15.0 237823 66 AC020886
c 38 40.8 12.4 38390 3 SC2H12
c 39 37 11.8 13684 94 MUSGABAT
c 40 37 11.2 39739 3 SCD16A
c 41 36.8 11.2 185300 2 AP000063
c 42 36.6 11.1 51440 12 AB025632
c 43 36.4 11.0 2437 3 SNAJ3310
c 44 36.4 11.0 2437 3 SAU77894
c 45 36.2 11.0 3073 94 AF195788
```

ALIGNMENTS

```
RESULT 1
AF244915/c
LOCUS AF244915 1302 bp mRNA MAM 16-OCT-2000
DEFINITION Canis familiaris Interleukin-13 mRNA, complete cds.
ACCESSION AF244915
VERSION AF244915.1 GI:7528273
KEYWORDS
SOURCE dog.
ORGANISM Canis familiaris
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
REFERENCE 1 (bases 1 to 1302)
AUTHORS Yang,S., Borroughs,K.L. and McDermott,M.J.
TITLE Canine Interleukin-13: molecular cloning of full-length cDNA and
expression of biologically active recombinant protein
JOURNAL J. Interferon Cytokine Res. 20 (9), 779-785 (2000)
MEDLINE 20485146
PUBMED 11032397
REFERENCE 2 (bases 1 to 1302)
AUTHORS Yang,S.
TITLE Direct Submission
JOURNAL Submitted (13-MAR-2000) Allergy and Immunology, Heska Corporation,
1613 Prospect Parkway, Fort Collins, CO 80525, USA
FEATURES
source
1..1302
/organism="Canis familiaris"
/db_xref="taxon:9615"
1..51
52..447
/codon_start=1
/product="interleukin-13"
/protein_id="AAF63204.1"
/db_xref="GI:7528274"
/translation="MAWLFTVVIATCLGLGLASPVTPSPFLKELIEELVNIQNQA
```

```
SLCNGSMVSVNLTAGMYCAALESILNVDCAIORQLKALCSQKPAAGQISSER
SDTKTEVLIQLVKNLLTYRGVYRHGNFR"
448..1302
BASE COUNT 337 a 318 c 340 g 307 t
ORIGIN
Query Match 96.1%; Score 317; DB 7; Length 1302;
Best Local Similarity 99.1%; Pred. NO. 1.1e-72;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 tctgaatttccatgcatgataactcccttaccatagtgagcaggtttttccaccaactg 60
|||||
DB 444 TCTGAATTTCCATGCGGATAAATCCCTTACATAGGTAGCAGGTTTTCACCACTG 385
QY 61 gatcaattcaatttgggtctcggtcggttcactggaat---ccctgcgcgggctt 117
|||||
DB 384 GATCACTTCAATTTGGTGCTCGGCTGCCTTCACTGGAATCTGCCCTCCGCGGCTT 325
QY 118 ttgagagcacagtgcttcaagatcctctgggttccttggatggcgtcagtcgagac 177
|||||
DB 324 TTGAGAGCACAGTGCTTTCAGCATCTCTGGGTCCTTTGGATGCGCTGCGAGAGAC 265
QY 178 attgatcagagattctagagctcgcagcatatgccggtcaggttgacgtccacac 237
|||||
DB 264 ATTGATCAGAGATTCTAGAGCTCGCAGTACATGCCGCGGTGAGTTGACGCTCCACAC 205
QY 238 catgtcgcgtttgcagaggtatgcctgattctgggtgatgttgaccagctccctcaatgag 297
|||||
DB 204 CATGCTGCCGTTGCAGAGGATGCTTGTGGTGATGTTGACCACTCTCTCAATGAG 145
QY 298 ctcttgaggggttgaggaggagtcacacagggt 330
|||||
DB 144 CTCTTTGAGGGTTGGGAGGAGTACACAGGGCT 112
```

RESULT 2

```
A29931/c
LOCUS A29931 336 bp DNA PAT 23-JUN-1995
DEFINITION Sequence coding for the mature cytokine like protein.
ACCESSION A29931
VERSION A29931.1 GI:1249019
KEYWORDS synthetic construct.
SOURCE synthetic construct.
ORGANISM artificial sequence.
REFERENCE 1 (bases 1 to 336)
AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le
Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.
TITLE Protein having cytokin type activity, recombinant DNA coding for
this protein, transformed cells and microorganisms
JOURNAL Patent: EP 0506574-A 3 30-SEP-1992;
ELF SANOFI
FEATURES
source
1..336
/organism="synthetic construct"
/db_xref="taxon:32630"
BASE COUNT 80 a 95 c 90 g 71 t
ORIGIN
Query Match 56.8%; Score 187.4; DB 9; Length 336;
Best Local Similarity 76.9%; Pred. NO. 9.3e-39;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
QY 3 tgaatttccatgcatgataactcccttaccatagtgagcaggtttttccaccaactgga 62
|||||
DB 334 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAGAGCAGGTCCTTTACAACTGGG 275
QY 63 tcaattcaatttgggtctcggtcgtctcactgaaa---tccctgcgcgggctttt 119
|||||
DB 274 CCACCTCGATTGTTGGTGCTCGGAGACATGCAGTGGGAAACTGCCCACTGAGACCTTGT 215
```


AUTHORS Minty,A.J.
 TITLE Direct Submission
 JOURNAL Submitted (02-NOV-1992) A.J. Minty, Sanofi-Elf Bio Recherches, Labège Inopole, Vole 1, BP 137, 31676 Labège Cedex, FRANCE
 REFERENCE 2 (bases 1 to 1282)
 AUTHORS Minty,A.J., Chailon,P., Derocq,J.M., Dumont,X., Guillemot,J.C., Kaghad,M., Labit,C., Leplatois,P., Liauzun,P., Miloux,B., Minty,C., Casellas,P., Loison,G., Lupker,J., Shire,D., Ferrara,P. and Caput,D.
 TITLE Interleukin-13 is a new human lymphokine regulating inflammatory and immune responses
 JOURNAL Nature 362 (6417), 248-250 (1993)
 MEDLINE 93211479
 FEATURES
 source Location/Qualifiers
 1..1282
 /organism="Homo sapiens"
 /db_xref="taxon:9606"
 /chromosome="5q 23-31"
 /cell_type="peripheral blood lymphocytes"
 15..455
 /gene="NC30"
 /gene="NC30"
 /product="NC30; alternative"
 /gene="NC30"
 /note="alternative; ATG at 15 is an alternative start codon"
 /codon_start=1
 /evidence=experimental
 /protein_id="CAA48823.1"
 /db_xref="GI:580330"
 /db_xref="SWISS-PROT:P35225"
 /translation="MHPLNPLLLALGLMALLTTVIALTCLGFGFASPGVPVPPSTALR ELIEELVNITQNKAPICNGSMVMSINLTAGMYCAALESINVSQSAIEKTRMLSG FCPHKVSAGQFSSLVHVRDTKIEVAQFVKDLLLHLKLFREGREN"
 57..455
 /gene="NC30"
 /note="alternative; ATG at 15 is an alternative start codon"
 /codon_start=1
 /evidence=experimental
 /protein_id="CAA48824.1"
 /db_xref="GI:673420"
 /db_xref="SWISS-PROT:P35225"
 /translation="MALLLTVIALTCLGFGFASPGVPVPPSTALRELIEELVNITQNK APLCNGSMVMSINLTAGMYCAALESINVSQSAIEKTRMLSGFCPHKVSAGQFSSL HVDRTKIEVAQFVKDLLLHLKLFREGREN"
 57..116
 /gene="NC30"
 /product="NC30; alternative"
 /gene="NC30"
 /evidence=experimental
 238
 /gene="NC30"
 /replace="a"
 /note="ATTTA motif"
 856..860
 /note="ATTTA motif"
 873..877
 /note="ATTTA motif"
 1134..1138
 /note="ATTTA motif"
 1153..1157
 /note="ATTTA motif"
 1264..1269
 /note="ATTTA motif"
 polyA_signal 293 a 341 c 337 g 311 t
 BASE COUNT 293 a 341 c 337 g 311 t
 ORIGIN
 Query Match 56.8%; Score 187.4; DB 92; Length 1282;
 Best Local Similarity 76.9%; Pred. No. 8.5e-39;
 Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 3 tgaatttccatggcgataaactcccttaccataggtgagcaggtttttccaccaactgga 62
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 450 TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGACGAGTCTCTTTACAACTGGG 391
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 63 tcaattcaattttggtgtctcggtcggttcactggaaa---tccctgcccggcggtttt 119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 390 CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAAACTGCCACGCTGAGACCTTGT 331
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 120 gagagcacagtgctttcagcatctctgggtcctcttgatggcgctgcagtcgagacat 179
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 330 GCGGCGAGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCCTGACACGT 271
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 180 tgatcagagattctagagctgcgcagtcacatgcgcggcggttcaggttgacgtccacacca 239
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 270 TGATCAGGATTCAGGGCTGCACAGTACATGCCAGCTGCAGCTTGATGCTCCATACCA 211
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 240 tgcgtccgttcagagggatgc---ctgattctgggtgatgtgaccagctctccaatga 296
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 210 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTCTGGGTGATGTTGACCAGCTCCTCAATGA 151
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 297 gctccttgagggttgggaggaggtcacagggc 329
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 150 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 118
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 RESULT 6
 LOCUS I34548 1290 bp DNA PAT 06-FEB-1997
 DEFINITION Sequence 1 from patent US 5596072.
 ACCESSION I34548
 VERSION I34548.1 GI:1825339
 KEYWORDS
 SOURCE Unknown.
 ORGANISM Unknown.
 REFERENCE
 1 (bases 1 to 1290)
 AUTHORS Culpepper,J., McKenzie,A., Dang,W. and Zurawski,G.
 TITLE Method of refolding human IL-13
 JOURNAL Patent: US 5596072-A 1 21-JAN-1997;
 FEATURES
 Location/Qualifiers
 source 1..1290
 /organism="unknown"
 BASE COUNT 308 a 335 c 336 g 311 t
 ORIGIN
 Query Match 56.8%; Score 187.4; DB 10; Length 1290;
 Best Local Similarity 76.9%; Pred. No. 8.5e-39;
 Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;
 QY 3 tgaatttccatggcgataaactcccttaccataggtgagcaggtttttccaccaactgga 62
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 438 TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGACGAGTCTCTTTACAACTGGG 379
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 63 tcaattcaattttggtgtctcggtcggttcactggaaa---tccctgcccggcggtttt 119
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 378 CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAAACTGCCACGCTGAGACCTTGT 319
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 120 gagagcacagtgctttcagcatctctgggtcctcttgatggcgctgcagtcgagacat 179
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 318 GCGGCGAGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCCTGACACGT 259
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 180 tgatcagagattctagagctgcgcagtcacatgcgcggcggttcaggttgacgtccacacca 239
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 258 TGATCAGGATTCAGGGCTGCACAGTACATGCCAGCTGTGAGGTGATGCTCCATACCA 199
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 240 tgcgtccgttcagagggatgc---ctgattctgggtgatgtgaccagctctccaatga 296
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 Db 198 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTCTGGGTGATGTTGACCAGCTCCTCAATGA 139
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
 QY 297 gctccttgagggttgggaggaggtcacagggc 329
 ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 138 GCTCCTGAGGCTGTAGAGGAGGCACAGGGC 106

RESULT 7

LOCUS A29930 336 bp DNA PAT 23-JUN-1995

DEFINITION Sequence coding for the mature cytokine like protein.

ACCESSION A29930

VERSION A29930.1 GI:1249018

KEYWORDS synthetic construct.

SOURCE synthetic construct.

ORGANISM 1 (bases 1 to 336)

REFERENCE 1 (bases 1 to 336)

AUTHORS Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le

TITLE Bouteiller,C., Leplatois,P., Magazin,M. and Minty,A.

PROTEIN having cytokine type activity, recombinant DNA coding for

JOURNAL this protein, transformed cells and microorganisms

PATENT: EP 0506574-A 2 30-SEP-1992;

ELF SANOFI

FEATURES

source Location/Qualifiers

1..336

/organism="synthetic construct"

/db_xref="taxon:32630"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 56.3%; Score 185.8; DB 9; Length 336;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

Qy 3 tgaatttcattggtgctgcgcgttcacatgagtgagcaggtttttccacaaactgga 62

Db 334 TCAACCGTCCCTCCGCGGAAAGTTCTTTAAATGTAAGAGCAGGTCTCTTTACAACACTGGG 275

Qy 63 tcaattcaatttgggtgctgcgcgttcacatgagtgagcaggtttttccacaaactgga 119

Db 274 CCACCTCGATTTGGTGTCTCGGACATGCAAGCTGGAAGAGCAGGTCTCTTTACAACACTGGG 215

Qy 120 gagagcacagtgcttcacacatcctcgtggttcacatgagtgagcaggtttttccacaaactgga 179

Db 214 GCGGCGAGATCCCGCTCAGCATCTCTGGGTCTCTCGATGSCACTGCAGCCTGACACGT 155

Qy 180 tgatcagagattcttagagctgcgcgttcacatgagtgagcaggtttttccacaaactgga 239

Db 154 TGATCAGGATTCAGGCTGCGGCTGACAGTACATGTCTGATGTCAGCTGTCAGCTGTCACCA 95

Qy 240 tgcctcaggttgcagaggtatgc---ctgattctgggtgctgcgcgttcacatgagtgagcaggtttttccacaaactgga 296

Db 94 TGCTGCCATTGCGAGCGGAGCCTCTCTGGGTCTCTGGGTGATGTGACAGCTCTCTCAATGA 35

Qy 297 gctccttgaggttgggaggtgagtcacagggc 329

Db 34 GCTCCTGAGGCTGTAGAGGAGGCACAGGGC 2

RESULT 9

LOCUS AF043334/c 417 bp mRNA PRI 21-FEB-1998

DEFINITION Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.

ACCESSION AF043334

VERSION AF043334.1 GI:2905619

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 417)

AUTHORS Jang,J.S. and Kim,B.E.

TITLE Direct Submission

JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea

COMMENT Nested PCR:

1) first PCR :

forward primer (5'-ctcaatcctcctctgttgca-3')

reverse primer (5'-tagtcaggtctgtctgtgc-3')

2) second PCR :

forward primer (5'-ctcatggcgtttgttgaccag-3')

reverse primer (5'-gatgcttcgaagtttcagttaa-3').

Location/Qualifiers

1..417

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_type="PHA-treated peripheral blood leukocyte"

1..417

/gene="IL13"

1..24

/gene="IL13"

/note="second PCR"

/PCR_conditions="94C-lmin, 50C-lmin, 72C-3min, 30 cycles; DeltaCycler II from Ericomp"

4..402

CDS

FEATURES

source Location/Qualifiers

1..336

/organism="unknown"

BASE COUNT 81 a 95 c 89 g 71 t

ORIGIN

Query Match 56.3%; Score 185.8; DB 10; Length 336;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

Qy 3 tgaatttcattggtgctgcgcgttcacatgagtgagcaggtttttccacaaactgga 62

Db 334 TGAACCGTCCCTCCGCGGAAAGTTCTTTAAATGTAAGAGCAGGTCTCTTTACAACACTGGG 275

Qy 63 tcaattcaatttgggtgctgcgcgttcacatgagtgagcaggtttttccacaaactgga 119

Db 274 CCACCTCGATTTGGTGTCTCGGACATGCAAGCTGGAAGAGCAGGTCTCTTTACAACACTGGG 215

Qy 120 gagagcacagtgcttcacacatcctcgtggttcacatgagtgagcaggtttttccacaaactgga 179

Db 214 GCGGCGAGATCCCGCTCAGCATCTCTGGGTCTCTCGATGSCACTGCAGCCTGACACGT 155

Qy 180 tgatcagagattcttagagctgcgcgttcacatgagtgagcaggtttttccacaaactgga 239

Db 154 TGATCAGGATTCAGGCTGCGGCTGACAGTACATGTCTGATGTCAGCTGTCAGCTGTCACCA 95

Qy 240 tgcctcaggttgcagaggtatgc---ctgattctgggtgctgcgcgttcacatgagtgagcaggtttttccacaaactgga 296

Db 94 TGCTGCCATTGCGAGCGGAGCCTCTCTGGGTCTCTGGGTGATGTGACAGCTCTCTCAATGA 35

Qy 297 gctccttgaggttgggaggtgagtcacagggc 329

Db 34 GCTCCTGAGGCTGTAGAGGAGGCACAGGGC 2

RESULT 9

LOCUS AF043334/c 417 bp mRNA PRI 21-FEB-1998

DEFINITION Homo sapiens interleukin 13 precursor (IL13) mRNA, complete cds.

ACCESSION AF043334

VERSION AF043334.1 GI:2905619

KEYWORDS human.

SOURCE

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.

REFERENCE 1 (bases 1 to 417)

AUTHORS Jang,J.S. and Kim,B.E.

TITLE Direct Submission

JOURNAL Submitted (15-JAN-1998) Protein Engineering, General Institute of Technology, Hyundai Pharm. Ind. Co., Ltd., 213 Sosa Bon 1-dong, Sosa-gu, Bucheon 422-231, Korea

COMMENT Nested PCR:

1) first PCR :

forward primer (5'-ctcaatcctcctctgttgca-3')

reverse primer (5'-tagtcaggtctgtctgtgc-3')

2) second PCR :

forward primer (5'-ctcatggcgtttgttgaccag-3')

reverse primer (5'-gatgcttcgaagtttcagttaa-3').

Location/Qualifiers

1..417

/organism="Homo sapiens"

/db_xref="taxon:9606"

/cell_type="PHA-treated peripheral blood leukocyte"

1..417

/gene="IL13"

1..24

/gene="IL13"

/note="second PCR"

/PCR_conditions="94C-lmin, 50C-lmin, 72C-3min, 30 cycles; DeltaCycler II from Ericomp"

4..402

CDS

/gene="IL13"
/codon_start=1
/product="interleukin 13 precursor"
/protein_id="AAC03535.1"
/db_xref="GI:2903620"
/translation="MALILTTVIALTCLGGFASPGVPPSTALRELIELVNITONQK
APLCNGSMVSNILTAGMYCAALESILNVSGCSAIEKTMRLGFCFKVKSAGQFSSL
HVRDTKIEVAQFVKDLLHLKLFREGFN"

sig_peptide

4..63

/gene="IL13"

mat_peptide

64..399

/gene="IL13"

primer_bind

/product="interleukin 13"

complement(394..417)

/note="second PCR"

91 a 121 c 108 g 97 t

BASE COUNT

ORIGIN

Query Match 56.3%; Score 185.8; DB 88; Length 417;

Best Local Similarity 76.6%; Pred. No. 2.4e-38;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

Qy 3 tgaattccatggcgataaaactcccttacataggtgagcaggtttttccaccaactgga 62

Db 397 TGAACCGTCCCTCGCGAAGTTCCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 338

Qy 63 tcaattcaatttgggtgtcgtcggtcgtctcactgga---tccctgcgcgggctttt 119

Db 337 CCACCTCGATTGGTGTCTCGGACATGCAAGCTGGAAACTGCCACGTGAGACCTTGT 278

Qy 120 gagagcacagtgtcttcagcatcctctgggtccttggatggcgtgagtcggagacat 179

Db 277 GCGGSCAGAAATCCGCCAGCATCCCTCTGGGTCTTCGATGGCACTGCGACCTGACACGT 218

Qy 180 tgalcagagattctagactcgcagatcacatccgcgcgcgcaggtgagtcgcctccacaca 239

Db 217 TGATCAGGAGTTCAGGGCTGCACAGTACATCCAGCTGTCTGAGTTGATGCTCCAAACCA 158

Qy 240 tgcctgcgttcagaggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296

Db 157 TGCTGCCATTGCAGAGCGAGCCCTCTGTTCTGGTGTGATGTTGACCACTCTCAATGA 98

Qy 297 gctccttgagggttgggagggagtcacagggc 329

Db 97 GCTCCCTGAGGCTGTAGAGGAGGCACAGGGC 65

RESULT 10

A29948/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

CDS

/db_xref="taxon:32630"

15..455

/codon_start=1

/transl_table=11

/product="protein with cytokine like activity"

/db_xref="taxon:32630"

15..455

/codon_start=1

/transl_table=11

/product="protein with cytokine like activity"

/db_xref="taxon:32630"

15..455

/protein_id="CAA01982.1"

/db_xref="GI:1249029"

/translation="MHPLNPLLLAALGMLALLTTVIALTCLGGFASPGVPPSTALR
ELIEELVNITONQKAPLCNGSMVSNILTAGMYCAALESILNVSGCSAIEKTMRLG
FCFKVKSAGQFSSLHVRDTKIEVAQFVKDLLHLKLFREGFN"

BASE COUNT 309 a 341 c 336 g 311 t

ORIGIN

Query Match

Best Local Similarity 56.3%; Score 185.8; DB 9; Length 1297;

Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

Qy 3 tgaattccatggcgataaaactcccttacataggtgagcaggtttttccaccaactgga 62

Db 450 TGAACCGTCCCTCGCGAAGTTCCTTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 391

Qy 63 tcaattcaatttgggtgtcgtcggtcgtctcactgga---tccctgcgcgggctttt 119

Db 390 CCACCTCGATTGGTGTCTCGGACATGCAAGCTGGAAACTGCCACGTGAGACCTTGT 331

Qy 120 gagagcacagtgtcttcagcatcctctgggtccttggatggcgtgagtcggagacat 179

Db 330 GCGGSCAGAAATCCGCCAGCATCCCTCTGGGTCTTCGATGGCACTGCGACCTGACACGT 271

Qy 180 tgaatcagattctagactcgcagatcacatccgcgcgcgcaggtgagtcgcctccacaca 239

Db 270 TGATCAGGAGTTCAGGGCTGCACAGTACATCCCTCTGGGTCTTCGATGGCACTGCGACCTGACACCA 211

Qy 240 tgcctgcgttcagaggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296

Db 210 TGCTGCCATTGCAGAGCGAGCCCTCTGTTCTGGTGTGATGTTGACCACTCTCAATGA 151

Qy 297 gctccttgagggttgggagggagtcacagggc 329

Db 150 GCTCCCTGAGGCTGTAGAGGAGGCACAGGGC 118

RESULT 11

158488/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

FEATURES

source

BASE COUNT

ORIGIN

Query Match

Best Local Similarity

Matches

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy

Db

Qy	120	gagagcagtgcttttcagcatctctgggtcctttggatggcgctgcagtcggagacat	179
Db	330	GCGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCATTGCAGCTGACACGT	271
Qy	180	tgatcagaagattctcagagctgcgcagtcacatgcggcgsgtcaggttgacgctcacacca	239
Db	270	TGATCAGGGATTCAGGGCTGCCACGTACATGTTCAGCTGTCAGGTTGATGCTCCATACCA	211
Qy	240	tgctgcgcttgccagaggatgc---ctgattctgggtgagtgtgaccagctccctcaatga	296
Db	210	TGCTGCCATTGCAGCGGAGGCTTCTGGTCTCGGTGATGTCACCAAGCTCCCTCAATGA	151
Qy	297	gctccttgagggttgggaggaggatcacagggc	329
Db	150	GCCTCCTTGAGGGCTGTAGAGGGAGGCACAGGC	118

RESULT	12			
A29950/c				
LOCUS	A29950	384 bp	DNA	PAT
				23-JUN-1995

LOCUS	A29950	384 bp	DNA	PAT#	23-JUN-1995
DEFINITION	Nucleic acid fragment B.				
ACCESSION	A29950				
VERSION	A29950.1	GI:1249030			
KEYWORDS	.				
SOURCE	synthetic construct.				
ORGANISM	synthetic construct				
	artificial sequence.				
REFERENCE	1 (bases 1 to 384)				
AUTHORS	Caput,D., Ferrara,P., Guillemot,J.C., Kaghad,M., Labit-le Boutellier,C., Leplatols,P., Magazin,M. and Minty,A.				
TITLE	Protein having cytokin type activity, recombinant DNA coding for this protein, transformed cells and microorganisms				
JOURNAL	Patent: EP 0506574-A 23 30-SEP-1992;				

FEATURES	Location/Qualifiers
source	1. .384
	/organism="synthetic construct"
	/db_xref="taxon:32630"
BASE COUNT	97 a 104 c 99 g 84 t
ORIGIN	
Query Match	55.88; Score 184.2; DB 9;
Best Local Similarity	76.3%; Pred. No. 6,3e-38;
Matches 254; Conservative	0; Mismatches 73; Indels 6; Gaps 2;

Query Match 55.8%; Score 184.2; DB 9; Length 384;
 Best Local Similarity 76.3%; Pred.No. 6.3e-38;
 Matches 234; Conservative 0; Mismatches 73; Indels 6; Gaps

QY 3 tgaatttcctggcgataaacctccctcacatagctgagcagggttttccaccactgga 62
 |||||
 Db 355 TGAACCGTCCCTCGCAAAAGTTCTTTAAATGTAAGAGCAGGTCTTTACAACTGGG 296
 |||||

	Qy	Db	Qy	Db
63	tcacttcaaat	ttttggtg	tctcggtg	cgcttcactg
	gaaa---	tcctctgc	cgcgact	tttt
119				
295	ccacctcgat	ttttggtg	tctcgacat	cgcaatg
	gcaactg	gcaactg	gcaactg	gcaactg
236				
120	gagacacag	tgtcttcag	catctctg	ggtgctt
	ggatg	ggtg	gctgcag	tgcggag
179				
235	gcsgggaga	aatccgct	cagcatcct	ctgggtctt
	cttcgcat	gttcgcat	gttcgcat	gttcgcat
176				

OY	180	tgatcagagattctaaagctgcacagcacatgccggcggtcaaggttgacgctccacaca	239
Db	175	TGATCAGGGATTCCAGGGCTGCACATCATGTCAAGTCTCAGGTTGATGCTCCATACA	116
OY	240	tgtcgctgttcagagaggaatgc---ctgattcttggtgtagtctgaccagctcctcaaaga	296
Db	115	TGCTGCCATTTCAGACGGAGCGCCTCTGGTCTTGCGGTGATGTTGACACGCTCCTCAATGA	56

Qy 297 gtccttgagggttgaggaggagtcacagggc 329
||||| ||||| ||||| ||||| ||||| |||||
Db 55 GTCCTCTGAGGGCCGTAGAGGGAGGCACAGGGC 23

RESULT 13
T58489/C

LOCUS	I58489	384 bp	DNA		07-OCT-1997
DEFINITION	Sequence 17 from patent US 5652123.				
ACCESSION	I58489				
VERSION	I58489.1 GI:2477727				
KEYWORDS	Unknown.				
SOURCE	Unknown.				
ORGANISM	Unclassified.				
REFERENCE	1 (bases 1 to 384)				
AUTHORS	Caput,D., Ferrara,P., Guillemot,J., Kaghad,M., Labit-Le Boutellier,C., Leplatois,P., Magazin,M. and Minty,A.				
TITLE	Protein having interleukin 13 activity, recombinant DNA coding for this protein, transformed cells and microorganisms				
JOURNAL	Patent: US 5652123-A 17 29-JUL-1997;				
FEATURES	Location/Qualifiers				
source	1..384				
	/organism="unknown"				
BASE COUNT	97	a	104	c	99 g
ORIGIN	84 t				

Query Match	55.8%	Score 184.2;	DB 10;	Length 384;
Best Local Similarity	76.3%	Pred. No. 6.3e-38;		
Matches 254;	Conservative	0;	Mismatches 73;	Indels 6;
				Gaps 2;

Qy 3 tgaatttcacatgcgataaacctcccttacatagtgagcagggttttccaccaactgga 62
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 355 TGAACCGTCCCTCGCGAAAAGTTCTTTAAATGTATAGAGCAGGTCCTTTACAACCTGGG 296

Qy 63 tcacttcaattttggtgtctcgcgttcactggaaa--tccctgccgcggcctttt 119
||| || | ||||| ||||| | ||||| ||| ||| |||
Db 295 CCACCTCGATTTTGGTGTCGCGGACATGCACAGCTGGAAAACGCCCCAGCTGAGACCTTGT 236

Qy 120 gagagcacagtgccttcagcatcctctgggtctcttgatgacgctgcagtcggagacat 179
| | | | | | | | | | | | | | | | | | | | | |
Db 235 GCGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTGCATGGCACTGCACGCCACACGT 176

Oy 180 tgatcagagattcttagagctgcgcatatgccggcggtcaggttgacgctccaccca 239
||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 175 TGATCAGGGATTCCAGGGGTCACACATACATGCAGCTGTCAAGTTGATGCTCATACCA 116

Qy 240 tgctgcggttcagaggatgc--ctgattctgggtgatgttgaccagctcctcaatga 296
||||| ||||| || | ||||| ||||| ||||| ||||| ||||| |||||
Db 115 TGCTGCCATTGCAGAGCGGAGCCTTCTGGTTCGTGGTGATGTTGACCACCTCCTCAATGA 56

QY 297 gctcctttaggggttgaggaggagtcacagggc 329
||||| ||||| | ||||| ||||| |||||
Db 55 GCTCCCTGAGGGCCGTAGAGGAGGCACAGGGC 23

RESULT	14
AR027065/c	
LOCUS	AR027065
DEFINITION	Sequence 4
ACCESSION	AR027065
VERSION	AR027065.1
KEYWORDS	GI:5937905
	DNA
	PAT
	29-SEP-1999

SOURCE
Unknown.

ORGANISM
Unclassified.

REFERENCE
1 (bases 1 to 425)

AUTHORS
Legoux, R., Maldonado, P. and Salome, M.

TITLE
Method for the extraction of periplasmic proteins from prokaryotic microorganisms in the presence of arginine

JOURNAL
Patent: US 5856142-A 4 05-JAN-1999;

FEATURES	source	Location/Qualifiers
		1. .425
		/organism="unknown"
BASE COUNT	100 a	116 c 110 g 99 t

Query Match 55.3%; Score 182.6; DB 9; Length 425;

Best Local Similarity 76.0%; Pred. No. 1.6e-37;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

```
Qy 3 tgaatttcacatgagcgtacacccctccctacatgagcaggtttttccacaaactgga 62
Db 397 TGAACCGTCCCTCGCGAAAAAGTTTCTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 338
Qy 63 tcaactcaattttggtctgcgtgcgttcaactgaaa---tccctgcgcgggctttt 119
Db 337 CCACCTCGATTTTGGTGCTCGGACATGCAAGCTGGAAACTGCCACAGCTGAGACCTTGT 278
Qy 120 gagagcacagtgtcttcagcatcctctgggtcctttgtagtgcgtgcagtcgagagacat 179
Db 277 GCGGCAGAAATCCGCTCAGCATCCTCTCGGTCTTCTCGATGGCACTGCAGCCTGACACGT 218
Qy 180 tgatcagagattctagagctgcgcagtcacatcccgcggtcaggttgacgctccacacca 239
Db 217 TGATCAGGGATTCCAGGCTGCACAGTACATGCCAGCTGTGAGGTTGATGCTCCATACCA 158
Qy 240 tgcctgcgttcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
Db 157 TCGTCCCATTCAGAGCGAGGCTTCTGCTTCTGGGTGATGTTGACCACTCCTCAATGA 98
Qy 297 gctcctgaggttgaggagaggtcacagggc 329
Db 97 GCTCCTGAGGCGACTACTGGGAGGCACAGGGC 65
```

RESULT 15

LOCUS I86198 425 bp DNA PAT 10-JUN-1998
DEFINITION Sequence 4 from patent US 5700665.
ACCESSION I86198
VERSION I86198.1 GI:3205916
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE
1 (bases 1 to 425)
Legoux,R., Maldonado,P. and Salome,M.
AUTHORS Method for the extraction of periplasmic proteins from prokaryotic
TITLE microorganisms in the presence of arginine
JOURNAL Patent: US 5700665-A 4 23-DEC-1997;
FEATURES
source
1. 425
/organism="unknown"
BASE COUNT 100 a 116 c 110 g 99 t
ORIGIN

Query Match 55.3%; Score 182.6; DB 10; Length 425;
Best Local Similarity 76.0%; Pred. No. 1.6e-37;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;

```
Qy 3 tgaatttcacatgagcgtacacccctccctacatgagcaggtttttccacaaactgga 62
Db 397 TGAACCGTCCCTCGCGAAAAAGTTTCTTAAATGTAAGAGCAGGTCCTTTACAAACTGGG 338
Qy 63 tcaactcaattttggtctgcgtgcgttcaactgaaa---tccctgcgcgggctttt 119
Db 337 CCACCTCGATTTTGGTGCTCGGACATGCAAGCTGGAAACTGCCACAGCTGAGACCTTGT 278
Qy 120 gagagcacagtgtcttcagcatcctctgggtcctttgtagtgcgtgcagtcgagagacat 179
Db 277 GCGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT 218
Qy 180 tgatcagagattctagagctgcgcagtcacatcccgcggtcaggttgacgctccacacca 239
Db 217 TGATCAGGGATTCCAGGCTGCACAGTACATGCCAGCTGTGAGGTTGATGCTCCATACCA 158
Qy 240 tgcctgcgttcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
Db 157 TCGTCCCATTCAGAGCGGAGGCTTCTGCTTCTGGGTGATGTTGACCACTCCTCAATGA 98
```

Qy 297 gctccttgaaggttgaggagggaggtcacagggc 329
Db 97 GCTCCTGAGGCGACTACTGGGAGGCACAGGGC 65

Search completed: May 13, 2001, 14:25:24
Job time: 19404 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:30:26 ; Search time 472.02 Seconds

(without alignments)
408.135 Million cell updates/sec

Title: US-09-451-527-106

Perfect score: 330

Sequence: 1 tctgaatttcctgcgat.....ggggaggaggtcacagggct 330

Scoring table:

IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 678276 seqs, 291890651 residues

Total number of hits satisfying chosen parameters: 1356552

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N_Geneseq_0401.*

- 1: /cgnl_8/gcgdata/geneseq/geneseq/NA1980.DAT.*
- 2: /cgnl_8/gcgdata/geneseq/geneseq/NA1981.DAT.*
- 3: /cgnl_8/gcgdata/geneseq/geneseq/NA1982.DAT.*
- 4: /cgnl_8/gcgdata/geneseq/geneseq/NA1983.DAT.*
- 5: /cgnl_8/gcgdata/geneseq/geneseq/NA1984.DAT.*
- 6: /cgnl_8/gcgdata/geneseq/geneseq/NA1985.DAT.*
- 7: /cgnl_8/gcgdata/geneseq/geneseq/NA1986.DAT.*
- 8: /cgnl_8/gcgdata/geneseq/geneseq/NA1987.DAT.*
- 9: /cgnl_8/gcgdata/geneseq/geneseq/NA1988.DAT.*
- 10: /cgnl_8/gcgdata/geneseq/geneseq/NA1989.DAT.*
- 11: /cgnl_8/gcgdata/geneseq/geneseq/NA1990.DAT.*
- 12: /cgnl_8/gcgdata/geneseq/geneseq/NA1991.DAT.*
- 13: /cgnl_8/gcgdata/geneseq/geneseq/NA1992.DAT.*
- 14: /cgnl_8/gcgdata/geneseq/geneseq/NA1993.DAT.*
- 15: /cgnl_8/gcgdata/geneseq/geneseq/NA1994.DAT.*
- 16: /cgnl_8/gcgdata/geneseq/geneseq/NA1995.DAT.*
- 17: /cgnl_8/gcgdata/geneseq/geneseq/NA1996.DAT.*
- 18: /cgnl_8/gcgdata/geneseq/geneseq/NA1997.DAT.*
- 19: /cgnl_8/gcgdata/geneseq/geneseq/NA1998.DAT.*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/NA1999.DAT.*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/NA2000.DAT.*
- 22: /cgnl_8/gcgdata/geneseq/geneseq/NA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	ID	Description
C 1	330	100.0	330	21	Canine mature inte
C 2	330	100.0	330	21	Canine mature inte
C 3	330	100.0	390	21	Canine interleukin
C 4	330	100.0	390	21	Canine interleukin
C 5	330	100.0	1269	21	Canine interleukin
C 6	330	100.0	1269	21	Canine interleukin
C 7	317	96.1	333	21	Canine mature inte
C 8	317	96.1	333	21	Canine mature inte
C 9	317	96.1	393	21	Canine interleukin
C 10	317	96.1	393	21	Canine interleukin
C 11	317	96.1	1302	21	Canine interleukin

12	317	96.1	1302	21	255556	Canine interleukin
C 13	240	72.7	272	21	255553	Canine interleukin
C 14	218	66.1	278	21	255554	Canine interleukin
C 15	187.4	56.8	336	13	Q28944	Gly41-Cytokine cod
C 16	187.4	56.8	1270	21	F21334	Human low adenosin
C 17	187.4	56.8	1270	21	A35212	Human adenosine re
C 18	187.4	56.8	1282	21	F21332	Human low adenosin
C 19	187.4	56.8	1282	21	A35210	Human adenosine re
C 20	187.4	56.8	1290	15	Q56692	Sequence encoding
C 21	187.4	56.8	6952	21	F21333	Human low adenosin
C 22	187.4	56.8	6952	21	A35211	Human adenosine re
C 23	187.4	56.8	14978	21	F21338	Human low adenosin
C 24	187.4	56.8	14978	21	A35216	Human adenosine re
C 25	185.8	56.3	336	13	Q28943	Asp41-Cytokine cod
C 26	185.8	56.3	1297	13	Q28947	Cytokine NC30. Q
C 27	151.4	45.9	1212	15	Q56693	Sequence encoding
C 28	71.4	21.6	5670	21	F21331	Human low adenosin
C 29	71.4	21.6	5670	21	F21337	Human low adenosin
C 30	71.4	21.6	5670	21	A35209	Human adenosine re
C 31	71.4	21.6	5670	21	A35215	Human adenosine re
C 32	39	11.8	166	21	255552	Canine interleukin
C 33	34	10.3	479	21	C38383	Zea mays DNA fragm
C 34	34	10.3	1896	21	248297	S. coelicolor Yesw
C 35	33.8	10.2	2792	20	X78074	Rat DTST cDNA. R
C 36	33.4	10.1	66	20	232227	Human interleukin
C 37	33.4	10.1	772	19	V48405	Dominant-negative
C 38	32.4	9.8	717	21	A93373	Enhanced green flu
C 39	32.4	9.8	717	21	A93374	Enhanced blue fluo
C 40	32.4	9.8	717	21	A93375	Enhanced cyan fluo
C 41	32.4	9.8	717	21	A27573	DNA encoding EGFP
C 42	32.4	9.8	717	21	A27574	DNA encoding EBFP
C 43	32.4	9.8	717	21	A27575	DNA encoding EGFP
C 44	32.4	9.8	720	21	C62377	CDNA encoding a gr
C 45	32.4	9.8	720	21	245644	DNA encoding the m

ALIGNMENTS

RESULT 1

255565/c
ID 255565 standard; cDNA; 330 BP.

AC 255565;

XX 14-MAR-2000 (first entry)

DT XX Canine mature interleukin-13 (IL-13) clone 78 cDNA.

DE XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.

XX Canis familiaris.

OS WO9961618-A2.

PN 02-DEC-1999.

PD XX 28-MAY-1999; 99WO-US11942.

PF XX 29-MAY-1998; 98US-0087306.

PR XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

DR P-PSDB; Y58224.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX Claim 11; Page 239-240; 264pp; English.


```
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX Sequence 330 BP; 88 A; 96 C; 82 G; 64 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgaatttcacatggcgataaaactcccttacatagatgagcaggtttttccacaaactg 60
DB 330 TCTGAATTTTCATGGCGATAACTCCCTTACATAGGTGACGAGGTTTTTCCACCAACTG 271

QY 61 gatcacttcaattttggtgtctcggtctggttcaactggaaatccctgcgcgggcttttg 120
DB 270 GATCATTCAATTTTGGTGTCTCGGTGCGTTCACCTGGAATCCCTGCGCGGGCTTTTG 211

QY 121 agagcacagtctttcagcactcctctggtctcttggatggcgctgagtcgagacatt 180
DB 210 AGAGCACAGTCTTTTACAGATCCTCTGGGTCTCTTGGATGGCGCTGCAGTCGAGACATT 151

QY 181 gatcagagattctagagctgcagatcatatccggcgatcaggttgacgtccacacatt 240
DB 150 GATCAGAGATTCTAGAGCTGCGCATATCGCCGGCGTTCAGTTGACGCTCCACACCAT 91

QY 241 gctgccgttgacaggggatgctgattctggtgattgttgaccagctctcgaatgagctc 300
DB 90 GCTGCCGTTGACAGGGGATGCTGATTCTGGGTGATGTGACCACTCTCTCAATGAGCTC 31

QY 301 cttgaggggttgggaggagtcacagggt 330
DB 30 CTTGAGGGTTGGGAGGAGTCACAGGGCT 1

RESULT 2
255566
ID 255566 standard; cDNA; 330 BP.
XX AC 255566;
XX AC 255566;
XX DT 14-MAR-2000 (first entry)
XX XX Canine mature interleukin-13 (IL-13) clone 78 cDNA complement.
XX DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX OS Canis familiaris.
XX XX WO961618-A2.
XX XX 02-DEC-1999.
XX PD
XX XX
```

```
PF 28-MAY-1999; 99WO-US11942.
XX XX
PR 29-MAY-1998; 98US-0087306.
XX XX
PA (HESK-) HESKA CORP.
XX XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX XX
XX WPI; 2000-072623/06.
DR P-PSDB; Y58224.
XX XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX Claim 1; Page 241; 264pp; English.
XX XX
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX Sequence 330 BP; 64 A; 82 C; 96 G; 88 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 330;
Best Local Similarity 100.0%; Pred. No. 1.3e-88;
Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgaatttcacatggcgataaaactcccttacataggtgagcaggtttttccacaaactg 60
DB 1 tctgaatttcacatggcgataaaactcccttacataggtgagcaggtttttccacaaactg 60

QY 61 gatcacttcaattttggtgtctcggtctggttcaactggaaatccctgcgcgggcttttg 120
DB 61 gatcacttcaattttggtgtctcggtctggttcaactggaaatccctgcgcgggcttttg 120

QY 121 agagcacagtctttcagcactcctctggtctcttggatggcgctgagtcgagacatt 180
DB 121 agagcacagtctttcagcactcctctggtctcttggatggcgctgagtcgagacatt 180

QY 181 gatcagagattctagagctgcagatcatatccggcgatcaggttgacgtccacacatt 240
DB 181 gatcagagattctagagctgcagatcatatccggcgatcaggttgacgtccacacatt 240

QY 241 gctgccgttgacaggggatgctgattctggtgattgttgaccagctctcgaatgagctc 300
DB 241 gctgccgttgacaggggatgctgattctggtgattgttgaccagctctcgaatgagctc 300

QY 301 cttgaggggttgggaggagtcacagggt 330
DB 301 cttgaggggttgggaggagtcacagggt 330

RESULT 3
255563/c
ID 255563 standard; cDNA; 390 BP.
XX XX
```

AC 255563;
 XX 14-MAR-2000 (first entry)
 DT Canine interleukin-13 (IL-13) clone 78 cDNA coding region.
 DE
 XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 XX WPI; 2000-072623/06.
 DR P-PSDB; Y58223.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PT
 PS Claim 11; Page 238-239; 264pp; English.
 XX
 XX Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 SQ Sequence 390 BP; 92 A; 117 C; 99 G; 82 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.4e-88;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 tctgaatttcacatgagcgtacatcccttaccatgagtgagcaggtttttccaccactg 60
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 390 TCTGAATTTTCATGCGGATAACTCCCTTACATAGGTGAGCAGGTTTTTCCACCACTG 331
 QY 61 gtcacttcacatttgggtctcggtcgctgcttaccatggaatccctgacgcgggtttg 120
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 330 GATCACTTCATTTTGGTGTCTCGGCTGGCTGCTTACATGGAATCCCTGCGCGGGCTTTG 271
 QY 121 agagcacagtgttttcagcatctctgggtcctttgagtcgctgcagtcgagacatt 180
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 270 AGAGCACAGTGTCTTCAGCATCTCTTGGTTCCTTTGGATGGCGCTGCAGTCGAGACATT 211
 QY 181 gatcagagattcttagagtcgagtcagtcagtcagtcgagtcgagtcagtcagtcacatt 240
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||

DB 210 GATCAGAGATTCTAGAGCTGCGCAGTACATGCGCGGTGAGTTGACGCTCCACACCAT 151
 QY 241 gctgccgttcagaggagtgatgctgattctgggtgattgtgaccagctcctcaatagctc 300
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 150 GCTCCGCTTCAGAGGGGATGCTGATTTGGGTGATGTGACCACTCCTCAATGAGCTC 91
 QY 301 cttgaggttggggagggagtcacagggct 330
 DB ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
 90 CTTGAGGTTTGGGAGGAGGAGTCACAGGGCT 61

RESULT 4
 255564
 ID 255564 standard; cDNA; 390 BP.
 XX
 AC 255564;
 XX
 DT 14-MAR-2000 (first entry)
 XX
 DE Canine interleukin-13 (IL-13) clone 78 cDNA coding region complement.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
 XX
 OS Canis familiaris.
 XX
 PN WO9961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 PF 28-MAY-1999; 99WO-US11942.
 XX
 PR 29-MAY-1998; 98US-0087306.
 XX
 PA (HESK-) HESKA CORP.
 XX
 PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
 XX
 XX WPI; 2000-072623/06.
 DR P-PSDB; Y58223.
 XX
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PT
 PS Claim 11; Page 239; 264pp; English.
 XX
 XX Sequences 255552-255560 and 255561-255566 represent cDNA
 CC sequences encoding canine interleukin-13 (IL-13) clones 80
 CC and 78 respectively. The invention relates to canine
 CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
 CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 SQ Sequence 390 BP; 82 A; 99 C; 117 G; 92 T; 0 other;

Query Match 100.0%; Score 330; DB 21; Length 390;
 Best Local Similarity 100.0%; Pred. No. 1.4e-88;
 Matches 330; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


```
XX (HESK-) HESKA CORP.
XX
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
DR P-PSDB; Y58223.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 1i; Page 237-238; 264pp; English.
XX
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumors, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
XX Sequence 1269 BP; 307 A; 340 C; 320 G; 302 T; 0 other;
SQ
```

```
XX Canine mature interleukin-13 (IL-13) clone 80 cDNA.
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX
XX Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
PI WPI; 2000-072623/06.
XX
XX P-PSDB; Y58222.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 1i; Page 233-234; 264pp; English.
XX
XX Sequences Z55552-Z55560 and Z55561-Z55566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumors, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
XX Sequence 333 BP; 89 A; 97 C; 83 G; 64 T; 0 other;
SQ
```

Query Match 96.1%; Score 317; DB 21; Length 333;
Best Local Similarity 99.1%; Pred. No. 9.1e-85;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

```
QY 1 tctgaatttcacatggcgataaactcccttaccatagtgagcaggtttttcaccacacg 60
Dd |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
333 TCTGAATTTTCATGGCGGATAAATCCCTTTACATAGGTGAGCAGGTTTTTTCACCAACTG 274
QY 61 gatcacttcaattttggtgtctcggtcgcttccactggaaat---ccctgcgcgggctt 117
Dd |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
273 GATCACTTCAATTTGGTGTCTCGGCTCGGTTCACATGGAAATCTGCCCTGCCGCGGCTT 214
QY 118 ttgagagcacagtgtctttcagcatcctctgggtcctttggatggcgtcagtcgagac 177
Dd |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
213 TTGAGAGCACAGTGTCTTTCAGCATCCTCTGGGTCTCTTTGGATGGCGCTCAGTCGAGAC 154
QY 178 attgatcagagattcttagagtcgcagtcagtcagtcagtcagtcagtcagtcagtc 237
Dd |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
153 ATTGATCAGAGATTCTAGAGCTGCGCAGTACATGCGCGGCTCAGGTTCAGCTCCACAC 94
QY 238 catgctgcgttgacagagggatgccttgattctgggtgatgttgaccagctcctcaatgag 297
```

RESULT 7
Z55559/c
ID Z55559 standard; cDNA; 333 BP.
XX
AC Z55559;
XX
DT 14-MAR-2000 (first entry)

```

|||||
93 CATGTCGCGTTGCAGAGGATCCCTGATTCGCGTGATGTTGACAGCTCCTCAATGAG 34
|||||
298 ctctttgaggggttggggagggagtcacagggct 330
|||||
33 CTCTCTTGAGCGGTTGGGAGGAGTACACAGGGCT 1

RESULT 8
255560
ID 255560 standard; cDNA; 333 BP.
XX AC 255560;
XX DT 14-MAR-2000 (first entry)
XX DE Canine mature Interleukin-13 (IL-13) clone 80 cDNA complement.
XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX OS Canis familiaris.
XX PN WO9961618-A2.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US11942.
XX PR 29-MAY-1998; 98US-0087306.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI: 2000-072623/06.
XX P-PSDB; Y5822.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX Claim 11; Page 235; 264pp; English.
XX Sequences 255552-255560 and 255561-255566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX modulators of activity, while the antibodies may be used in detection,
XX and in drug targeting.
XX Sequence 333 BP; 64 A; 83 C; 97 G; 89 T; 0 other;

Query Match 96.1%; Score 317; DB 21; Length 333;
Best Local Similarity 99.1%; Pred. No. 9.1e-85;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;

93 1 tctgaatttcctgagcgtataactcccttcacatagtgagcaggtttttccaccaactg 60
|||||
298 ctctttgaggggttggggagggagtcacagggct 330
|||||
33 CTCTCTTGAGCGGTTGGGAGGAGTACACAGGGCT 1

```

```

Db 1 tctgaatttcctgagcgtataactcccttcacatagtgagcaggtttttccaccaactg 60
QY 61 gatcaactcaatttttggtgtcggctgcgttcaactggaataat----ccctgccgcgggctt 117
|||||
Db 61 gatcaactcaatttttggtgtcggctgcgttcaactggaataatgcctgcgggctt 120
|||||
QY 118 ttgagagcacagtcttcaagcatcctctggctccttcttgatgagcgtcagtcggagac 177
|||||
Db 121 ttgagagcacagtcttcaagcatcctctggctccttcttgatgagcgtcagtcggagac 180
|||||
QY 178 attgacagagattctagagctgcgcagtagcatgccgcggtcaggttgacgctccacac 237
|||||
Db 181 attgacagagattctagagctgcgcagtagcatgccgcggtcaggttgacgctccacac 240
|||||
QY 238 catgctgcggttcagagggatgcctgattcctgggtgattgaccagctcctcaatgag 297
|||||
Db 241 catgctgcggttcagagggatgcctgattcctgggtgattgaccagctcctcaatgag 300
|||||
QY 298 ctctttgaggggttggggagggagtcacagggct 330
|||||
Db 301 ctctttgaggggttggggagggagtcacagggct 333

RESULT 9
255557/G
ID 255557 standard; cDNA; 393 BP.
XX AC 255557;
XX DT 14-MAR-2000 (first entry)
XX DE Canine interleukin-13 (IL-13) clone 80 cDNA coding region.
XX KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX OS Canis familiaris.
XX PN WO9961618-A2.
XX PD 02-DEC-1999.
XX PF 28-MAY-1999; 99WO-US11942.
XX PR 29-MAY-1998; 98US-0087306.
XX PA (HESK-) HESKA CORP.
XX PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI: 2000-072623/06.
XX P-PSDB; Y58221.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX Claim 11; Page 232-233; 264pp; English.
XX Sequences 255552-255560 and 255561-255566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX can also be used for the recombinant production of a protein, while

```


PN WO9961618-A2.
XX 02-DEC-1999.
PD 28-MAY-1999; 99WO-US11942.
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX SIm G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX P-PSDB; Y58221.
XX Claim 11; Page 229-230; 264pp; English.
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha), and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
XX Sequence 1302 BP; 337 A; 318 C; 340 G; 307 T; 0 other;
SQ
Query Match 96.1%; Score 317; DB 21; Length 1302;
Best Local Similarity 99.1%; Pred. No. 1.5e-84;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 tctgaatttcacatgagcgtatcccttaccatagatgagcaggttttccacaaactg 60
Db 444 TCTGAATTTCCATGGCGGATTAACCTCCCTTACATAGGTGACAGGTTTTCACCAACTG 385
QY 61 gatcactcaattttggtgtctgcgctcgtttcaactggaaat---ccctgcgcgggctt 117
Db 384 GATCATTCAATTTTGGTGTCTCGGCTCGTTCATCTGAAATTCGCCCTGCGCGGGCTT 325
QY 118 ttgagagcacagtctttcacatcctctggtcctttggatggcgtcagtcggagac 177
Db 324 TTGAGAGCACAGTCTTTTACATCTCTGGGTCTCTTGGATGGGCGTGCAGTCGGAGAC 265
QY 178 attgatcagagattctagagctgcgcagatccgcggtcaggttgagcgtccacac 237
Db 264 ATTGATCAGAGATTCTAGAGCTGCCAGTACATGCCGGGTCAGGTGACGCTCCACAC 205
QY 238 catgctgcgttgagagggatgcttgatctgggtgattgttgacagctcctcaatgag 297
Db 204 CATGCTGCCGTTGCAGAGGGATGCTTGATTCTGCGTGTGATTGACCACTCTCAATGAG 145
QY 298 ctcttgagggttgggggagtgacacagggct 330
Db 144 CTCCTTGAGGTTGGGAGGAGTACACAGGCT 112

RESULT 12
Z55556
ID 255556 standard; cDNA; 1302 BP.
XX AC 255556;
XX 14-MAR-2000 (first entry)
XX Canine interleukin-13 (IL-13) clone 80 cDNA complement.
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX Key Location/Qualifiers
FH complement (856..1251)
FT /*tag= a
FT /product= "Canine IL-13 clone 80"
XX WO9961618-A2.
XX 02-DEC-1999.
XX 28-MAY-1999; 99WO-US11942.
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX P-PSDB; Y58221.
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX Claim 11; Page 231-232; 264pp; English.
XX Sequences 255552-255560 and 255561-255566 represent cDNA
CC sequences encoding canine interleukin-13 (IL-13) clones 80
CC and 78 respectively. The invention relates to canine
CC IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
CC feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
XX Sequence 1302 BP; 307 A; 340 C; 318 G; 337 T; 0 other;
SQ
Query Match 96.1%; Score 317; DB 21; Length 1302;
Best Local Similarity 99.1%; Pred. No. 1.5e-84;
Matches 330; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
QY 1 tctgaatttcacatgagcgtatcccttaccatagatgagcaggttttccacaaactg 60
Db 859 tctgaatttcacatgagcgtatcccttaccatagatgagcaggttttccacaaactg 918
QY 61 gatcactcaattttggtgtctgcggtgagttcactggaaat---ccctgcgcgggctt 117

```
Db 919 gatcaattcaatttgggtctcggtcgcttcaactggaatactgcccgcggggtt 978
Qy 118 ttgagagcacagtgtcttcagcaccctcttggtctcttggaatgctgcagtcggagac 177
Db 979 ttgagagcacagtgtcttcagcaccctcttggtctcttggaatgctgcagtcggagac 1038
Qy 178 attgacacagattcttagagctgcgcagtcacatgccgcgggtcaggttgacgctccacac 237
Db 1039 attgacacagattcttagagctgcgcagtcacatgccgcgggtcaggttgacgctccacac 1098
Qy 238 catgctgcgcgttgcagagggatgcctgattctggtgatgttgaccagctctcaatgag 297
Db 1099 catgctgcgcgttgcagagggatgcctgattctggtgatgttgaccagctctcaatgag 1158
Qy 298 ctctctgaggggttggggagggagtcacagggct 330
Db 1159 ctctctgaggggttggggagggagtcacagggct 1191

RESULT 13
ID Z5553/c
XX Z5553 standard; cDNA; 272 BP.
AC Z5553;
XX
XX
XX 14-MAR-2000 (first entry)
XX Canine interleukin-13 (IL-13) cDNA fragment nCaIL13-272.
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX WO9961618-A2.
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 228; 264pp; English.
XX
XX Sequences Z5552-Z5556 and Z55561-Z55566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
XX vaccines for therapeutic or prophylactic regulation of an immune
XX response in animals (particularly cats, dogs, horses and humans).
XX They may be used to treat autoimmune or infectious diseases including
XX allergies, tumours, inflammation and graft rejection, and to increase
XX the response from a co-administered antigen. The nucleotide sequences
XX can also be used for the recombinant production of a protein, while
XX nucleotide fragments are useful as probes, as amplification primers and
XX as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
XX The proteins may be used to raise antibodies and to screen for
XX modulators of activity, while the antibodies may be used in detection,
```

```
CC and in drug targeting.
XX
XX Sequence 272 BP; 64 A; 91 C; 69 G; 48 T; 0 other;
SQ
Query Match 72.7%; Score 240; DB 21; Length 272;
Best Local Similarity 98.8%; Pred. No. 5.7e-62;
Matches 253; Conservative 0; Mismatches 0; Indels 3; Gaps 1;
Qy 78 tgcctcgcgtcgcgttcaactggaaat---ccctgcgcgcgggctttttgagagcacagtgcctt 134
Db 272 TGTCTCGGCTCGGTTCACTGGAAATCTGCCCTGCGCGGCTTTTGAGAGCAGAGTCTT 213
Qy 135 taagcatcctctgggtcctcttgatggcgctgcagtcggagacattgatcagagattcta 194
Db 212 TCAGCATCTCTGGTCTCTTGGATGGCGCTCAGTCGGAGACATTGATCAGAGATCTCA 153
Qy 195 gactgcgcagtcacatgccgcgggtcaggttgacgctccacaccatgctgcggttcaga 254
Db 152 GAGCTGCGCAGTACATGCCGCGGTCAAGTTGACGCTCCACACCATGCTGCCGTTGCAGA 93
Qy 255 gggatgcctgattcgggtgatgttgaccagctcctcctcaatgagctcttgagggttgggg 314
Db 92 GGGATGCCCTGATTCTGGGTGATGTTGACCAGCTCCTCAATGAGCTCCTTGAGGGTTGGGG 33
Qy 315 agggagtcacagggct 330
Db 32 AGGGAGTCACAGGGCT 17

RESULT 14
ID Z5554/c
XX Z5554 standard; cDNA; 278 BP.
AC Z5554;
XX
XX 14-MAR-2000 (first entry)
XX Canine interleukin-13 (IL-13) cDNA probe.
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
XX immunoregulation; tumour; cancer; autoimmune disease; vaccine; ss.
XX Canis familiaris.
XX WO9961618-A2.
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 11; Page 229; 264pp; English.
XX
XX Sequences Z5552-Z5556 and Z55561-Z55566 represent cDNA
XX sequences encoding canine interleukin-13 (IL-13) clones 80
XX and 78 respectively. The invention relates to canine
XX IL-4, canine or feline Flt-3 ligand, canine or feline CD40, canine or
XX feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
XX interferon-alpha (IFN-alpha) and feline granulocyte macrophage
XX colony-stimulating factor (GM-CSF), and nucleotides which encode these
XX immunoregulatory proteins. The proteins, their associated
XX nucleic acids, specific antibodies and inhibitors may be used as
```


CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 CC
 CC Sequence 278 BP; 58 A; 93 C; 69 G; 58 T; 0 other;

Query Match 66.1%; Score 218; DB 21; Length 278;
 Best Local Similarity 100.0%; Pred. No. 1.9e-55;
 Matches 218; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 113 ggcctttgagagacagtgctttcagcatcctctgggtcctttgagtgagcgctgacgtcg 172
 DB 278 ggccttttgcagacacagtgcttttcagcattccttgggtcctttggatgctgacgtcg 219
 QY 173 gagacattgatcagagattcagagctgcagctacatccgcgctcaggttgacgtc 232
 DB 218 GAGACATTGATCAGAGATTCTAGAGCTGGCAGTACATCCCGCGGTGAGGTGACGCTC 159
 QY 233 cacaccatgctgccgtttgcagagggatgctgattctggtgattgtgaccagctctca 292
 DB 158 CACACCATGCTGCCGTTGCAGAGGGATGCTGATCTGSGTGATGTTGACAGGCTCCTCA 99
 QY 293 atgagctccttgagggctgaggagggaggtcagacagggct 330
 DB 98 ATGAGCTCCTTGAGGGTTGGGGAGGGAGTACAGGGGCT 61

RESULT 15

Q28944/c
 ID Q28944 standard; DNA; 336 BP.

XX AC Q28944;

XX 24-FEB-1993 (first entry)

XX Gly41-Cytokine coding sequence Na1'.

XX Interleukin; chemotaxis; immunomodulation; inflammation; ss.

XX Key Location/Qualifiers
 XX mat_peptide 1..336

FT /*tag= a

FT /note= "encodes Gly at position 41 of cytokine"

XX EP506574-A.

XX 30-SEP-1992.

XX 27-MAR-1992; 92EP-0400858.

XX 29-MAR-1991; 91FR-0003904.

PR 08-JAN-1992; 92FR-0000137.

XX (SNFI) ELF SANOFI.

XX Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
 PI Leplatois P, Magazin M, Minly A;

XX WPI; 1992-325841/40.

DR P-PSDB; R27347.

XX New cytokine having immunomodulatory activity - useful for
 PT treating tumours and infectious or inflammatory conditions

XX

PS Claim 11; Page 60; 78pp; French.

XX T lymphocytes were induced by phorbol-2-myristate-3-acetate (PMA)
 CC and phytohemagglutinin (PHA). Poly (A)+ RNA was isolated from the
 CC cells and reverse transcribed to cDNA. The cDNA was subjected to
 CC hybridisation with polyA RNA from the monkey kidney cell line
 CC COS3. DNA specific for peripheral blood mononuclear cells (PBMC)
 CC (i.e. which did not hybridise) was cloned in pSEI to construct a
 CC DNA bank. The bank was screened with cDNA prepared from PBMC which
 CC had been stimulated with PMA (and opt.PHA) and with a mixture of
 CC oligonucleotides specific to other cytokines. One positive clone
 CC (i.e. which hybridised more strongly to cells induced with PHA and
 CC PMA, c.f. PMA alone, and did not hybridise to known cytokine
 CC probes) was designated pSEI-NC30. It included a 1282 bp ORF with
 CC two potential ATG initiation codons and four potential signal
 CC sequence cleavage sites. A second positive clone differed only in
 CC the identity of codon 41 which was GGC (Gly) in stead of GAC (Asp).
 CC See Q28941-Q28947.

XX Sequence 336 BP; 80 A; 95 C; 90 G; 71 T; 0 other;

Query Match 56.8%; Score 187.4; DB 13; Length 336;
 Best Local Similarity 76.9%; Pred. No. 2.4e-46;
 Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 3 tgaatttcctgagcagataaaacccctctacataggtgagcaggtttttcaccaactgga 62
 DB 334 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAGAGCAGGTCCCTTTACAACTGGG 275
 QY 63 tcaactcaatttgggtgctcgcgctgcgtcactggaaa---tccctgcgcgggctttt 119
 DB 274 CCACCTCGATTGTTGGTGTCTCGGACATGCAAGCTGGAAAACTGCCACGCTGAGACCTTGT 215
 QY 120 gagagcacagtgtttcagcatcctctggtcctttggtgagcgctcagtcgagacat 179
 DB 214 GCGGGCAGAAATCCGCTCAGCATCTCTGGGTCTTCTCGATGGGCACCTGCACGCTGACACGT 155
 QY 180 tgatcagagattctagagctgcagtcagtcacatgcgcggcggttcaggttgacgtccacacca 239
 DB 154 TGATCAGGGGATTCAGGGCTGCACAGTACATGCCAGCTGTCAGGTTGATGCTCCATACCA 95
 QY 240 tgctgcgcttgacagaggatgc---ctgattctgggtgattgaccagctcctcaatga 296
 DB 94 TGCTGCCATTGCAGAGCGGAGCCTTCTGTTCTGGGTGATGTTGACCAAGCTCCTCAATGA 35
 QY 297 gctccttgaggttgaggagggatcacaggc 329
 DB 34 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 2

Search completed: May 13, 2001, 14:30:27
 Job time: 18342 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 14:21:47 ; Search time 226.02 Seconds
(without alignments)
254.928 Million cell updates/sec

Title: US-09-451-527-106
Perfect score: 330
Sequence: 1 tctgaatttcctgcgat.....ggggagggagtcacagggt 330

Scoring table:
IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 302621 seqs, 87301344 residues

Total number of hits satisfying chosen parameters: 605242

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_NA:*
1: /cgnl_7/ptodata/1/ina/5A_COMB.seq:*
2: /cgnl_7/ptodata/1/ina/5B_COMB.seq:*
3: /cgnl_7/ptodata/1/ina/6A_COMB.seq:*
4: /cgnl_7/ptodata/1/ina/6B_COMB.seq:*
5: /cgnl_7/ptodata/1/ina/PCTUS_COMB.seq:*
6: /cgnl_7/ptodata/1/ina/backfiles1.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	187.4	56.8	336	1	US-08-371-121-24
C 2	187.4	56.8	1290	1	US-08-012-543-1
C 3	187.4	56.8	1290	5	PCT-US93-07645A-1
C 4	187.4	56.8	1290	5	PCT-US93-07645-1
C 5	185.8	56.3	336	1	US-08-371-121-2
C 6	185.8	56.3	1297	1	US-08-371-121-15
C 7	184.2	55.8	384	1	US-08-371-121-17
C 8	182.6	55.3	425	1	US-08-594-469-4
C 9	182.6	55.3	425	2	US-08-906-957-4
C 10	182.6	55.3	4410	1	US-08-594-469-1
C 11	182.6	55.3	4410	2	US-08-906-957-1
C 12	151.4	45.9	447	1	US-08-371-121-26
C 13	151.4	45.9	1212	1	US-08-012-543-3
C 14	151.4	45.9	1212	5	PCT-US93-07645A-3
C 15	151.4	45.9	1212	5	PCT-US93-07645-3
C 16	33.4	10.1	1322	4	US-09-128-450-27
C 17	32.4	9.8	720	4	US-09-094-359-3
C 18	32.4	9.8	720	4	US-09-094-359-7
C 19	32.4	9.8	720	4	US-09-172-063-11
C 20	32.4	9.8	720	4	US-09-172-063-13
C 21	32.4	9.8	762	1	US-08-532-390-40
C 22	32.4	9.8	762	4	US-08-717-294-40
C 23	32.4	9.8	768	4	US-09-094-359-11
C 24	32.4	9.8	850	4	US-09-062-102-2
C 25	32.4	9.8	972	4	US-09-172-063-27
C 26	32.4	9.8	972	4	US-09-172-063-29
C 27	32.4	9.8	1095	4	US-09-085-305-5

C 28	32.4	9.8	1929	2	US-08-818-253-1	Sequence 1, Appli
C 29	32.4	9.8	1929	2	US-08-818-253-5	Sequence 5, Appli
C 30	32.4	9.8	1929	4	US-08-818-252-1	Sequence 1, Appli
C 31	32.4	9.8	1929	4	US-08-818-252-5	Sequence 5, Appli
C 32	32.4	9.8	1959	2	US-08-818-253-3	Sequence 3, Appli
C 33	32.4	9.8	1959	4	US-08-818-253-3	Sequence 3, Appli
C 34	32.4	9.8	1971	2	US-08-818-253-7	Sequence 7, Appli
C 35	32.4	9.8	1971	4	US-08-818-252-7	Sequence 7, Appli
C 36	32.4	9.8	7938	4	US-09-331-581-14	Sequence 14, Appli
C 37	32	9.7	1926	2	US-08-978-182-2	Sequence 2, Appli
C 38	32	9.7	1926	2	US-09-205-681-2	Sequence 2, Appli
C 39	31.8	9.6	35081	2	US-08-752-760A-1	Sequence 1, Appli
C 40	31.4	9.5	398	4	US-09-060-758-630	Sequence 630, App
C 41	31.2	9.5	720	4	US-09-094-359-5	Sequence 5, Appli
C 42	31.2	9.5	720	4	US-09-094-359-9	Sequence 9, Appli
C 43	31.2	9.5	720	4	US-09-172-063-12	Sequence 12, Appli
C 44	31.2	9.5	720	4	US-09-172-063-14	Sequence 14, Appli
C 45	31.2	9.5	720	4	US-09-172-063-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1

US-08-371-121-24/c
; Sequence 24, Application US/083711121
; Patent No. 5652123

GENERAL INFORMATION:

APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTEILLER, Christine
APPLICANT: MAGAZIN, Marilyn

TITLE OF INVENTION: Protein having a cytokine type

TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
transformed cells and microorganisms.

NUMBER OF SEQUENCES: 27

CORRESPONDENCE ADDRESS:

ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/371,121

FILING DATE:

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/938,161

FILING DATE: 30-NOV-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: PCT/FR92/00280

FILING DATE: 27-MAR-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR-91 00137

FILING DATE: 08-JAN-1992

PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 03904

FILING DATE: 29-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: SAXE, Bernhard D.

REGISTRATION NUMBER: 28,665

REFERENCE/DOCKET NUMBER: 16781/383

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202) 672-5300

TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-24

Query Match 56.8%; Score 187.4; DB 1; Length 336;
Best Local Similarity 76.9%; Pred. No. 2.1e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

Qy 3 tgaatttcacatgagcgaataaacctccctcacatagtgagcaggtttttccaccaactgga 62
Db 334 TGAACCGTCCCTCGCGAANAAGTTCTTTAATGTAGAGCAGGTCTTTACANAAGTGGG 275
Qy 63 tcaattcaatttgggtgtcgtcgcttcaactggaaa---tccctgcgcggggtttt 119
Db 274 CCACCTCGATTTGGTGTCTCGGACATGCAAGCTGGAANAAGTCCCAAGCTGAGACCTTGT 215
Qy 120 gagagcacagtgcttttcagacatcctctgggttcctttggatggcgtgcagtcggagacat 179
Db 214 GCGGCGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGCGACTGCGAGCCTGACACGT 155
Qy 180 tgatcagagattctagagctgcgcagtcacatcccgcggtcaggttgacgtccacacca 239
Db 154 TGATCAGGATTCAGGCGCTGCACAGTACATGCCAGCTGTCAGGTGTGTCCTCCATACCA 95
Qy 240 tgcctcccttgcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
Db 94 TCTCCCATTCAGAGCGAGCGCTTCTGGTTCGTGGGTGATGTTGACCACTCCTCAATGA 35
Qy 297 gctccttgagggttgggagggagtcacagggc 329
Db 34 GCTCCCTGAGGCGCTGATAGAGGAGGCACAGGGC 2

RESULT 2
US-012-543-1/c
Sequence 1, Application US/08012543
Patent No. 596072
GENERAL INFORMATION:
APPLICANT: Culpepper, Janice
APPLICANT: McKenzie, Andrew
APPLICANT: Dang, Warren
APPLICANT: de Waal Malefyt, Rene
APPLICANT: Heath, Andrew
APPLICANT: Aversa, Gregorio
APPLICANT: Briere, Francine
APPLICANT: Banchereau, Jacques
APPLICANT: de Vries, Jan
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: Human Interleukin-13
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,543
FILING DATE: 01-FEB-1993

CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933,416
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0302K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
SEQUENCE CHARACTERISTICS:
LENGTH: 1290 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: CDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 45..443
US-08-012-543-1

Query Match 56.8%; Score 187.4; DB 1; Length 1290;
Best Local Similarity 76.9%; Pred. No. 3.5e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

Qy 3 tgaatttcacatgagcgaataaacctccctcacatagtgagcaggtttttccaccaactgga 62
Db 438 TGAACCGTCCCTCGCGAANAAGTTCTTTAATGTAGAGCAGGTCTTTACANAAGTGGG 379
Qy 63 tcaattcaatttgggtgtcgtcgcttcaactggaaa---tccctgcgcggggtttt 119
Db 378 CCACCTCGATTTGGTGTCTCGGACATGCAAGCTGGAANAAGTCCCAAGCTGAGACCTTGT 319
Qy 120 gagagcacagtgcttttcagacatcctctgggttcctttggatggcgtgcagtcggagacat 179
Db 318 GCGGCGAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGCGACTGCGAGCCTGACACGT 259
Qy 180 tgatcagagattctagagctgcgcagtcacatcccgcggtcaggttgacgtccacacca 239
Db 258 TGATCAGGATTCAGGCGCTGCACAGTACATGCCAGCTGTCAGGTGTGTCCTCCATACCA 199
Qy 240 tgcctcccttgcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
Db 198 TGCTGCCATTGCAGCGGAGCGCTTCTGGTTCGTGGGTGATGTTGACCACTCCTCAATGA 139
Qy 297 gctccttgagggttgggagggagtcacagggc 329
Db 138 GCTCCCTGAGGCGCTGATAGAGGAGGCACAGGGC 106

RESULT 3
PCT-US93-07645A-1/c
Sequence 1, Application PC/TUS9307645A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Human Interleukin-13
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07645A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012543
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010977

;; FILING DATE: 29-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/933416
;; FILING DATE: 21-AUG-1992
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1290 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
PCT-US93-07645A-1

Query Match 56.8%; Score 187.4; DB 5; Length 1290;
Best Local Similarity 76.9%; Pred. No. 3.5e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 3 tgaattccatggcgataaaaccccttacataggtgagcaggtttttccaccaactgga 62
DB 438 TGAACCGTCCCTCGCGAAAAGTTCTTTAAATGTAAGAGCAGGTCCTTTACAACTGGG 379

QY 63 tcaattcaattttgtctcggtcggttcactgaaa---tcctgcgcgcggtttt 119
DB 378 CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAGCTGCCAGCTGAGACCTTGT 319

QY 120 gagagcacagtgcttcacagcctctctgggtcctttggatggcgctcagtcgagacat 179
DB 318 GCGGCGAGAAATCCGCTCAGCATCTCTGGGTCTCTCGATGGCATGCGACCTGACACGT 259

QY 180 tgatcacagattctagagctgcagctacatgcgcggcggttcaggttcacacacca 239
DB 258 TGATCAGGATTTCCAGGGCTGCACAGTACATGCCAGCTGCAGGTGATGCTCCATACCA 199

QY 240 tctgcctgttcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
DB 198 TGTGCTGCAATTCGACGGGCTTCTGGTCTCTGGGTGATGTTGACCACTCCTCAATGA 139

QY 297 gctccttgagggttcggggagggaggtcacagggc 329
DB 138 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 106

RESULT 4
PCT-US93-07645-1/c
;; Sequence 1, Application PC/TUS9307645
;; GENERAL INFORMATION:
;; APPLICANT:
;; TITLE OF INVENTION: Human Interleukin-13
;; NUMBER OF SEQUENCES: 6
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: Apple Macintosh
;; OPERATING SYSTEM: Macintosh 6.0.5
;; SOFTWARE: Microsoft Word 5.1a
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: PCT/US93/07645
;; FILING DATE: 19930818
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/012543
;; FILING DATE: 01-FEB-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 08/010977
;; FILING DATE: 29-JAN-1993
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/933416
;; FILING DATE: 21-AUG-1992
;; INFORMATION FOR SEQ ID NO: 1:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1290 base pairs
;; TYPE: nucleic acid
;; STRANDEDNESS: double
;; TOPOLOGY: linear
PCT-US93-07645-1

Query Match 56.8%; Score 187.4; DB 5; Length 1290;
Best Local Similarity 76.9%; Pred. No. 3.5e-50;
Matches 256; Conservative 0; Mismatches 71; Indels 6; Gaps 2;

QY 3 tgaattccatggcgataaaaccccttacataggtgagcaggtttttccaccaactgga 62
DB 438 TGAACCGTCCCTCGCGAAAAGTTCTTTAAATGTAAGAGCAGGTCCTTTACAACTGGG 379

QY 63 tcaattcaattttgtctcggtcggttcactgaaa---tcctgcgcgcggtttt 119
DB 378 CCACCTCGATTTTGGTGTCTCGGACATGCAAGCTGGAAGCTGCCAGCTGAGACCTTGT 319

QY 120 gagagcacagtgcttcacagcctctctgggtcctttggatggcgctcagtcgagacat 179
DB 318 GCGGCGAGAAATCCGCTCAGCATCTCTGGGTCTCTCGATGGCATGCGACCTGACACGT 259

QY 180 tgatcacagattctagagctgcagctacatgcgcggcggttcaggttcacacacca 239
DB 258 TGATCAGGATTTCCAGGGCTGCACAGTACATGCCAGCTGCAGGTGATGCTCCATACCA 199

QY 240 tctgcctgttcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
DB 198 TGTGCTGCAATTCGACGGGCTTCTGGTCTCTGGGTGATGTTGACCACTCCTCAATGA 139

QY 297 gctccttgagggttcggggagggaggtcacagggc 329
DB 138 GCTCCCTGAGGGCTGTAGAGGGAGGCACAGGGC 106

RESULT 5
US-08-371-121-2/c
;; Sequence 2, Application US/08371121
;; Patent No. 5652123
;; GENERAL INFORMATION:
;; APPLICANT: CAPUT, Daniel
;; APPLICANT: FERRARA, Pascual
;; APPLICANT: GUILLEMOT, Jean-Claude
;; APPLICANT: LEPLATOIS, Pascal
;; APPLICANT: MINTY, Adrian
;; APPLICANT: KAGHAD, Mourad
;; APPLICANT: LABIT-LE BOUTEILLER, Christine
;; APPLICANT: MAGAZIN, Marilyn
;; TITLE OF INVENTION: Protein having a cytokine type
;; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
;; NUMBER OF SEQUENCES: 27
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: FOLEY & LARDNER
;; STREET: 3000 K Street, N.W., Suite 500
;; CITY: Washington, D.C.
;; COUNTRY: USA
;; ZIP: 20007-5109
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/371,121
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US 07/938,161
;; FILING DATE: 30-NOV-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: PCT/FR92/00280
;; FILING DATE: 27-MAR-1992
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: FR 91 00137
;; FILING DATE: 08-JAN-1992
;; PRIOR APPLICATION DATA:

APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 336 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-371-121-2

Query Match 56.3%; Score 185.8; DB 1; Length 336;
Best Local Similarity 76.6%; Pred. No. 6.7e-50;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;
QY 3 tgaatttcacatggcgataaaactcccttacataggtgagcaggtttttccaccactgga 62
DB 334 TGAACCGCTCCCTCGCGAAAAAGTTCTTTAAATGTAAAGAGCAGGTCCTTTACAAACTGGG 275
QY 63 tcaattcaatttggtgtcgtcgcttcactgga---tcctgcgcggtgtttt 119
DB 274 CCACCTCGATTGTGTCGAGACATCAAGCTGGAAACTGCCAGCTGAGACCTTGT 215
QY 120 gagagcacagtgtcttagacatccctgtggtcttttggtggtgcgtgcagtcggagacat 179
DB 214 GCGGCGAAGTCCGCTAGCATCCTCTGGTCTTCTCGATGGCAGCTGCAGCCTGACACGT 155
QY 180 tgatcacagattctagaactgcagatcacatccgcggtcaggttgagctccacacca 239
DB 154 TGATCAGGATTCCAGGCTGCACAGTACATGTACGTCTCAGTTGATGCTCCATACCA 95
QY 240 tgcctccgttcagagggatgc---ctgattctggtggtgattgacacagctcctcaatga 296
DB 94 TGCTGCCATTGCAGAGCGAGCCTTCTGGTCTGGTGATGTGACCACTCCTCAATGA 35
QY 297 gctccttgaggggttgggagggagtcacagggc 329
DB 34 GCTCCTCAGGGCTGTAGAGGAGGCACAGGC 2

RESULT 6
US-08-371-121-15/c
Sequence 15, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOIS, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTELLIER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: SAXE, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 1297 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 15..452
FEATURE:
NAME/KEY: mat_peptide
LOCATION: 117..452
US-08-371-121-15

Query Match 56.3%; Score 185.8; DB 1; Length 1297;
Best Local Similarity 76.6%; Pred. No. 1.1e-49;
Matches 255; Conservative 0; Mismatches 72; Indels 6; Gaps 2;

QY 3 tgaatttcacatggcgataaaactcccttacataggtgagcaggtttttccaccactgga 62
DB 450 TGAACCGCTCCCTCGCGAAAAAGTTCTTTAAATGTAAAGAGCAGGTCCTTTACAAACTGGG 391
QY 63 tcaattcaatttggtgtcgtcgcttcactgga---tcctgcgcggtgtttt 119
DB 390 CCACCTCGATTGTGTCGCGACATCAAGCTGGAAACTGCCAGCTGAGACCTTGT 331
QY 120 gagagcacagtgtcttagacatccctgtggtcttttggtggtgcgtgcagtcggagacat 179
DB 330 GCGGCGAAGTCCGCTAGCATCCTCTGGTCTTCTCGATGGCAGCTGCAGCCTGACACGT 271
QY 180 tgatcacagattctagaactgcagatcacatccgcggtcaggttgagctccacacca 239
DB 270 TGATCAGGATTCCAGGCTGCACAGTACATGTACGTCTCAGTTGATGCTCCATACCA 211
QY 240 tgcctccgttcagagggatgc---ctgattctggtggtgattgacacagctcctcaatga 296
DB 210 TGCTGCCATTGCAGAGCGAGCCTTCTGGTCTGGTGATGTGACCACTCCTCAATGA 151
QY 297 gctccttgaggggttgggagggagtcacagggc 329
DB 150 GCTCCTCAGGGCTGTAGAGGAGGCACAGGC 118

RESULT 7

US-08-371-121-17/c
: Sequence 17, Application US/08371121
: Patent No. 5652123
: GENERAL INFORMATION:
: APPLICANT: CAPUT, Daniel
: APPLICANT: FERRARA, Pascual
: APPLICANT: GUILLEMOT, Jean-Claude
: APPLICANT: LEPLATOIS, Pascal
: APPLICANT: MINTY, Adrian
: APPLICANT: KAGHAD, Mourad
: APPLICANT: LABIT-LE BOUTELLER, Christine
: APPLICANT: MAGAZIN, Marillyn
: TITLE OF INVENTION: Protein having a cytokine type
: TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
: TITLE OF INVENTION: transformed cells and microorganisms.
: NUMBER OF SEQUENCES: 27
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: FOLEY & LARDNER
: STREET: 3000 K Street, N.W., Suite 500
: CITY: Washington, D.C.
: COUNTRY: USA
: ZIP: 20007-5109
: COMPUTER READABLE FORM: disk
: MEDIUM TYPE: Floppy
: COMPUTER: IBM PC compatible
: OPERATING SYSTEM: PC-DOS/MS-DOS
: SOFTWARE: PatentIn Release #1.0, version #1.25
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/371,121
: FILING DATE:
: CLASSIFICATION: 435
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: US 07/938,161
: FILING DATE: 30-NOV-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: PCT/FR92/00280
: FILING DATE: 27-MAR-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 91 00137
: FILING DATE: 08-JAN-1992
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: FR 91 03904
: FILING DATE: 29-MAR-1991
: ATTORNEY/AGENT INFORMATION:
: NAME: SAXE, Bernhard D.
: REGISTRATION NUMBER: 28,665
: REFERENCE/DOCKET NUMBER: 16781/383
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: (202) 672-5300
: TELEFAX: (202) 672-5399
: TELEX: 904136
: INFORMATION FOR SEQ ID NO: 17:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 384 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: double
: TOPOLOGY: linear
: MOLECULE TYPE: DNA (genomic)
: US-08-371-121-17

Query Match 55.88; Score 184.2; DB 1; Length 384;
Best Local Similarity 76.38; Pred. No. 2.3e-49;
Matches 254; Conservative 0; Mismatches 73; Indels 6; Gaps 2;

Qy	3	lgaaatttccatggtgcataaaactccccccttacataggtgagcgggtttttccaccaactgga	62
Db	355	tgaacccgtccctcgcaaaaaggttctttttaaatgttaagacgaggctcttttacaacactggg	296
Qy	63	tcacttcaatttgggtgtctcgctgcgttcaactggaaa---tccctgcgcgcgggctttt	119
Db	295	ccacctcgatttttgggtgtctcgacacatgcaagcttgaaaactgccccagctgagacctctgt	236

Qy	120	gagagcacagtgttttcagcatcctctgggtctcttggatggcgctgcagtcggagacat	179
Db	235	CGGGCAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT	176
Qy	180	tgatcagagattctagagctgcgcagttacatgccggcggtcgaagttgcagctccacacca	239
Db	175	TGATCAGGGATTCAGGGCTGCACAGTACATGTCAGCTGTCAGGTTGATGCTCCATACCA	116
Qy	240	tgtctgcggttcgcagaggatgc---ctgattctgggtgatgttgaccagcgtctctcaatga	296
Db	115	TGCTGCCATTGCAGAGCGGAGCCCTCTGGTCTTGGGTGATGTTGACCACTCCTCAATGA	56
Qy	297	gtctcttgagggttgaggaggagtcacagggc	329
Db	55	GCTCCCTTGAGGGCCGTAGAGGGAGGCACAGGCG	23

RESULT

US-08-594-469-4/c
Sequence 4, Application US/08594469
Patent No. 5700665
GENERAL INFORMATION:
APPLICANT: LEGOUX, Richard
APPLICANT: MALDONADO, Paul
APPLICANT: SALOME, Marc
TITLE OF INVENTION: Method for the extraction of
TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
TITLE OF INVENTION: presence of arginine
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bacon & Thomas
STREET: 625 Slaters Lane - Fourth Floor
CITY: Alexandria
STATE: Virginia
COUNTRY: USA
ZIP: 22314
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/594,469
FILING DATE:

```

1 FILING DATE:
2 CLASSIFICATION: 435
3 PRIORITY APPLICATION DATA:
4 APPLICATION NUMBER: FR 95 01083
5 FILING DATE: 31-JAN-1995
6 ATTORNEY/AGENT INFORMATION:
7 NAME: FICHTER, Richard E
8 REGISTRATION NUMBER: 26,382
9 REFERENCE/DOCKET NUMBER: REF/LEGOUX
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: (703) 683-0500
12 TELEFAX: (703) 683-1080
13 INFORMATION FOR SEQ ID NO: 4:
14 SEQUENCE CHARACTERISTICS:
15 LENGTH: 425 base pairs
16 TYPE: nucleic acid
17 STRANDEDNESS: single
18 TOPOLOGY: linear
19 MOLECULE TYPE: DNA (genomic)
20 US-08-594-469-4

```

Query Match	55.3%	Score 182.6;	DB 1;	Length 425;
Best Local Similarity	76.0%	Pred. No. 7.5e-49;		
Matches 253; Conservative	0;	Mismatches 74;	Indels 6;	Gaps 2;

Qy 3 tgaatatccatgcgataaaactccccttacataggtgagcagggttttaccacaactgga 62
 |||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| | ||| |
Dβ 397 TGACCGTCCCTCGGANAAGTTTCNTTAATGTGAAGACAGTGCTTTACAACACTGGG 388

```
QY 63 tcactcaatttggtgctcgcgtcctcactgaaa---tcctaccgcgggctttt 119
Db 337 CCACCTCCGATTTGGTCTCGGACATCAAGCTGGAAACTGCCAGCTGAGACCTTGT 278
QY 120 gagagcacagtgccttcagcatcctctgggtccttttgatggcgcgtgcagtcggagacat 179
Db 277 GCGGCGAGAAATCCGCTCAGCATCCTCTGGGTCTTCTCGATGCATGCGAGCTGACAGCT 218
QY 180 tgatcagagattctagagctgcgcagtcacatccgcgcgtgcaggttgacgtctccacacca 239
Db 217 TGATCAGGAGTTCCAGGCTGCACAGTAGTACATGCCAGCTGTAGGTGTGATGCTCCATACCA 158
QY 240 tgcctgcctttcagagggatgc---ctaatctgggtgatgttgaccagctcctcaatga 296
Db 157 TGCTGCCATTCCAGACGGAGCCCTTCTGGTCTTGGGTGATGTTGACCAAGCTCCTCAATGA 98
QY 297 gctccttgaggggttgaggagggagtcacagggc 329
Db 97 GCTCCCTGAGGCGAGTACTGTGGGAGGCACAGGGC 65

RESULT 9
US-08-906-957-4/c
; Sequence 4, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906.957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 425 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-4
```

Query Match

55.3%; Score 182.6; DB 2; Length 425;

```
Best Local Similarity 76.0%; Pred. No. 7 5e-49;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;
QY 3 tgaatttccatggcgataaactcccttacatagtgagcaggtttttccaccaactgga 62
Db 397 TGAACCGTCCCTCGCGAAAAAGTTTCTTTAAATGTAAGAGCAGGTCTCTTTACAAACTGGG 338
QY 63 tcactcaatttggtgctcgcgtcctcactgaaa---tcctaccgcgggctttt 119
Db 337 CCACCTCCGATTTGGTCTCGGACATCAAGCTGGAAACTGCCAGCTGAGACCTTGT 278
QY 120 gagagcacagtgccttcagcatcctctgggtccttttgatggcgcgtgcagtcggagacat 179
Db 217 TGATCAGGAGTTCCAGGCTGCACAGTAGTACATGCCAGCTGTAGGTGTGATGCTCCATACCA 158
QY 240 tgcctgcctttcagagggatgc---ctaatctgggtgatgttgaccagctcctcaatga 296
Db 157 TGCTGCCATTCCAGACGGAGCCCTTCTGGTCTTGGGTGATGTTGACCAAGCTCCTCAATGA 98
QY 297 gctccttgaggggttgaggagggagtcacagggc 329
Db 97 GCTCCCTGAGGCGAGTACTGTGGGAGGCACAGGGC 65

RESULT 10
US-08-594-469-1/c
; Sequence 1, Application US/08594469
; Patent No. 5700665
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/594,469
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
```


US-08-594-469-1

Query Match 55.3%; Score 182.6; DB 1; Length 4410;
Best Local Similarity 76.0%; Pred. No. 1.8e-48;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;
Qy 3 tgaattccatgagcgcataaaactcccttaccatagtgagcagggtttttccaccactgga 62
Db 734 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAAGACGAGGTCTTTTACAAACTGGG 675
Qy 63 tcacttcaattttggtctcgctcgcttccactgga---tcctcgccgagggctttt 119
Db 674 CCACCTCGATTGTTGGTCTCGACATGCAAGCTGGAAACTGCCACGTGAGACCTTGT 615
Qy 120 gagagcacagtgtttcagacatcctctgggtcttggatggcgctcagctcgagagacat 179
Db 614 CGCGGCAGAAATCCGCTCAGCATCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT 555
Qy 180 tgatcagagattctagagctgcagctacatgcgcggcgtcaggttgacgctccacacca 239
Db 554 TGATCAGGAGATTCCAGGGTGCACATGATGACAGTGTGAGGTTGATGCTCCATACCA 495
Qy 240 tctgcggttcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
Db 494 TCGTCCATTGACAGCGGAGCCCTTCTGGTCTGGGATGATGACACAGCTCCTCAATGA 435
Qy 297 gctccttgaggttgggggagggagtcacagggc 329
Db 434 GCTCCTGAGGCGACGTACTGGGAGGCACAGGGC 402

RESULT 11
US-08-906-957-1/c
; Sequence 1, Application US/08906957
; Patent No. 5856142
; GENERAL INFORMATION:
; APPLICANT: LEGOUX, Richard
; APPLICANT: MALDONADO, Paul
; APPLICANT: SALOME, Marc
; TITLE OF INVENTION: Method for the extraction of
; TITLE OF INVENTION: periplasmic proteins of prokaryotic microorganisms in the
; TITLE OF INVENTION: presence of arginine
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Bacon & Thomas
; STREET: 625 Slaters Lane - Fourth Floor
; CITY: Alexandria
; STATE: Virginia
; COUNTRY: USA
; ZIP: 22314
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/906,957
; FILING DATE: 06-AUG-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/594,469
; FILING DATE:
; APPLICATION NUMBER: FR 95 01083
; FILING DATE: 31-JAN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: FICHTER, Richard E
; REGISTRATION NUMBER: 26,382
; REFERENCE/DOCKET NUMBER: REF/LEGOUX
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703) 683-0500
; TELEFAX: (703) 683-1080
; INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
; LENGTH: 4410 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-906-957-1
Query Match 55.3%; Score 182.6; DB 2; Length 4410;
Best Local Similarity 76.0%; Pred. No. 1.8e-48;
Matches 253; Conservative 0; Mismatches 74; Indels 6; Gaps 2;
Qy 3 tgaattccatgagcgcataaaactcccttaccatagtgagcagggtttttccaccactgga 62
Db 734 TGAACCGTCCCTCGCGAAAAAGTTCTTTAAATGTAAAGACGAGGTCTTTTACAAACTGGG 675
Qy 63 tcacttcaattttggtctcgctcgcttccactgga---tcctcgccgagggctttt 119
Db 674 CCACCTCGATTGTTGGTCTCGGACATGCAAGCTGGAAACTGCCACGTGAGACCTTGT 615
Qy 120 gagagcacagtgtctcagacatcctctgggtcttggatggcgctcaggttgacgctccacacca 179
Db 614 CGCGGCAGAAATCCGCTCAGCATCTCTGGGTCTTCTCGATGGCACTGCAGCCTGACACGT 555
Qy 180 tgatcagagattctagagctgcagctacatgcgcggcgtcaggttgacgctccacacca 239
Db 554 TGATCAGGAGATTCCAGGGTGCACATGATGACAGTGTGAGGTTGATGCTCCATACCA 495
Qy 240 tctgcggttcagagggatgc---ctgattctgggtgatgttgaccagctcctcaatga 296
Db 494 TCGTCCATTGACAGCGGAGCCCTTCTGGTCTGGGATGATGACACAGCTCCTCAATGA 435
Qy 297 gctccttgaggttgggggagggagtcacagggc 329
Db 434 GCTCCTGAGGCGACGTACTGGGAGGCACAGGGC 402

RESULT 12
US-08-371-121-26/c
; Sequence 26, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMET, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 13, 2001, 11:40:59 ; Search time 5997.24 Seconds
(without alignments)
480.707 Million cell updates/sec

Title: US-09-451-527-106
Perfect score: 330
Sequence: 1 tctgaatttcacatggcgat.....ggggaggaggtcacagggct 330

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 9623517 seqs, 4368049070 residues

Total number of hits satisfying chosen parameters: 19247034

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:

- 1: gb_est1:*
- 2: gb_est2:*
- 3: gb_est3:*
- 4: gb_est4:*
- 5: gb_est5:*
- 6: gb_est6:*
- 7: gb_est7:*
- 8: gb_est8:*
- 9: gb_est9:*
- 10: gb_est10:*
- 11: gb_est11:*
- 12: gb_est12:*
- 13: gb_est13:*
- 14: gb_est14:*
- 15: gb_est15:*
- 16: gb_est16:*
- 17: gb_est17:*
- 18: gb_est18:*
- 19: gb_est19:*
- 20: gb_est20:*
- 21: gb_est21:*
- 22: gb_est22:*
- 23: gb_est23:*
- 24: gb_est24:*
- 25: gb_est33:*
- 26: gb_est34:*
- 27: gb_est35:*
- 28: gb_est36:*
- 29: gb_est37:*
- 30: gb_est38:*
- 31: gb_est39:*
- 32: gb_est40:*
- 33: em_estba:*
- 34: em_estfun:*
- 35: em_esthum1:*
- 36: em_esthum2:*
- 37: em_esthum3:*
- 38: em_esthum4:*
- 39: em_esthum5:*
- 40: em_esthum6:*
- 41: em_esthum7:*
- 42: em_esthum8:*
- 43: em_esthum9:*

- 44: em_esthum10:*
- 45: em_esthum11:*
- 46: em_esthum12:*
- 47: em_esthum13:*
- 48: em_esthum14:*
- 49: em_esthum15:*
- 50: em_esthum16:*
- 51: em_esthum17:*
- 52: em_esthum18:*
- 53: em_esthum19:*
- 54: em_esthum20:*
- 55: em_esthum21:*
- 56: em_esthum22:*
- 57: em_esthum23:*
- 58: em_esthum24:*
- 59: em_esthum25:*
- 60: em_esthum26:*
- 61: em_esthum27:*
- 62: em_esthum28:*
- 63: em_estin1:*
- 64: em_estin2:*
- 65: em_estin3:*
- 66: em_estin4:*
- 67: em_estin5:*
- 68: em_estomi:*
- 69: em_estom2:*
- 70: em_estov1:*
- 71: em_estov2:*
- 72: em_estpl1:*
- 73: em_estpl2:*
- 74: em_estpl3:*
- 75: em_estpl4:*
- 76: em_estpl5:*
- 77: em_estpl6:*
- 78: em_estpl7:*
- 79: em_estpl8:*
- 80: em_estpl9:*
- 81: em_estpl10:*
- 82: em_estro1:*
- 83: em_estro2:*
- 84: em_estro3:*
- 85: em_estro4:*
- 86: em_estro5:*
- 87: em_estro6:*
- 88: em_estro7:*
- 89: em_estro8:*
- 90: em_estro9:*
- 91: em_estro10:*
- 92: em_estro11:*
- 93: em_estro12:*
- 94: em_estro13:*
- 95: em_estro14:*
- 96: em_estro15:*
- 97: em_estro16:*
- 98: em_estro17:*
- 99: em_estro18:*
- 100: em_estro19:*
- 101: em_estro20:*
- 102: gb_est25:*
- 103: gb_est26:*
- 104: gb_est27:*
- 105: gb_est28:*
- 106: gb_est29:*
- 107: gb_est30:*
- 108: gb_est31:*
- 109: gb_est32:*
- 110: gb_est41:*
- 111: gb_est42:*
- 112: gb_est43:*
- 113: gb_est44:*
- 114: gb_est45:*
- 115: gb_est46:*
- 116: gb_est47:*

117: gb_est48:*
118: gb_est49:*
119: gb_est50:*
120: gb_est51:*
121: gb_est52:*
122: gb_est53:*
123: gb_est54:*
124: gb_est55:*
125: gb_est56:*
126: gb_est57:*
127: gb_est58:*
128: gb_est59:*
129: gb_est60:*
130: gb_est61:*
131: gb_est62:*
132: gb_est63:*
133: gb_est64:*
134: gb_est65:*
135: gb_est66:*
136: gb_est67:*
137: gb_est68:*
138: gb_est69:*
139: gb_est70:*
140: gb_est71:*
141: gb_est72:*
142: gb_est73:*
143: gb_est74:*
144: gb_est75:*
145: gb_est76:*
146: gb_est77:*
147: gb_est78:*
148: gb_est79:*
149: gb_est80:*
150: gb_est81:*
151: gb_est82:*
152: gb_est83:*
153: gb_est84:*
154: gb_est85:*
155: gb_est86:*
156: gb_est87:*
157: gb_est88:*
158: gb_est89:*
159: gb_est90:*
160: gb_est91:*
161: gb_est92:*
162: gb_est93:*
163: gb_est94:*
164: gb_est95:*
165: gb_est96:*
166: gb_est97:*
167: gb_est98:*
168: gb_est99:*
169: gb_est100:*
170: gb_est101:*
171: gb_est102:*
172: gb_est103:*
173: gb_est104:*
174: gb_est105:*
175: gb_est106:*
176: gb_est107:*
177: gb_est108:*
178: gb_est109:*
179: gb_est110:*
180: gb_est111:*
181: gb_est112:*
182: gb_est113:*
183: gb_est114:*
184: gb_est115:*
185: gb_est116:*
186: gb_est117:*
187: gb_est118:*
188: gb_est119:*
189: gb_est120:*

190: em_gss_pln1:*
191: em_gss_pln2:*
192: em_gss_pro:*
193: em_gss_rod1:*
194: em_gss_rod2:*
195: em_gss_rod3:*
196: em_gss_rod4:*
197: em_gss_rod5:*
198: em_gss_vrt1:*
199: em_gss_vrt2:*
200: em_gss_vrt3:*
201: gb_gss1:*
202: gb_gss2:*
203: gb_gss3:*
204: gb_gss4:*
205: gb_gss5:*
206: gb_gss6:*
207: gb_gss7:*
208: gb_gss8:*
209: gb_gss9:*
210: gb_gss10:*
211: gb_gss11:*
212: gb_gss12:*
213: gb_gss13:*
214: gb_gss14:*
215: gb_gss15:*
216: gb_gss16:*
217: gb_gss17:*
218: gb_gss18:*
219: gb_gss19:*
220: gb_gss20:*
221: gb_gss21:*
222: gb_gss22:*
223: gb_gss23:*
224: gb_gss24:*
225: gb_gss25:*
226: gb_gss26:*
227: gb_gss27:*
228: gb_gss28:*
229: gb_gss29:*
230: gb_gss30:*
231: gb_gss31:*
232: gb_gss32:*
233: gb_gss33:*
234: gb_gss34:*

pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
C 1	39	11.8	477	218	AZ261971	AZ261971 RPCT-23-1
C 2	39	11.8	521	215	AZ027551	AZ027551 RPCT-23-3
C 3	36.4	11.0	277	137	BE593226	BE593226 WSL_99_B0
C 4	36.4	11.0	537	166	BE357229	BE357229 DGL_147_B
C 5	35.2	10.7	757	174	BG260311	BG260311 602371427
C 6	34.4	10.4	462	143	BF039993	BF039993 BP250023B
C 7	34.4	10.4	507	138	BE705147	BE705147 SC02_08f0
C 8	34.2	10.4	535	161	BE032541	BE032541 131940 MA
C 9	34.2	10.4	546	161	BE032543	BE032543 131942 MA
C 10	34.2	10.4	570	24	A1746678	A1746678 ul06005.y
C 11	34.2	10.4	965	217	AZ201624	AZ201624 SP_0053_A
C 12	34.2	10.4	2275	14	AF034173	AF034173 AF034173
C 13	34	10.3	370	166	BE363650	BE363650 WSL_64_G1
C 14	34	10.3	562	166	BE361027	BE361027 DGL_69_A0
C 15	33.8	10.2	341	163	BE127683	BE127683 DEPA1432
C 16	33.8	10.2	498	150	BF606532	BF606532 273595 MA
C 17	33.6	10.2	577	166	BE402120	BE402120 CSB004F06
C 18	33.6	10.2	714	166	BE414190	BE414190 SCU007.CO

Db 330 GTTGACCACTCGCGCGCTGCGTGCAGAGAACCCACCCAGCGCGGTGTCGCCGGG 271

QY 286 ctctcaatgagctccttggagg 307

Db 270 CTCCCGGAGCCTCCCATGGG 249

RESULT 5

BG260311 757 bp mRNA EST 13-FEB-2001

LOCUS NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4479367 5', mRNA sequence.

ACCESSION BG260311

VERSION BG260311.1 GI:12770127

KEYWORDS EST.

SOURCE human.

ORGANISM Homo sapiens

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 757)

AUTHORS NIH-MGC <http://img.ncbi.nih.gov/>.

TITLE National Institutes of Health, Mammalian Gene Collection (MGC)

JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D. Tel: (301) 496-1350 Email: Robert.Strausberg@nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov> Plate: LLAM10311 row: f column: 08 High quality sequence stop: 736.

FEATURES source Location/Qualifiers 1..757 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:4479367" /clone_lib="NIH_MGC_93" /tissue_type="transitional cell papilloma, cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI; Site 2: SalI; Cloned unidirectionally; oligo-dT primed. Average insert size 1.7 kb. Library enriched for full-length clones and constructed by Life Technologies. Note: this is a NIH_MGC Library." BASE COUNT 186 a 200 c 201 g 170 t

Query Match 10.7%; Score 35.2; DB 174; Length 757; Best Local Similarity 49.0%; Pred. No. 9.5; Matches 94; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 3 tgaatttccttgccggaataactcccccttacataggtgagcaggtttttaccacactgga 62

Db 497 TCAAGTTTCTTGCGCCGCCAGAGATGCACATCTCAAGAAGTGGGGCTTCCACCAAGTTCA 556

QY 63 tcactcaatttgggtgtctcgctgctgcttcaactggaatccctcgccgcggttttgag 122

Db 557 ATGCTCATCAATTTGAAGACATGCTGGCTGCAAAAGCGGCTCATCCAGATGGCTTGTGGG 616

QY 123 agcacagtgcttccagcactctctgggttccttggatggcgctgcagtcgagacattga 182

Db 617 GTCAAGTAGATACACCCAGTCGTGGGCCCTCTGGACAAAGTGGCGGCCCTGGCACTCA 676

QY 183 tcagagattcta 194

Db 677 TGAGGGCCTTCCA 688

RESULT 6

BF039993/c 462 bp mRNA EST 10-OCT-2000

LOCUS BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA clone BP250023B10D12 5', mRNA sequence.

ACCESSION BF039993

VERSION BF039993.1 GI:10757048

KEYWORDS EST.

SOURCE COW.

ORGANISM Bos taurus

REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovinae; Bos. 1 (bases 1 to 462)

AUTHORS Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson, J.H.

TITLE Bovine ESTs

JOURNAL Unpublished (2000)

COMMENT Contact: Lewin, H. A. W. M. Keck Center for Comparative and Functional Genomics University of Illinois at Urbana-Champaign 340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL 61801, USA Tel: 217 333 5998 Fax: 217 244 5617 Email: h-lewin@uiuc.edu Funding for cattle EST sequencing was provided by the USDA National Research Initiative, Animal Genome Resource Grant AG 99-3205-8534 to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED from Washington University Genome Center. Vector Trimmi g: Cross_match from Washington University Genome Center PHRAP suite. This sequence is vector free and at least 200 bp in length. PCR Primers FORWARD: TAATACCACTCATTATAGGG BACKWARD: ATTAACCCCTCACTAAAG Insert Length: 462 Std Error: 0.00 Plate: BP250023B10 row: D column: 12 Seq primer: AGCGATAACAAATTCACACAGGA High quality sequence stop: 462.

FEATURES source Location/Qualifiers 1..462 /organism="Bos taurus" /db_xref="taxon:9913" /clone="BP250023B10D12" /clone_lib="Soares normalized bovine placenta" /sex="female" /lab_host="DH10B" /note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI; Site 2: NotI; The cDNA library was contributed by the Soares laboratory and it was constructed and normalized as described by Bonaldo, M.F., Lennon, G. and Soares, M.B. (1996), Genome Research 6(9): 791-806." BASE COUNT 110 a 153 c 123 g 73 t 3 others

Query Match 10.4%; Score 34.4; DB 143; Length 462; Best Local Similarity 49.2%; Pred. No. 14; Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 134 ttcagcatcctctgggtccttggatggcgctgcagtcgagacattgatcagagattct 193

Db 285 TTCTGCTTTCAGCTTGGCCCTTTAGANCTCGCGGAGAGCCGCCCTTCCCCACAGGGTGTCC 226

QY 194 agagctgcgcagtcacatgccggcggttgacgctccacacattgcctcgttgcaq 253

Db 225 AGCTCGATGGGCAGCAGCTCCGTGTGTGGTTGATGTGTGGCGCAGGTGGAGCTGATG 166

QY 254 aggatgcctgattctcgttggtgatgttgaccagctcctcaatgagctccttgagggttggg 313

Db 165 TCGGAGCGGTGCTCTCCAGGATGATGCCAGGTGCTCACTGAACCTCCATCATCAGTTGCC 106


```

Db 330 GTTACCCACTCGCGGGCGTGGTGCAGAGAACCCGACCCGCGGATGTGCGCGGG 271
QY 286 ctctcaatgagctccttgagg 307
Db 270 CTCCCGGAGCCTCTCCATGGG 249

RESULT 5
BG260311 757 bp mRNA EST 13-FEB-2001
LOCUS 602371427F1 NIH_MGC_93 Homo sapiens cDNA clone IMAGE:4479367 5',
DEFINITION mRNA sequence.
ACCESSION BG260311
VERSION BG260311.1 GI:12770127
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1 (bases 1 to 757)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Tel: (301) 496-1550
Email: Robert.Strausberg@nih.gov
Tissue Procurement: ATCC
cDNA Library preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM10311 row: f column: 08
High quality sequence stop: 736.
Location/Qualifiers
1. .757
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:4479367"
/clone_lib="NIH_MGC_93"
/tissue_type="transitional cell papilloma, cell line"
/lab_host="DH10B (phage-resistant)"
/Note="Organ: bladder; Vector: pCMV-SPORT6; Site 1: NotI;
Site 2: SalI; Cloned unidirectionally; oligo-dT primed.
Average insert size 1.7 kb. Library enriched for
full-length clones and constructed by Life Technologies.
Note: this is a NIH_MGC Library."
BASE COUNT 186 a 200 c 201 g 170 t
ORIGIN

Query Match 10.7%; Score 35.2; DB 174; Length 757;
Best Local Similarity 49.0%; Pred. No. 9.5;
Matches 94; Conservative 0; Mismatches 98; Indels 0; Gaps 0;

QY 3 tgaatttcctgagcgaataaactcccttcacataggtgagcaggtttttcaccaactgga 62
Db 497 TCAAGTTTCTGGCGCCGAGAGATGCATCTCAAAAGAGTGGGGCTTCACCAAGTTCA 556

QY 63 tcacttcaatttgggtgtctcggtcggttcactggaatccctcgccgcggttttgag 122
Db 557 ATGCTGATCAATTTGAAGACATGCTGGCGTAAAGCGGCTCATCCAGATGGCTTTGGG 616

QY 123 agcacagtctttcagcaccctcttggtctcttggtgagcgctgagtcgagacattga 182
Db 617 GTCAAGTAGATACACCCAGTCGTTGGGCCCTCTGGACAAAGTGGCGGCCCTGSCACTCA 676

QY 183 tcagagattcta 194
Db 677 TGAGGCGCTTCCA 688

```

RESULT 6

```

BF039993/c 462 bp mRNA EST 10-OCT-2000
LOCUS BP250023B10D12 Soares normalized bovine placenta Bos taurus cDNA
DEFINITION clone BP250023B10D12 5', mRNA sequence.
ACCESSION BF039993
VERSION BF039993.1 GI:10757048
KEYWORDS EST.
SOURCE cow.
ORGANISM Bos taurus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovidae; Bovinae; Bos.
REFERENCE 1 (bases 1 to 462)
AUTHORS Lewin, H.A., Soares, M.B., Rebeiz, M., Pardinas, J., Liu, L. and Larson,
J.H.
TITLE Bovine ESTs
JOURNAL Unpublished (2000)
COMMENT Contact: Lewin, H. A.
W. M. Keck Center for Comparative and Functional Genomics
University of Illinois at Urbana-Champaign
340 Edward R. Madigan Laboratory, 1201 W. Gregory Dr., Urbana, IL
61801, USA
Tel: 217 333 5998
Fax: 217 244 5617
Email: h-lewin@uiuc.edu
Funding for cattle EST sequencing was provided by the USDA National
Research Initiative, Animal Genome Resource Grant AG 99-3205-8534
to H. A. Lewin and J. E. Womack. Base Calling/Quality Scores: PHRED
from Washington University Genome Center. Vector trimmi g:
Cross_match from Washington University Genome Center PHRAP suite.
This sequence is vector free and at least 200 bp in length.
PCR primers
FORWARD: TAATACGACTCCTATAGGG
BACKWARD: ATTAACCTCTCAATAAG
Insert Length: 462 Std Error: 0.00
Plate: BP250023B10 row: D column: 12
Seq primer: AGCGATAACAATTTTCACACAGGA
High quality sequence stop: 462.
Location/Qualifiers
1. .462
/organism="Bos taurus"
/db_xref="taxon:9913"
/clone="BP250023B10D12"
/clone_lib="Soares normalized bovine placenta"
/sex="female"
/lab_host="DH10B"
/Note="Organ: placenta; Vector: pT7T3Pac; Site 1: EcoRI;
Site 2: NotI; The cDNA library was contributed by the
Soares laboratory and it was constructed and normalized
as described by Bonaldo, M.F., Lennon, G. and Soares,
M.B. (1996), Genome Research 6(9): 791-806."
BASE COUNT 110 a 153 c 123 g 73 t 3 others
ORIGIN

Query Match 10.4%; Score 34.4; DB 143; Length 462;
Best Local Similarity 49.2%; Pred. No. 14;
Matches 89; Conservative 0; Mismatches 92; Indels 0; Gaps 0;

QY 134 ttccagcctccttggtctcttggtgagcgctgcagtcgagacattgatcagagattct 193
Db 285 TTCTCTTTCAGTTGGCCCTTTAGANCTCGCGAAGCGCCCTTGGCCACAGGGTGTCC 226

QY 194 agagctgcgcagtcacatgccggcggttcagttgagcctccacacatgctgcgttgca 253
Db 225 AGCTCGATGGGAGCAGCTCCGCTGTGTGTTGATGTTGTTGGCGCAGGTGGAGCTGATG 166

QY 254 agggatgctgattctcgtggtgatgttgaccagctcctcaatgagctccttgagggt 313
Db 165 TCGAGCGGTGCTCTCCAGGATGATGGCCAGGTGCTCACTGAACCTCCATCAGCTTGGC 106

```


Dd 1587 RSYSSYCKRCKWYKKTGSTSMKSAGGWGRWRARAARWMYSWSMRRASARMRMRYMWG 1528

Oy 139 catcctcggttcctttgatggcgctgcagtcgacattatcatcacagtacctt 193
::l:::::::::: :ll:: :::::::::::::: ::::::::::: |||
Dd 1527 MMKYCYMMRWNGYTKTGKKTYRKYMRCAYMYCMYYMYWKTTTTT 1473

RESULT 13
BE363650/c
LOCUS BE363650 370 bp mRNA EST 20-JUL-2000
DEFINITION WSI_64_G10.gl_A002 Water-stressed 1 (WSI) Sorghum bicolor cDNA,
mRNA sequence.
ACCESSION BE363650
VERSION BE363650.1 GI:9305207
KEYWORDS EST.
SOURCE sorghum.
ORGANISM Sorghum bicolor
Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae;
Andropogoneae; Sorghum.
REFERENCE 1 (bases 1 to 370)
AUTHORS Cordonnier-pratt,M.-M., Gingle,A., Marsala,C., Sudman,M. and Pratt,L.H.

TITLE An EST database from Sorghum: water-stressed plants
JOURNAL Unpublished (2000)
COMMENT Contact: Cordonnier-Pratt MM
Department of Botany
The University of Georgia
Plant Sciences Building, Rm. 2502, Athens, GA 30602-7271, USA
Tel: 706 542 1860
Fax: 706 542 1805
Email: mmpratt@uga.edu

Sequences have been trimmed to exclude PolyA, vector and regions below Phred quality 16. The threshold for highest quality sequence is 20.
Seq primer: PolyTMix
High quality sequence start: 32
High quality sequence stop: 368
POLYA=Yes,

FEATURES source Location/Qualifiers
1..370
 /organism="Sorghum bicolor"
 /db_xref="taxon:4558"
 (clone_lib="Water-stressed 1 (WSI)"
 /note="Organ: Mix of 5-week old plants on days 7 & 8 after water was withheld; Vector: Lambda zap; Site_l: XhoI; Site_r: EcoRI; The library was made from poly-A RNA in the cloning vector lambda ZAP II. Clones to be sequenced were prepared by mass excision."
BASE COUNT 76 a 110 c 130 g 54 t
ORIGIN

Query Match 10.3%; Score 34; DB 166; Length 370;
Best Local Similarity 56.1% Pred.No.18;
Matches 64; Conservative 0; Mismatches 50; Indels 0; Gaps 0;

Oy 205 gtacatgccggcgtagtgaggtaaacaccataccactctcccgttgacagggagtgctg 264
||| |||| | |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db 167 GTCCATGGCAGCGGC GGCTTC CGCCTCAAGAAGGTGACGAAGCGAAGGAGCGGTG 108
||||| |||| | |||| | |||| | |||| | |||| | |||| | ||||
Oy 265 attctgggtgatgttgaccagctctcaaatgaagctctcttgtgggtgtggagagg 318
||||| |||| | |||| | |||| | |||| | |||| | |||| | ||||
Db 107 CTTC TGGCTGGACTG TGCCAGCGGCCGCTTTG ACCTGCTCTTG ACCTCGCCGAAGGG 54

RESULT 14
BE361027/c
LOCUS BE361027 562 bp mRNA EST 20-JUL-2000
DEFINITION DGI_69_A02.bl_A002 Dark Grown 1 (DG1) Sorghum bicolor cDNA, mrna
sequence.
ACCESSION BE361027
VERSION BE361027.1 GI:9302584

Tel: 0064 9 373 5600
Fax: 0064 9 373 2189

Query Match 10.2%; Score 33.8; DB 163; Length 341;
Best Local Similarity 55.1%; Pred. No. 20;
Matches 65; Conservative 0; Mismatches 53; Indels 0;

	Qy	213	cggcggctgaagttgacgcgtccaccacacatctgccgttcagagggatcgctcatcttggg	272
	Db	281	CGMCGGCTTCCGGTGAAGTTCTCCCCCTTCGTGGTGCTGACTGTATGCTGCTTGTATGG	222
	Qy	273	tgaattgaccagctcctcaatgagctccttgagggcttggggagggagtcacagagct	330
	Db	221	TGATAATTACACAGTGCAGCAAGTCTTCTGGTGTCTGTACTGATGCACCGGCCCT	164

Search completed: May 13, 2001, 11:41:00
Job time: 16535 sec

Query Match
10.3%; Score 34; DB 166; Length 562;

[illegible]

RESULT	15				
LOCUS	BE127683/c				
DEFINITION	DEPA1432 Rat Lambda ZAP Express Library Rattus norvegicus cDNA 5', mRNA sequence.	341 bp	mRNA	EST	15-JUN-2000
ACCESSION	BE127683				
VERSION	BE127683.1	GI:8550422			
KEYWORDS	EST.				
SOURCE	Norway rat.				
ORGANISM	Rattus norvegicus				
	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;				
	Rattus.				

REFERENCE AUTHORS	TITLE	JOURNAL	COMMENT
1 (bases 1 to 341) Slegman, M.A., Murison, J.G., Strachan, L., Kumble, K.D., Glenn, M.P., McGrath, A., Grierson, A., Havukkala, I., Tan, P.L.J. and Watson, J.D.	Expressed sequence tags of cDNA clones from rat dermal papilla cells	unpublished (2000)	Biotechnology Contact: Slegman MA
			Genesis Research and Development Corporation Limited P.O. Box 50, 1 Fox St, Parnell, Auckland, New Zealand

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 14:22:00 ; Search time 79.9 seconds
(without alignments)
93.722 Million cell updates/sec

Title: US-09-451-527-92
Perfect score: 663
Sequence: 1 MALWLTWIALTCGLGLASP.....QLVKNLLTYRGVYRHGNER 131

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : A_Geneseq_0401.*
- 1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
 - 6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
 - 7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT.*
 - 8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
 - 9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT.*
 - 10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT.*
 - 11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT.*
 - 12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT.*
 - 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT.*
 - 16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT.*
 - 17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT.*
 - 18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /cgnl_8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	663	100.0	131	21	Y58221 Canine interleukin
2	647.5	97.7	130	21	Y58223 Canine interleukin
3	561	84.6	110	21	Y58222 Canine mature inte
4	545.5	82.3	110	21	Y58224 Canine mature inte
5	463.5	69.9	132	15	R48624 Sequence of human
6	456.5	68.9	146	13	R27348 Cytokine NC30. R
7	382.5	57.7	112	13	R27347 Protein with cytok
8	382.5	57.7	112	17	R92793 Human interleukin-
9	378.5	57.1	131	15	R48625 Sequence of mouse
10	375.5	56.6	112	13	R27346 Protein with cytok
11	367	55.4	111	17	R92794 Human interleukin-

12	295.5	44.6	111	17	R92795 Murine p600. Mus
13	81	12.2	20	13	R27345 Cytokine signal pe
14	81	12.2	34	13	R27344 Human secreted pro
15	78.5	11.8	665	21	B38312 Gene 38 human secr
16	78.5	11.8	667	21	B38311 TIP120. Rattus ra
17	78.5	11.8	1230	18	W15764 Human ORFX ORF1944
18	78.5	11.8	1230	21	B42180 Human interleukin
19	78	11.8	21	20	Y49702 Recombinantlly prod
20	77.5	11.7	482	19	W62025 Placentl-derived
21	75.5	11.4	482	13	R20641 Human platelet der
22	75.5	11.4	482	17	R77531 Recombinantlly prod
23	75.5	11.4	482	19	W62026 Streptococcus pneu
24	72	10.9	356	21	Y81649 Arabidopsis thalia
25	71.5	10.8	141	21	G35063 Amino acid sequenc
26	71.5	10.8	382	21	Y84919 Human secreted pro
27	71	10.7	279	21	B44998 Drosophila mitofus
28	71	10.7	718	20	W84067 Aquaticine I. The
29	70	10.6	513	11	R04585 T.aquaticus Aquari
30	70	10.6	513	12	R13181 Aqualyzin I. Ther
31	70	10.6	513	16	R67653 A human proliferat
32	69.5	10.5	237	21	Y84892 Amino acid sequenc
33	69.5	10.5	715	20	Y30341 HIV-1-NC7 envelope
34	69.5	10.5	2404	20	W30640 Wheat sulfite redu
35	69	10.4	286	21	Y58998 Human secreted pro
36	68	10.3	221	21	Y91434 Human heparin-bind
37	67	10.1	634	20	Y21548 Human colon cancer
38	66	10.0	101	21	B53687 Arabidopsis thalia
39	66	10.0	283	21	G45469 Arabidopsis thalia
40	66	10.0	299	21	G30635 Arabidopsis thalia
41	66	10.0	299	21	G45468 Arabidopsis thalia
42	66	10.0	312	21	G30634 Arabidopsis thalia
43	66	10.0	357	21	G30633 Arabidopsis thalia
44	66	10.0	1032	21	G45673 Arabidopsis thalia
45	66	10.0	1045	21	G45672 Arabidopsis thalia

ALIGNMENTS

RESULT 1
Y58221
ID Y58221 standard; Protein; 131 AA.
XX
AC Y58221;
XX
XX 14-MAR-2000 (first entry)
XX
XX Canine interleukin-13 (IL-13) clone 80.
DE Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
XX WO9961618-A2.
XX
XX 02-DEC-1999.
XX
XX 28-MAY-1999; 99WO-US11942.
XX
XX 29-MAY-1998; 98US-0087306.
XX
XX (HESK-) HESKA CORP.
XX
XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI: 2000-072623/06
XX
XX N-PSDB; 255555, 255556, 255557, 255558.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 3i; Page 231; 264pp; English.
PS

XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine IL-5, canine IL-13, feline
CC canine or feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, and inhibitors which may be used as
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.

XX Sequence 131 AA;
SQ

Query Match 100.0%; Score 663; DB 21; Length 131;
Best Local Similarity 100.0%; Pred. No. 5.6e-68;
Matches 131; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALWLTVVVIALTCIGLASPSVPTSPPTLKEIEELVNITQNASLCSGMSWVSNLTAG 60
DB 1 malwltvvialtciglaspsvptspptlkeieelvnitqnaslcsngmswvsnltag 60
QY 61 MYCAALESINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVQLVKNLITY 120
DB 61 mycaaleslinvsdcsaigrtrmkalcsqkpaagqissersrtdtkievqlvknllty 120
QY 121 VRGVYRHGNFR 131
DB 121 vrgvyrhgnfr 131

RESULT 2
Y58223
ID Y58223 standard; Protein; 130 AA.
AC Y58223;
XX
XX 14-MAR-2000 (first entry)
DE Canine interleukin-13 (IL-13) clone 78.
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
XX Canis familiaris.
OS
PN WO9961618-A2.
XX
XX 02-DEC-1999.
PD
XX 28-MAY-1999; 99WO-US11942.
PF
XX 29-MAY-1998; 98US-0087306.
PR
XX (HESK-) HESKA CORP.
PA
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR N-PSDB; 255561, 255562, 255563, 255564.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumours or autoimmune disease

XX Claim 3i; Page 237; 264pp; English.
PS
XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine IL-5, canine IL-13, feline
CC canine or feline CD134 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, and inhibitors which may be used as
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.

XX Sequence 130 AA;
SQ

Query Match 97.7%; Score 647.5; DB 21; Length 130;
Best Local Similarity 99.2%; Pred. No. 3.3e-66;
Matches 130; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MALWLTVVVIALTCIGLASPSVPTSPPTLKEIEELVNITQNASLCSGMSWVSNLTAG 60
DB 1 malwltvvialtciglaspsvptspptlkeieelvnitqnaslcsngmswvsnltag 60
QY 61 MYCAALESINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVQLVKNLITY 120
DB 61 mycaaleslinvsdcsaigrtrmkalcsqkpaag-qissersrtdtkievqlvknllty 119
QY 121 VRGVYRHGNFR 131
DB 120 vrgvyrhgnfr 130

RESULT 3
Y58222
ID Y58222 standard; Protein; 111 AA.
XX
XX AC Y58222;
XX
XX 14-MAR-2000 (first entry)
DE Canine mature interleukin-13 (IL-13) clone 80.
XX
XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
XX Canis familiaris.
OS
PN WO9961618-A2.
XX
XX 02-DEC-1999.
PD
XX 28-MAY-1999; 99WO-US11942.
PF
XX 29-MAY-1998; 98US-0087306.
PR
XX (HESK-) HESKA CORP.
PA
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
XX WPI; 2000-072623/06.
DR N-PSDB; 255559, 255560.
XX

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 useful for treating or preventing e.g. tumors or autoimmune disease

PS Claim 3i; Page 234; 264pp; English.

XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
 CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
 CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
 CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
 CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 111 AA;

Query Match 84.6%; Score 561; DB 21; Length 111;

Best Local Similarity 100.0%; Pred. No. 2e-56;

Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 SPVTPSPTLKELIEELVNTQNASLNGSMVSNLTAGMYCAALESINVSDCSAIOR 80
 DB 1 spvtpspptkelielvnitqnaslncngsmvsnltagmycaalesinvsdcsaigr 60
 QY 81 TQMLKALCSQKPAAGQISSERSRDTKIEVLQVKNLLTYVRGVYRHGNFR 131
 DB 61 tqmlkalcsqkpaagqissersrtdkievqlvknlltyvrgvyrhgnfr 111

RESULT 4

Y58224
 ID Y58224 standard; Protein; 110 AA.

XX Y58224;

XX 14-MAR-2000 (first entry)

XX Canine mature interleukin-13 (IL-13) clone 78.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.

XX WO9961618-A2.

XX 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

XX 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

XX Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI; 2000-072623/06.

DR N-PSDB; 255565, 255566.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease

XX
 PS
 XX

Claim 3i; Page 240; 264pp; English.

CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
 CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
 CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
 CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
 CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.

XX Sequence 110 AA;

Query Match 82.3%; Score 545.5; DB 21; Length 110;

Best Local Similarity 99.1%; Pred. No. 1.1e-54;

Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 21 SPVTPSPTLKELIEELVNTQNASLNGSMVSNLTAGMYCAALESINVSDCSAIOR 80
 DB 1 spvtpspptkelielvnitqnaslncngsmvsnltagmycaalesinvsdcsaigr 60

QY 81 TQMLKALCSQKPAAGQISSERSRDTKIEVLQVKNLLTYVRGVYRHGNFR 131

DB 61 tqmlkalcsqkpaag-qissersrtdkievqlvknlltyvrgvyrhgnfr 110

RESULT 5

R48624

ID R48624 standard; Protein; 132 AA.

XX R48624;

XX 14-SEP-1994 (first entry)

XX Sequence of human interleukin-13 (IL-13).

XX Interleukin-13; lymphokine; immunological disorder; therapy;
 KW diagnostic.

XX Homo sapiens.

XX WO9404680-A.

XX 03-MAR-1994.

XX 18-AUG-1993; 93WO-US07645.

XX 21-AUG-1992; 92US-0933416.

XX 29-JAN-1993; 93US-0010977.

XX 01-FEB-1993; 93US-0012543.

XX (SCHE) SCHERING CORP.

XX Aversa G, Banchereau J, Briere F, Coffman RL, Cooks BG;

XX Culpepper, Dang W, De Vries J, De Waal Malefyt R;

XX Doherty TM, Heath A, McKenzie A, Punnonen J, Zurawski G;

XX WPI; 1994-083197/10.

XX N-PSDB; Q56692.

at position 41 which is either Asp or Gly. The cytokine acts on monocytes and B lymphocytes and is useful in treatment of tumours and some infections and inflammatory conditions.
See Q28941-Q28947.

Sequence 112 AA;

Query Match 57.7%; Score 382.5; DB 13; Length 112;
Best Local Similarity 70.0%; Pred. No. 4.7e-36;
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

Qy 22 PVTPSPTLKELIEELVNITQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIOR 80
||| | :||||| ||||| | ||||| :||||| ||||| ||||| ||||| ||||| :||| :|

Db 2 pvpstairelieelvnitqkqaplcngsmvwsinltagmycaalesinvsdcsaiek 61
||| | :||||| ||||| | ||||| :||||| ||||| ||||| ||||| ||||| :||| :|

Qy 81 TQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVRHGNF 130
|||| | :||| | ||||| | ||||| :||| :|

Db 62 tqrmisgfcphkvsagqfsslhvrdtkievagfvkdllhlklifregrf 111

RESULT 8

R92793
ID R92793 standard; Protein; 112 AA.

XX R92793;

AC R92793;

DT 24-MAY-1996 (first entry)

DE Human interleukin-13 mutein 1.

XX Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;
KW diagnosis; therapy; cancer; inflammation; degenerative disease.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 11 /note= "Glu at position 11 may be replaced by an
FT amidated amino acid, including Lys"

FT Misc-difference 64 /note= "Arg at position 64 may be replaced by an
FT acidic amino acid, including Asp"

XX WO9604306-A2.

XX 15-FEB-1996.

XX 31-JUL-1995; 95WO-US089950.

XX 01-AUG-1994; 94US-0284393.

XX (SCHE) SCHERING CORP.

XX Zurawski G, Zurawski SM;

XX WPI; 1996-129335/13.

XX Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
XX murine P600 contg. amino acid substitutions. - useful for the
XX diagnosis and treatment of cancer, inflammation, etc.

XX Claim 12; Page 46; 52pp; English.

XX Muteins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain
XX amino acid substitutions at amino acid position 11 in helix A and/or
XX at position 64 in helix C. They are obtd. by site-directed
XX mutagenesis of natural IL-13 sequences. The muteins antagonise the
XX activity of IL-13 or IL-4. They have partial cytokine agonist
XX activity, exhibit less than 80% maximal agonist activity of natural
XX IL-2, and/or antagonize cytokine activity by least about 50% when
XX present at a 100-fold excess. They and other cytokine muteins
XX (see also R92790-92, R92795-802) are useful in the screening of

CC cytokine and cytokine receptor levels, and in the diagnosis or
CC treatment of e.g. inflammation, cancer, and degenerative disorders.
XX
SQ Sequence 112 AA;

Query Match 57.7%; Score 382.5; DB 17; Length 112;
Best Local Similarity 70.0%; Pred. No. 4.7e-36;
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

Qy 22 PVTPSPTLKELIEELVNITQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIOR 80
||| | :||||| ||||| | ||||| :||||| ||||| ||||| ||||| ||||| :||| :|

Db 2 pvpstairelieelvnitqkqaplcngsmvwsinltagmycaalesinvsdcsaiek 61
||| | :||||| ||||| | ||||| :||||| ||||| ||||| ||||| ||||| :||| :|

Qy 81 TQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKNLLTYVRGVRHGNF 130
|||| | :||| | ||||| | ||||| :||| :|

Db 62 tqrmisgfcphkvsagqfsslhvrdtkievagfvkdllhlklifregrf 111

RESULT 9

R48625
ID R48625 standard; Protein; 131 AA.

XX R48625;

AC R48625;

DT 14-SEP-1994 (first entry)

DE Sequence of mouse p600.

XX Interleukin-13; lymphokine; p600; immunological disorder; therapy;
KW diagnostic.

XX Mus musculus.

XX WO9404680-A.

XX 03-MAR-1994.

XX 18-AUG-1993; 93WO-US07645.

XX 21-AUG-1992; 92US-0933416.

XX 29-JAN-1993; 93US-0010977.

XX 01-FEB-1993; 93US-0012543.

XX (SCHE) SCHERING CORP.

XX Aversa G, Bancheireau J, Briere F, Coffman RL, Cooks BG;
XX Culpepper, Dang W, De Vries J, De Waal Malefyt R;
XX Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;

XX WPI; 1994-083197/10.

XX N-PSDB; Q56693.

XX Purified interleukin-13 proteins and antibodies - obtd. using
XX mouse gene encoding related protein p600

XX Disclosure; Page 128-129; 135pp; English.

XX An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction
XX digest of the mouse p600 cDNA clone was isolated. This fragment,
XX which encompasses most of the coding region of the mouse p600 cDNA,
XX was radioactively labelled and hybridised with filter lifts prepd.
XX from a cDNA library made from a clone of an A10 T cell line. One
XX clone, designated PA 10.66, was subcloned into M13 and sequenced.
XX This sequence encodes human IL-13.

XX Sequence 131 AA;

Query Match 57.1%; Score 378.5; DB 15; Length 131;
Best Local Similarity 59.0%; Pred. No. 1.7e-35;
Matches 79; Conservative 19; Mismatches 29; Indels 7; Gaps 3;

```
QY 1 MALWLVVIALTCLGLASPSVTPSP-----TLKELIEELVNITONQASLCNGSMVWSVN 56
DB 1 malwvtavialaclggaapgvprsvslptlklleielvsnitqdcplcngsmwsvd 60
QY 57 LTAGMYCAALESINVSQSAIQRTQRMKALCSQKPAAGQISSRSRDTKIEVIQLVKN 116
DB 61 laaggfvaldslniscnalyrtqrlhglcnrk-aptvss--lpdtkievahfuk 117
QY 117 LLTVRGVYRHGNF 130
DB 118 llsytkqlfrhgp 131

RESULT 10
R27346
ID R27346 standard; Protein; 112 AA.
AC R27346;
XX
XX
DT 24-FEB-1993 (first entry)
XX
XX Protein with cytokine activity encoded by Nal.
XX
XX -Interleukin; chemotaxis; immunomodulation; inflammation.
XX
XX EP506574-A.
XX
XX 30-SEP-1992.
XX
XX 27-MAR-1992; 92EP-0400858.
XX
XX 29-MAR-1991; 91FR-0003904.
XX
XX 08-JAN-1992; 92FR-0000137.
XX
XX (SNFI ) ELF SANOFI.
XX
XX Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
XX Lepilaotus P, Magazin M, Minty A;
XX
XX WPI; 1992-325841/40.
XX
XX N-PSDB; Q28943.
XX
XX New cytokine having immunomodulatory activity - useful for
XX treating tumours and infectious or inflammatory conditions
XX
XX Claim 1; Page 60; 78pp; French.
XX
XX This protein is one of two possible forms of a new cytokine
XX produced by T lymphocytes induced by phorbol-2-myristate-3-acetate
XX and phytohaemagglutinin. The proteins differ only in the amino acid
XX at position 41 which is either Asp or Gly. The cytokine acts on
XX monocytes and B lymphocytes and is useful in treatment of tumours
XX and some infections and inflammatory conditions.
XX See Q28941-Q28947.
XX
XX Sequence 112 AA;

Query Match 56.6%; Score 375.5; DB 13; Length 112;
Best Local Similarity 69.1%; Pred. No. 3e-35;
Matches 76; Conservative 11; Mismatches 22; Indels 1; Gaps 1;

QY 22 PVTPTSPTLKEIEELVNITONQ-ASLCNGSMVWSVNLTAGMYCAALESINVSQSAIQ 80
DB 2 pvpstaltrelleielvntqkqplcngsmwsvntadmycaaleslinvsgcsaiek 61
QY 81 TQRMKALCSQKPAAGQISSRSRDTKIEVIQLVKNLLTYVRGVYRHGNF 130
DB 62 tqrmalsgfcphkvsagfsslhvrdtkievagfvkdlllhkklfregfr 111

RESULT 11
R27346
ID R27346 standard; Protein; 112 AA.
XX
```

```
ID R92794 standard; Protein; 111 AA.
XX
XX R92794;
XX
XX 24-MAY-1996 (first entry)
XX
XX Human interleukin-13 mutein 2.
XX
XX Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;
XX diagnosis; therapy; cancer; inflammation; degenerative disease.
XX
XX Synthetic.
XX
XX Key Location/Qualifiers
XX Misc-difference 11 /note= "Glu at position 11 may be replaced by an
XX FT amidated amino acid, including Lys"
XX FT Misc-difference 64 /note= "Arg at position 64 may be replaced by an
XX FT acidic amino acid, including Asp"
XX
XX WO9604306-A2.
XX
XX 15-FEB-1996.
XX
XX 31-JUL-1995; 95WO-US08950.
XX
XX 01-AUG-1994; 94US-0284393.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Zurawski G, Zurawski SM;
XX
XX WPI; 1996-129335/13.
XX
XX Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
XX murine P600 contg. amino acid substitutions. - useful for the
XX diagnosis and treatment of cancer, inflammation, etc.
XX
XX Claim 12; Page 46; 52pp; English.
XX
XX Muteins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain
XX amino acid substitutions at amino acid position 11 in helix A and/or
XX at position 64 in helix C. They are obtd. by site-directed
XX mutagenesis of natural IL-13 sequences. The muteins antagonise the
XX activity of IL-13 or IL-4. They have partial cytokine agonist
XX activity, exhibit less than 80% maximal agonist activity of natural
XX IL-2, and/or antagonize cytokine activity by least about 50% when
XX present at a 100-fold excess. They and other cytokine muteins
XX (see also R92790-92, R92795-802) are useful in the screening of
XX cytokine and cytokine receptor levels, and in the diagnosis or
XX treatment of e.g. inflammation, cancer, and degenerative disorders.
XX
XX Sequence 111 AA;

Query Match 55.4%; Score 367; DB 17; Length 111;
Best Local Similarity 69.1%; Pred. No. 2.8e-34;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 22 PVTPTSPTLKEIEELVNITONQ-ASLCNGSMVWSVNLTAGMYCAALESINVSQSAIQ 80
DB 2 pvpstaltrelleielvntqkqplcngsmwsvntadmycaaleslinvsgcsaiek 61
QY 81 TQRMKALCSQKPAAGQISSRSRDTKIEVIQLVKNLLTYVRGVYRHGNF 130
DB 62 tqrmalsgfcphkvsag-fsslhvrdtkievagfvkdlllhkklfregfr 110

RESULT 12
R92795
ID R92795 standard; Protein; 111 AA.
XX
```

AC R92795;
 XX
 DT 24-MAY-1996 (first entry)
 XX
 DE Murine P600.
 XX
 KW Cytokine; mutein; P600; interleukin-13; IL-13; agonist; antagonist;
 KW diagnosis; therapy; cancer; inflammation; degenerative disease.
 XX
 OS Mus musculus.
 XX
 FH Key Location/Qualifiers
 FT Misc-difference 67
 ET /note= "Arg at position 67 may be replaced by an
 ET acid amino acid, including Asp"
 FN
 PN WO9604306-A2.
 XX
 PD 15-FEB-1996.
 XX
 PF 31-JUL-1995; 95WO-US089950.
 XX
 PR 01-AUG-1994; 94US-0284393.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Zurawski G, Zurawski SM;
 XX
 DR WPI; 1996-129335/13.
 XX
 PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
 PT murine P600 contg. amino acid substitutions. - useful for the
 PT diagnosis and treatment of cancer, inflammation, etc.
 XX
 PS Claim 12; Page 46; 52pp; English.
 XX
 CC Muteins of mouse P600 (R92795) contain amino acid substitutions at
 CC amino acid position 67 in helix C. They are obtd. by site-directed
 CC mutagenesis of natural P600 sequences. The muteins antagonise the
 CC activity of IL-13 or IL-4. They have partial cytokine agonist
 CC activity, exhibit less than 80% maximal agonist activity of natural
 CC IL-2, and/or antagonize cytokine activity by least about 50% when
 CC present at a 100-fold excess. They and other cytokine muteins
 CC (see also R92790-94, R92796-802) are useful in the screening of
 CC cytokine and cytokine receptor levels, and in the diagnosis or
 CC treatment of e.g. inflammation, cancer, and degenerative disorders.
 XX
 SQ Sequence 111 AA;

Query Match 44.6%; Score 295.5; DB 17; Length 111;
 Best Local Similarity 55.9%; Pred. No. 4e-26;
 Matches 62; Conservative 18; Mismatches 28; Indels 3; Gaps 2;

Qy 20 PSPVTPSPTLKELIEELVNITQASLNGSMVSNLTAGMYCAALESINVSDCSAIQ 79
 Db 4 prsvslptlkllelelnitqdeplcngsmvsvdlaagfcvaldsitniscnaly 63

Qy 80 RTQRLKALCSQKPAAGQISSRSRDTKEVTLQVKNLLTYRGVYRHGNF 130
 Db 64 rtqrlhglcnrk-apttvs--lpotkievahftklisytckqlfrhgp 111

RESULT 13
 R27345
 ID R27345 standard; peptide; 20 AA.
 XX
 AC R27345;
 XX
 DT 24-FEB-1993 (first entry)
 XX
 DE Cytokine signal peptide b4.

KW Interleukin; chemotaxis; immunomodulation; inflammation.
 XX
 PN EP506574-A.
 XX
 PD 30-SEP-1992.
 XX
 PF 27-MAR-1992; 92EP-0400858.
 XX
 PR 29-MAR-1991; 91FR-0003904.
 PR 08-JAN-1992; 92FR-0000137.
 XX
 PA (SNFI) ELF SANOFI.
 XX
 PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
 PI Leplatois P, Magazin M, Minty A;
 XX
 DR WPI; 1992-325841/40.
 DR N-PSDB; Q28941.
 XX
 PT New cytokine having immunomodulatory activity - useful for
 PT treating tumours and infectious or inflammatory conditions
 XX
 PS Claim 12; Page 61; 78pp; French.
 XX
 CC The b4 peptide is a preferred signal peptide to be fused to the
 CC N-terminus of the new cytokine. The last two amino acids (Ser-Pro)
 CC are opt. absent; when absent the signal peptide is designated b3.
 CC See Q28942-Q28947.
 XX
 SQ Sequence 20 AA;

Query Match 12.2%; Score 81; DB 13; Length 20;
 Best Local Similarity 85.0%; Pred. No. 0.012;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 1 MALWLTVVIALTCGLGASP 20
 Db 1 malllttvialtcglgasp 20

RESULT 14
 R27344
 ID R27344 standard; peptide; 34 AA.
 XX
 AC R27344;
 XX
 DT 21-MAY-1998 (first entry)
 XX
 DE Cytokine signal peptide b2.
 XX
 KW Interleukin; chemotaxis; immunomodulation; inflammation.
 XX
 OS Homo sapiens.
 XX
 PN EP506574-A.
 XX
 PD 30-SEP-1992.
 XX
 PF 27-MAR-1992; 92EP-0400858.
 XX
 PR 29-MAR-1991; 91FR-0003904.
 PR 08-JAN-1992; 92FR-0000137.
 XX
 PA (SNFI) ELF SANOFI.
 XX
 PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
 PI Leplatois P, Magazin M, Minty A;
 XX
 DR WPI; 1992-325841/40.
 DR N-PSDB; Q28941.
 XX
 PT New cytokine having immunomodulatory activity - useful for

PT treating tumours and infectious or inflammatory conditions
 XX
 PS Claim 12; Page 61; 78pp; French.
 XX
 CC The b2 peptide is a preferred signal peptide to be fused to the
 CC N-terminus of the new cytokine. The last two amino acids (Ser-Pro)
 CC are opt. absent; when absent the signal peptide is designated bl.
 CC See Q28942-Q28947.
 XX
 SQ Sequence 34 AA;
 Query Match 12.28; Score 81; DB 13; Length 34;
 Best Local Similarity 85.0%; Pred. No. 0.025;
 Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 OY 1 MALWLTVVVIALTCGLGLASP 20
 DB 15 malllttvialtcglgfpasp 34
 RESULT 15
 B38312
 ID B38312 standard; Protein; 665 AA.
 XX
 AC B38312;
 XX
 DT 30-JAN-2001 (first entry)
 XX
 DE Human secreted protein sequence encoded by gene 38 SEQ ID NO:168.
 XX
 KW Human; secreted protein; diagnosis; immunosuppressive; antiarthritic;
 KW antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic;
 KW cerebroprotective; nootropic; neuroprotective; antibacterial; virucide;
 KW fungicide; ophthalmological; gene therapy; autoimmune disease; infection;
 KW hyperproliferative disorder; cardiovascular disorder; angiogenesis;
 KW cerebrovascular disorder; nervous system disorder; ocular disorder;
 KW wound healing; skin aging; food additive; preservative.
 XX
 OS Homo sapiens.
 XX
 PN WO200058469-A1.
 XX
 PD 05-OCT-2000.
 XX
 PF 23-MAR-2000; 2000WO-US07579.
 XX
 PR 26-MAR-1999; 99US-0126509.
 PR 07-JAN-2000; 2000US-0174853.
 XX
 PA (HUMA-) HUMAN GENOME SCI INC.
 XX
 PI Rosen CA, Ruben SM, Komatsoulis G;
 XX
 DR WPI; 2000-594642/56.
 XX
 PT Isolated nucleic acid molecule encoding a human secreted protein is
 PT used in preventing, treating or ameliorating a medical condition -
 XX
 PS Disclosure; Page 407-409; 416pp; English.
 XX
 CC The polynucleotide sequences given in C69455 to C69502 encode the human
 CC secreted proteins given in B38203 to B38250. B38251 to B38320 represent
 CC human secreted polypeptide sequences and proteins homologous to them,
 CC which are given in the exemplification of the present invention. Human
 CC secreted proteins have activities based on the tissues and cells the
 CC genes are expressed in. Example of activities include: immunosuppressive;
 CC antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant;
 CC vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial;
 CC virucide; fungicide; and ophthalmological. The polynucleotides and
 CC polypeptides can be used to prevent, treat or ameliorate a medical
 CC condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs,
 CC chickens or sheep. They are also used in diagnosing a pathological

CC condition or susceptibility to a pathological condition. Disorders which
 CC are diagnosed or treated include autoimmune diseases, hyperproliferative
 CC disorders, cardiovascular disorders, cerebrovascular disorders,
 CC angiogenesis, nervous system disorders, infections caused by bacteria,
 CC viruses and fungi and ocular disorders. The polypeptides can also be used
 CC to aid wound healing and epithelial cell proliferation, to prevent skin
 CC aging due to sunburn, to maintain organs before transplantation, for
 CC supporting cell culture of primary tissues, to regenerate tissues and in
 CC chemotaxis. The polypeptides can also be used as a food additive or
 CC preservative to increase or decrease storage capabilities. C69446 to
 CC C69454 and B38202 represent sequences used in the exemplification of the
 CC present invention.
 XX
 SQ Sequence 665 AA;
 Query Match 11.8%; Score 78.5; DB 21; Length 665;
 Best Local Similarity 31.0%; Pred. No. 2.7;
 Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;
 OY 5 LTVVIALTCGLGLASPPVTPPTLKELEELVN-ITQNASLCSNGSMV-----WSV 55
 DB 479 lttvkaitliag--splkidlrpvigegvpilasflrknqraiklqtlalsaldilliknysd 536
 OY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSOKPAAGQISSERSRDTKIEVIQ 112
 DB 537 sitaamidavldelpplisesdmhvsqmaiflittlakvypss---lsklsqsilnelig 593
 OY 113 LVKNLL 118
 DB 594 lvrsl 599
 Search completed: May 13, 2001, 17:47:33
 Job time: 12333 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 14:26:17 ; Search time 42.06 seconds
(without alignments)
59.834 Million cell updates/sec

Title: US-09-451-527-92
Perfect score: 663
Sequence: 1 MALWLTWVIALTCGLGLASP.....QLVKNLLTYRGVYRHGNGR 131

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgnl_7/ptodata/1/1aa/5A-COMB.pep.*
2: /cgnl_7/ptodata/1/1aa/5B-COMB.pep.*
3: /cgnl_7/ptodata/1/1aa/6A-COMB.pep.*
4: /cgnl_7/ptodata/1/1aa/6B-COMB.pep.*
5: /cgnl_7/ptodata/1/1aa/PCTUS-COMB.pep.*
6: /cgnl_7/ptodata/1/1aa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	463.5	69.9	132	1	US-08-012-543-2
2	463.5	69.9	132	5	PCT-US93-07645A-2
3	463.5	69.9	132	5	PCT-US93-07645-2
4	456.5	68.9	146	1	US-08-371-121-16
5	382.5	57.7	112	1	US-08-284-393B-4
6	382.5	57.7	112	5	PCT-US95-08950-4
7	378.5	57.1	131	1	US-08-012-543-4
8	378.5	57.1	131	1	US-08-371-121-25
9	378.5	57.1	131	5	PCT-US93-07645A-4
10	378.5	57.1	131	5	PCT-US93-07645-4
11	375.5	56.6	112	1	US-08-371-121-1
12	371.5	56.0	112	1	US-08-284-393B-15
13	367	55.4	111	1	US-08-284-393B-5
14	367	55.4	111	5	PCT-US95-08950-5
15	356	53.7	111	1	US-08-284-393B-15
16	295.5	44.6	111	1	PCT-US95-08950-6
17	295.5	44.6	111	5	PCT-US95-08950-6
18	288.5	43.5	111	1	US-08-284-393B-16
19	81	12.2	20	1	US-08-371-121-8
20	81	12.2	34	1	US-08-371-121-6
21	71	10.7	718	4	US-09-090-808-2
22	70	10.6	18	1	US-08-371-121-7
23	70	10.6	32	1	US-08-371-121-5
24	70	10.6	1754	1	US-07-745-206A-13
25	70	10.6	1754	2	US-08-311-363-13
26	65.5	9.9	477	2	US-08-770-544-16
27	64.5	9.7	268	2	US-08-176-414B-2

28	64.5	9.7	268	2	US-08-687-559-25	Sequence 25, Appl
29	64	9.7	168	3	US-09-188-579-85	Sequence 85, Appl
30	64	9.7	206	3	US-09-041-889-6	Sequence 6, Appl
31	64	9.7	206	3	US-08-837-058-6	Sequence 6, Appl
32	64	9.7	228	4	US-08-569-221A-2	Sequence 2, Appl
33	63.5	9.6	338	1	US-07-809-457A-16	Sequence 16, Appl
34	63.5	9.6	338	1	US-08-553-943-16	Sequence 16, Appl
35	63.5	9.6	338	5	PCT-US91-09437-16	Sequence 16, Appl
36	63.5	9.6	1461	2	US-08-993-228-10	Sequence 10, Appl
37	63	9.5	599	1	US-08-232-619-2	Sequence 2, Appl
38	63	9.5	599	5	PCT-US95-04075-2	Sequence 2, Appl
39	63	9.5	731	1	US-08-731-716-2	Sequence 2, Appl
40	63	9.5	848	4	US-08-976-255-10	Sequence 10, Appl
41	63	9.5	871	2	US-08-775-009-35	Sequence 35, Appl
42	62	9.4	496	2	US-08-696-349-2	Sequence 2, Appl
43	62	9.4	496	5	PCT-US96-13156-2	Sequence 2, Appl
44	62	9.4	1117	2	US-08-841-483-6	Sequence 6, Appl
45	61.5	9.3	338	3	US-08-722-184-4	Sequence 4, Appl

ALIGNMENTS

RESULT 1
US-08-012-543-2
; Sequence 2, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-543-2

Qy	22	PVTSPETLKELEELVNITQNO-ASGCSGSMVSVNLTAGMYCAALESINVSQCSATOR	806
Db	2	PVPFSTALRELIEELVNITQNOKAPLCSGSMVSVNLTAGMYCAALESINVSQCSATRK	611
Qy	81	TORMLKALCSOKPAGOSQSSERSDRTKIEVTLVKNNLITYRGVYVRHGNF	130
Db	62	TORMLSGFCPHKVSAGQFSSLHVDRDKIEVAQFVKDOLLHLKLPFGPF	111

RESULT 6
 PCT-US95-08950-4
 : Sequence 4, Application PC/TUS9508950
 : GENERAL INFORMATION:
 : APPLICANT: Zurawski, Sandra M.
 : APPLICANT: Zurawski, Gerard
 : TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
 : NUMBER OF SEQUENCES: 13
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: DNAX Research Institute
 : STREET: 901 California Avenue
 : CITY: Palo Alto
 : STATE: California
 : COUNTRY: USA
 : ZIP: 94304-1104
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: PatentIn Release #1.0, Version #1.25
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: PCT/US95/08950
 : FILING DATE:
 : CLASSIFICATION:
 : PRIOR APPLICATION DATA:
 : APPLICATION NUMBER: US 08/284,393
 : FILING DATE: 01-AUG-1994
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Ching, Edwin P.
 : REGISTRATION NUMBER: 34,090
 : REFERENCE/DOCKET NUMBER: DX0389
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: 415-852-9196
 : TELEFAX: 415-496-1200
 : INFORMATION FOR SEQ ID NO: 4:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 112 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: linear

COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08950
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,393
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,030
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear


```

COMPUTER READABLE FORM:
ZIP: 20007-5109
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25

```


RESULT 15

```

Query Match      53.7%; Score 356; DB 1; Length 111;
Best Local Similarity 67.3%; Pred. No. 8.4e-36;
Matches 74; Conservative 12; Mismatches 22; Indels 2; Gaps 2;

Qy   22 PVTSPILKELIELVNITQNQ-ASLNGSMVWSVNLTAGMYCAALESLINVSCSAIQR 80
     ||| :|||:|||:||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|
Db   2 PVPESTALRKLEELVNITQNQAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEK 61

Qy   81 TORMLKALCOKPAAGQISSRSRDTKIEVLQLVKNNLLTYVRGVYRHGNF 130
     ||| :||| :||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   62 TDQLSGFCPHKVSAQ-FSSLHVHVDRTKIEVAQFVKDLLHLKLFLREGFR 110

```


Result No.	Query	Score	Match	Length	DB	ID	Description
1	463.5	69.9	146	1	A47481	interleukin-13 pre	
2	378.5	57.1	131	2	E30552	T-cell activation	
3	378	57.0	131	2	I52290	interleukin-13 - r	
4	78.5	11.8	1230	1	T42735	TBP-interacting pr	
5	75.5	11.4	482	1	S03904	platelet-derived e	
6	75.5	11.4	505	2	E83551	conserved hypothet	
7	75	11.3	430	2	S77393	cell division prot	
8	74	11.2	261	2	S52110	sepiapterin reduct	
9	74	11.2	262	2	A36024	sepiapterin reduct	
10	73.5	11.1	586	2	T51211	hypothetical prote	
11	73	11.0	701	2	S17196	transcription fact	
12	73	11.0	1806	2	T23298	hypothetical prote	
13	72.5	10.9	425	2	T50355	hypothetical prote	
14	72	10.9	211	1	HSPG1T	histone H1t - pig	
15	72	10.9	431	2	S47538	acrosin (EC 3.4.21	
16	71.5	10.8	382	1	A60112	42K membrane antig	
17	71	10.7	261	2	JQ1176	sepiapterin reduct	
18	70.6	10.6	382	2	S15578	ipac protein - Shi	
19	70	10.6	513	1	A35742	aqualysin (EC 3.4.	
20	70	10.6	677	2	S15667	transcription fact	
21	70	10.6	2195	2	T34284	hypothetical prote	
22	69.5	10.5	267	2	JC1339	movement protein -	
23	69.5	10.5	1057	2	T38694	probable translati	
24	69	10.4	208	2	I70195	histone H1t - rhes	
25	69	10.4	323	1	GHRB	Ig gamma chain C r	
26	69	10.4	1026	2	T05882	hypothetical prote	
27	68.5	10.3	494	2	F82660	penicillin binding	
28	68.5	10.3	559	2	T00714	hypothetical prote	
29	68.5	10.3	2606	2	T03159	large tegument pro	

Db 15 MALLTTVTIALTCLGGFASPGVPPTALRELIELVNITONKAPLCNGSMWVSINLTA 74
QY 60 GWCAALESINVSDCAIQTORMLKALCSOKPAAGQISSERSRDTKIEVQLVKNLT 119
Db 75 GWCAALESINVSDCAIQTORMLKALCSOKPAAGQISSERSRDTKIEVQLVKNLT 134
QY 120 YRGVYRHHGNF 130
Db 135 HLKLLFREGRF 145

RESULT 2
T-cell activation protein p60 precursor - mouse
C:Species: Mus musculus (house mouse)
C>Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 16-Jul-1999
C:Accession: E30552
R:Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142: 679-687, 1989
A:Title: A family of small inducible proteins secreted by leukocytes are members of a new class of various activation processes.
A:Reference number: A30552; MUID:89093958
A:Accession: E30552
A:Molecule type: mRNA
A:Residues: 1-131 <BRO>
A:Cross-references: GB:M23504; NID:g533246; PIDN:AAA40149.1; PID:g533247
C:Superfamily: Interleukin-13

Query Match 57.1%; Score 378.5; DB 2; Length 131;
Best Local Similarity 59.0%; Pred. No. 2.3e-30;
Matches 79; Conservative 19; Mismatches 29; Indels 7; Gaps 3;

QY 1 MALWLTVVIALTCLGGIASPVPPTSP---TLKELIEELVNITONKASLCNGSMWVSN 56
Db 1 MALWTVAVLALACGLGAAPGVPVRSVSLPLTLKELIEELSNITODQTPLCNGSMWVSD 60
QY 57 LTAGMYCAALESINVSDCAIQTORMLKALCSOKPAAGQISSERSRDTKIEVQLVKN 116
Db 61 LAAGGFCVALDSLTNISCNAIYRTORILHGLCNK-APTTVSS--LPDTRKIEVAHFITK 117
QY 117 LTYVYRGVYRHHGNF 130
Db 118 LLSYTKQLFRHGP 131

RESULT 3
Interleukin-13 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I52290
R:Lakkis, F.G.; Cruet, E.N.
Biochem. Biophys. Res. Commun. 197, 612-618, 1993
A:Title: Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expression
A:Reference number: I52290; MUID:94092138
A:Accession: I52290
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-131 <RES>
A:Cross-references: GB:I26913; NID:g438875; PIDN:AAA16478.1; PID:g438876
C:Genetics:
A:Gene: IL-13
C:Superfamily: Interleukin-13

Query Match 57.0%; Score 378; DB 2; Length 131;
Best Local Similarity 59.0%; Pred. No. 2.6e-30;
Matches 79; Conservative 20; Mismatches 27; Indels 8; Gaps 4;

QY 1 MALWLTVVIALTCLGGIASPVP---TPSPTLKELIEELVNITONK-ASLCNGSMWVSN 55
Db 1 MALWTVAVLALACGLGATPGVVRRTSPVVALRELIELSNITODQTPSLCNSMWSV 60

QY 56 NLTAGMYCAALESINVSDCAIQTORMLKALCSOKPAAGQISSERSRDTKIEVQLVKN 115
Db 61 DUTAGGFCVALESINISSNAIHRITRLINGLCNOK--ASDVASS-PPDTKIEVAQFTS 117
QY 116 NLTYVYRGVYRHHGN 129
Db 118 KLLNTYSKQLFRYGH 131

RESULT 4
T42735
TBP-interacting protein TIP120 - rat
C:Species: Rattus norvegicus (Norway rat)
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42735
R:Yogotsawa, S.; Makino, Y.; Yoshida, T.; Kishimoto, T.; Muramatsu, M.; Tamura, T.
Biochem. Biophys. Res. Commun. 229, 613-617, 1996
A:Title: Molecular cloning of a novel 120-kDa TBP-interacting protein.
A:Reference number: 222253; MUID:97127450
A:Accession: T42735
A:Status: preliminary; translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 1-1230 <YOG>
A:Cross-references: EMBL:D87671; NID:g1799569; PIDN:BAAL3432.1; PID:g1799570
C:Genetics:
A:Gene: tip120
C:Function:
A:Description: considered to participate in transcription regulation through the interaction with TBP

Query Match 11.8%; Score 78.5; DB 2; Length 1230;
Best Local Similarity 31.0%; Pred. No. 14;
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;

QY 5 LTVVIALTCLGGIASPVPPTSPPTLKEELVN-ITONKASLCNGSMV-----WSV 55
Db 626 LTVVIALTLIAG--SPLKIDLPVIGEGVPIILASFLRNKQNRALKGLTSLALDILIKNSD 693
QY 56 NLTAGMYCAALES---LINVSDCAIQTORMLKALCSOKPAAGQISSERSRDTKIEVQ 112
Db 684 SLTAAMIDAVLDLPLISESDMHVSQMAISFLTLLAKVYPSS---LSKISGILNELIG 740
QY 113 LVKNLL 118
Db 741 LVRSPL 746

RESULT 5
S03904
platelet-derived endothelial cell growth factor precursor [validated] - human
N:Contains: Thymidine phosphorylase (EC 2.4.2.4)
C:Species: Homo sapiens (man)
C>Date: 23-Oct-1998 #sequence_revision 23-Oct-1998 #text_change 08-Dec-2000
C:Accession: S03904; JX0275; A60966
R:Ishikawa, F.; Miyazono, K.; Hellman, U.; Drexler, H.; Wernstedt, C.; Haglward, K.; Nature 338, 557-562, 1989
A:Title: Identification of angiogenic activity and the cloning and expression of platelet-derived endothelial cell growth factor precursor
A:Reference number: S03904; MUID:89181955
A:Accession: S03904
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-482 <ISH>
A:Note: 471-Ser was also found
R:Sumizawa, T.; Furukawa, T.; Haraguchi, M.; Yoshimura, A.; Takeyasu, A.; Ishizawa, M.
J. Biochem. 114, 9-14, 1993
A:Title: Thymidine phosphorylase activity associated with platelet-derived endothelial cell growth factor precursor
A:Reference number: JX0275; MUID:94012588
A:Accession: JX0275
A:Molecule type: mRNA
A:Residues: 125-244 <SUM>
A:Experimental source: placenta

R:Usuki, K.; Norberg, L.; Larsson, E.; Miyazono, K.; Hellman, U.; Wernstedt, C.; Rubin, Cell Regul. 1, 577-596, 1990
A:Title: Localization of platelet-derived endothelial cell growth factor in human placenta
A:Reference number: A60966; MUID:91175877
A:Accession: A60966
A:Molecule type: protein
A:Residues: 6-14 <USU>
C:Genetics:
A:Gene: GDB:ECGF1
A:Cross-references: GDB:127754; OMIM:131222
A:Map position: 22q13-22q13
C:Superfamily: thymidine phosphorylase
C:Keywords: angiogenesis; glycosyltransferase; growth factor; mitogen; pentosyltransferase
F:6-482/Product: platelet-derived endothelial cell growth factor, placental form #status
F:11-482/Product: platelet-derived endothelial cell growth factor, platelet form #status
F:63/Binding site: carbohydrate (Asn) (covalent) #status absent

Query Match 11.4%; Score 75.5; DB 1; Length 482;
Best Local Similarity 25.4%; Pred. No. 9.3;
Matches 33; Conservative 19; Mismatches 49; Indels 29; Gaps 5;

Qy 5 LTVVIALTCGLGLASPVPPTPTLKELIEELVNITQNASLCSGSMVSVNLTAGMYCA 64
Db 285 LEVEALLCMDS-AGP-----PDLRLVTTL-----GGALLMLSGHAGTQAQG 326
Qy 65 ALESILNVSDCSAQTQRM-----KALCSQKPAAGQISSERSRDTKIEVIQLV 114
Db 327 AARVAALDDGSGALGRFERMLAAQGVDPGLARALCSGSPAERQLLPRAREQE-ELLAPA 365
Qy 115 KNLTYVRGV 124
Db 386 DGTVELVRAL 395

RESULT 6
E83551
conserved hypothetical protein PA0752 [imported] - Pseudomonas aeruginosa (strain PA01)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83551
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warriner, P.; Hickey, M.J.; Boman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lim, L.; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an opportunistic pathogen
A:Reference number: A82950; MUID:20437337
A:Accession: E83551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <STO>
A:Cross-references: GB:AE004510; GB:AE004634; PIDN:RAG04141.1; GSPDB:GN001
A:Experimental source: strain PA01
C:Genetics:
A:Gene: PA0752

Query Match 11.4%; Score 75.5; DB 2; Length 505;
Best Local Similarity 24.6%; Pred. No. 9.8;
Matches 34; Conservative 25; Mismatches 42; Indels 37; Gaps 6;

Qy 4 WTVVIALTCGLGLASPVPPTPTLKELIEELVNITQNASLCSGSMV-----SVNLT 58
Db 150 FVLWVFAIVCLGCMAGDRP-----LKTLLAALLGLFLSSVGIDANSYVFTGDSIHLA 203
Qy 59 AGM-YCAALESILNVSDC-----SAQTQRMKALCSQKPAAGQISSERSRDT 106
Db 204 DGIQFVLVLGLFVSVEILLLEKTHHGQEA VKATGRM---LFFKREA----- 249

Qy 107 KIEVIQLVKNLTYVRGV 124
Db 250 SVLLVNLRCGLLGVNGV 267

RESULT 7
S77393
cell division protein ftsZ - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S77393
R:Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yas DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis S.
A:Reference number: S74322; MUID:97061201
A:Accession: S77393
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-430 <KAN>
A:Cross-references: EMBL:D90906; GB:AB001339; NID:gl652492; PIDN:BAAL17496.1; PID:gl65
A:Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C:Genetics:
A:Gene: ftsZ
C:Superfamily: cell division protein ftsZ
C:Keywords: cell division; GTP binding
F:161-167/Region: tubulin/FtsZ GTP/GDP-binding (G-G-G-T-G-[ST]-G) motif
F:262-269/Region: GTP hydrolyzing

Query Match 11.3%; Score 75; DB 2; Length 430;
Best Local Similarity 26.4%; Pred. No. 9.2;
Matches 28; Conservative 19; Mismatches 31; Indels 28; Gaps 5;

Qy 19 SPSVPVTPSPITKELIEELV--NITQ-----ASLCSGSMVSVNLTAG 60
Db 46 TPTFASPSPNLKR--DQIVPSNIAKIKIVGGCCNAVNRMIASGVTFIDFWAINTDS- 102

Qy 61 MYCAALESILNVSDCSAQTQRMKAL-CSQKPAAGQISSERSRD 105
Db 103 -----QALVTNAPDCIQCKLTRLGAGCNPAIGQKAAEESRD 142

RESULT 8
S52110
sepiapterin reductase (EC 1.1.1.153) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 18-Feb-2000
C:Accession: S52110; PH1578
R:Ota, A.; Ichinose, H.; Nagatsu, T. Biochim. Biophys. Acta 1260, 320-322, 1995
A:Title: Mouse sepiapterin reductase: an enzyme involved in the final step of tetrahy
A:Reference number: S52110; MUID:95178553
A:Accession: S52110
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <OTA>
R:Waier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I. Exp. Cell Res. 204, 217-222, 1993
A:Title: Detection of a novel sepiapterin reductase mRNA: Assay of mRNA in various ce
A:Reference number: A49174; MUID:93178546
A:Accession: PH1578
A:Molecule type: mRNA
A:Residues: 209-255 <MAI>
C:Comment: This enzyme catalyzes the reduction of both C1' and C2' oxo group.
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 11.2%; Score 74; DB 2; Length 261;
Best Local Similarity 22.2%; Pred. No. 6.5;
Matches 32; Conservative 27; Mismatches 55; Indels 30; Gaps 6;

Db 177 ARDMLYQVLAVEEPSVRVLSYAPG 200

RESULT 10
T51211
hypothetical protein B24M22.70 [imported] - Neurospora crassa
C:Species: Neurospora crassa
C:Date: 28-Jul-2000 #sequence_revision 28-Jul-2000 #text_change 02-Sep-2000
C:Accession: T51211
R:Schulte, U.; Aign, V.; Hoheisel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakatura submitted to the Protein Sequence Database, July 2000
A:Reference number: 225286
A:Accession: T51211
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-586 <SCH>
A:Cross-references: EMBL:AL390354; GSPDB:GN001116; NCSP:B24M22.70
A:Experimental source: strain OR74A
C:Genetics:
A:Gene: NCSP:B24M22.70
A:Map position: 6
C:Superfamily: indoleacetamide hydrolase

Query Match . 11.1% Score 73.5; DB 2; Length 586;
Best Local Similarity 28.2%; Pred. No. 18;
Matches 35; Conservative 15; Mismatches 33; Indels 41; Gaps 9;

QY 4 WLTVVIAL-TCLG-GLASPS-----PVTPTLKELIELVNITNQ 43
||||| | : ||| : ||| : ||| : ||| : ||| : ||| : ||
Db 9 WLTVATAGICLGAALSTPTEDIKPKNCPTNVLPFVPCGSFK--LEE-ATIDDMQ 65
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||
QY 44 ASLCNGSMWNSVNLTAGYCAALESINVSDCSAIQRTQRLMKALCSQKP----AAGQIS 99
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||
Db 66 AMNNGSLT-SVOLVG---CYVLRTF-----QTDLVINSLLOYNPDAISIAAQMD 111
||| : ||| : ||| : ||| : ||| : ||| : ||| : ||| : ||

QY 100 SERS 103
:::
Db 112 AERA 115

RESULT 11
SI7196
transcription factor UB2 - African clawed frog
N:Alternate names: upstream binding factor 2
C:Species: Xenopus laevis (African clawed frog)
C:Date: 07-Apr-1994 #sequence_revision 07-Apr-1994 #text_change 24-Sep-1999
C:Accession: SI7196; SI7977; SI6329
R:Bachvarov, D.; Normandeau, M.; Moss, T.
FEBS Lett. 288, 55-59, 1991
A:Title: Heterogeneity in the Xenopus ribosomal transcription factor xUBF has a molec
A:Reference number: SI7196; MUID:91348289
A:Accession: SI7196
A>Status: nucleic acid sequence not shown
A:Molecule type: mRNA
A:Residues: 1-701 <BAC>
A:Cross-references: EMBL:X59863
R:Moss, T.
submitted to the EMBL Data Library, May 1991
A:Reference number: SI7977
A:Accession: SI7977
A:Molecule type: mRNA
A:Residues: 1-31, 'H', 33-701 <MOS>
A:Cross-references: EMBL:X59863; NID:g65264; PIDN:CAA42523.1; PID:g65265
R:McStay, B.; Hu, C.H.; Pitkaard, C.S.; Reeder, R.H.
EMBO J. 10, 2297-2303, 1991
A:Title: xUBF and Rib1 are both required for formation of a stable polymerase I promo
A:Reference number: SI6329; MUID:91293106
A:Accession: SI6329
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-537, 'y', 539-668, 'D', 670-701 <MCS>
A:Cross-references: EMBL:X57561; NID:g65200; PIDN:CAA40794.1; PID:g65201

RESULT 13
T50355
hypothetical protein SPBC21C3.11 [imported] - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 09-Jun-2000 #sequence_revision 09-Jun-2000 #text_change 09-Jun-2000
C:Accession: T50355
R:Seeger, K.; Harris, D.; Lyne, M.; Rajandream, M.A.; Barrell, B.G.
submitted to the EMBL Data Library, February 2000
A:Reference number: Z25064
A:Accession: T50355
A:Status: preliminary; translated from GB/EMBL/DBJ

C;Superfamily: acrosin; trypsin homology

C; keywords: glycoprotein; hydrolase; serine proteinase
F; 40-283/Domain: trypsin homology <TRY>

Query Match 10.9%; Score 72; DB 2; Length 431;
Best Local Similarity 32.3%; Pred. No. 18;
Matches 20; Conservative 8; Mismatches 26; Indels 8; Gaps 2;
QY 10 ALTCL---GGLASPSVTPSTLKELELVNITONQASLCNGSMWVSVNLTAGMYCAAL 66
Db 172 AOTCYVAGWGYVKNAPRPSPTLMEARVDLINL-----ELCNSTOMYNGRITASNLCAGY 226
QY 67 ES 68
Db 227 PS 228

Search completed: May 13, 2001, 21:48:37
Job time: 26246 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:59:23 ; Search time 44.64 Seconds
(without alignments)
100.526 Million cell updates/sec

Title: US-09-451-527-92

Perfect score: 663

Sequence: 1 MALWLTVVIALTCGLGLASP.....QLVKNLLTYVRGVYRHGNFR 131

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	463.5	69.9	132	1 IL13_HUMAN	P35225 homo sapien
2	427.5	64.5	132	1 IL13_BOVIN	Q9XSV9 bos taurus
3	378.5	57.1	131	1 IL13_MOUSE	P42109 mus musculus
4	378	57.0	131	1 IL13_RAT	P42203 rattus norv
5	75.5	11.4	482	1 TYPH_HUMAN	P19971 homo sapien
6	75	11.3	430	1 FTSZ_SYNY3	P73456 synechocyst
7	74	11.2	261	1 SPRE_MOUSE	Q64105 mus musculus
8	74	11.2	262	1 SPRE_RAT	P18297 rattus norv
9	73	11.0	701	1 UBF2_XENLA	P25980 xenopus lae
10	73	11.0	1164	1 FHOS_HUMAN	Q9Y613 homo sapien
11	72	10.9	211	1 HLT_PIG	P06348 sus scrofa
12	72	10.9	431	1 ACRO_RABIT	P48038 oryctolagus
13	71.5	10.8	382	1 IPAC_SHIFL	P18012 shigella fl
14	71	10.7	261	1 SPRE_HUMAN	P35270 homo sapien
15	70.5	10.6	192	1 FLHC_SALTY	O52222 salmonella
16	70	10.6	382	1 IPAC_SHIDY	Q03946 shigella dy
17	70	10.6	513	1 AQL1_THEAQ	P08594 thexmus aqu
18	70	10.6	677	1 UBF1_XENLA	P25979 xenopus lae
19	69	10.4	207	1 HLT_MACMU	P40286 macaca mula
20	69	10.4	323	1 GC_RABIT	P01870 oryctolagus
21	68	10.3	1004	1 YG21_YEAST	P53067 saccharomyc
22	67	10.1	481	1 YA88_SCHPO	Q09775 schizosacch
23	67	10.1	510	1 MUTL1_THEMA	P74925 thermotoga
24	66.5	10.0	585	1 YM67_CAEEL	P34528 caenorhabdi
25	66	10.0	1037	1 ACRD_ECOLI	P24177 escherichia
26	66	10.0	1234	1 MFD_MYCTU	P96380 mycobacteri
27	65.5	9.9	326	1 YIE1_YEAST	P40531 saccharomyc
28	65.5	9.9	1681	1 CLH_CAEEL	P34574 caenorhabdi
29	65	9.8	99	1 FIL1_ANTMA	Q38737 antirrhinum
30	65	9.8	203	1 YM91_AEEL	P34530 caenorhabdi
31	65	9.8	268	1 MOVF_TWVR	P70737 tobacco mos
32	65	9.8	272	1 ATPD_STRLI	P50008 streptomyces
33	65	9.8	512	1 Y4UC_RHISN	Q53197 rhizobium s

RESULT 1

ID	IL13_HUMAN	STANDARD;	PRT;	132 AA.
AC	P35225; O43644;			
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-13 PRECURSOR (IL-13).			
GN	IL13 OR NC30.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Euthera; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93211479; PubMed=8096327;			
RA	Minty A.J., Chalon P., Derocq J.M., Dumont X., Guillemot J.C.,			
RA	Kaghad M., Labit C., Leplatois P., Liauzun P., Miloux B.,			
RA	Minty C., Casellas P., Loison G., Lupker J., Shire D., Ferrara P.,			
RA	Caput D.;			
RT	"Interleukin-13 is a new human lymphokine regulating inflammatory and			
RT	immune responses.";			
RL	Nature 362:248-250(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93234572; PubMed=8097324;			
RA	McKenzie A.N., Culppepper J.A., Waal Malefyt R., Briere F.,			
RA	Punnonen J., Aversa G., Sato A., Dang W., Cocks B.G., Menon S.,			
RA	de Vries J.E., Banchereau J., Zurawski G.R.;			
RT	"Interleukin 13, a T-cell-derived cytokine that regulates human			
RT	monocyte and B-cell function.";			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:3735-3739(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Delganov G., Lewis D.B., Lovett M., Burr J., Bort S., Short D.,			
RA	McGurn M., Gibson C.;			
RA	Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUP=Blood;			
RA	MEDLINE=95237624; PubMed=7721105;			
RA	Smirnov D.V., Smirnova M.G., Korobko V.G., Frolova E.I.;			
RT	"Tandem arrangement of human genes for interleukin-4 and			
RT	interleukin-13: resemblance in their organization.";			
RL	Gene 155:277-281(1995).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Jang J.S., Kim B.E.;			
RA	Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	3D-STRUCTURE MODELING.			
RA	MEDLINE=95132583; PubMed=7530359;			
RA	Bamorough P., Duncan D., Richards W.G.;			
RT	"Predictive modelling of the 3-D structure of interleukin-13.";			
RL	Protein Eng. 7:1077-1082(1994).			
RN	[7]			

34	65	9.8	713	1 - PMIP_HUMAN	O99797 homo sapien
35	65	9.8	891	1 YB33_SCHPO	O14338 schizosacch
36	64.5	9.7	268	1 MOVF_TWVR	P03583 tobacco mos
37	64.5	9.7	268	1 MOVF_TWVR	Q91275 tobacco mos
38	64.5	9.7	268	1 MOVF_TWVR	Q98746 tobacco mos
39	64.5	9.7	338	1 1A1D_PSEFL	O51813 pseudomonas
40	64.5	9.7	538	1 RO60_XENLA	P42700 xenopus lae
41	64	9.7	168	1 PTP_NPVAC	P24656 autographa
42	64	9.7	206	1 HIT_HUMAN	P22492 homo sapien
43	64	9.7	228	1 MP64_MYCTU	P19996 mycobacteri
44	64	9.7	381	1 RHG6_MOUSE	O54834 mus musculus
45	64	9.7	587	1 RHG6_HUMAN	O43182 homo sapien

ALIGNMENTS


```
RP VARIANT GLN-130.
RX MEDLINE-20164293; PubMed-10699178;
RA Helnzmann A., Mao X.-Q., Akaiwa M., Kreomer R.T., Gao P.-S.,
RA Ohshima K., Umeshita K., Abe Y., Braun S., Yamashita T., Roberts M.H.,
RA Sugimoto R., Arima K., Arinobu Y., Yu B., Kruse S., Enomoto T.,
RA Dake Y., Kawai M., Shimazu S., Sasaki S., Adra C.N., Kitaichi M.,
RA Inoue H., Yamauchi K., Tomichi N., Kurimoto F., Hamasaki N.,
RA Hopkin J.M., Izuhara K., Shirakawa T., Deichmann K.A.;
RA "Genetic variants of IL-13 signalling and human asthma and atopy."
RL Hum. Mol. Genet. 9:549-559(2000).
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES.
CC -1- SURCELLULAR LOCATION: SECRETED.
CC -1- POLYMORPHISM: GLN AT POSITION 130 IS A SIGNIFICANT RISK FACTOR FOR
CC ASTHMA DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06801; AAA36107.1; -.
DR EMBL; X69079; CAA48824.1; -.
DR EMBL; X69079; CAA48823.1; ALT_INIT.
DR EMBL; U31120; AAB01681.1; -.
DR EMBL; U10307; AAB83738.1; -.
DR EMBL; AF043334; AAC03535.1; -.
DR PIR; A47481; A47481.
DR PDB; 3ITS; 15-JAN-95.
DR MIM; 147683; -.
DR InterPro; IPR001325; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 132 INTERLEUKIN-13.
FT DISULFID 48 76
FT DISULFID 64 90
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 130 130 R -> Q.
FT CONFLICT 45 45 /FTid=VAR_010037.
FT CONFLICT 87 87 A -> R (IN REF. 4).
FT CONFLICT 98 98 S -> G (IN REF. 5).
FT CONFLICT 98 98 MISSING (IN REF. 4).
SQ SEQUENCE 132 AA; 14319 MW; 123FDCAB87FD78B CRC64;

Query Match 69.9%; Score 463.5; DB 1; Length 132;
Best Local Similarity 71.8%; Pred. No. 8.1e-40;
Matches 94; Conservative 11; Mismatches 25; Indels 1; Gaps 1;

QY 1 MALMLTVVIALTCGLGLASPSVPTPTLKLIEELVNITQNO-ASLCNGSMWVSNLTA 59
DB 1 MALMLTVVIALTCGLGLASPSVPTPTLKLIEELVNITQNO-KAPLCNGSMWVSNLTA 60
QY 60 GMYCAALESINVDSCSAIQRTQRMKALCSQKPAAGQISSRSRDTKIEVLQVKNLLT 119
DB 61 GMYCAALESINVDSCSAIEKRTQRMKALCSQKPAAGQISSRSRDTKIEVLQVKNLLT 120
QY 120 YVRGVYRHGNF 130
DB 121 HLKLFREGRF 131

RESULT 2
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
```

```
IL13_BOVIN
ID IL13_BOVIN STANDARD; PRT; 132 AA.
AC Q9XSV9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13).
GN IL13
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
SEQUENCE FROM N.A.
RA Buikamp J., Jann O., Fries R.;
RT "The bovine interleukin-13 gene: genomic organization, chromosomal
RT location and evolution of the promoter."
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS. MAY
CC BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY
CC SIMILARITY).
CC -1- SURCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ13241; CAB4636.1; -.
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 132 INTERLEUKIN-13.
FT DISULFID 48 76 BY SIMILARITY.
FT DISULFID 64 90 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 132 AA; 14623 MW; 723BD42375C161F3 CRC64;

Query Match 64.5%; Score 427.5; DB 1; Length 132;
Best Local Similarity 66.4%; Pred. No. 3.3e-36;
Matches 87; Conservative 16; Mismatches 27; Indels 1; Gaps 1;

QY 1 MALMLTVVIALTCGLGLASPSVPTPTLKLIEELVNITQNO-ASLCNGSMWVSNLTA 59
DB 1 MALMLTVVIALTCGLGLASPSVPTPTLKLIEELVNITQNO-KAPLCNGSMWVSNLTA 60
QY 60 GMYCAALESINVDSCSAIQRTQRMKALCSQKPAAGQISSRSRDTKIEVLQVKNLLT 119
DB 61 GMYCAALESINVDSCSAIQRTQRMKALCSQKPAAGQISSRSRDTKIEVLQVKNLLT 120
QY 120 YVRGVYRHGNF 130
DB 121 HSRIVFRNERF 131

RESULT 3
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
```

GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;
RA Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
RT "A family of small inducible proteins secreted by leukocytes are
RT members of a new superfamily that includes leukocyte and
RT fibroblast-derived inflammatory agents, growth factors, and
RT indicators of various activation processes.";
RL J. Immunol. 142:679-687(1989).
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M23504; AAA40149.1; -
DR PIR: E30552; E30552.
DR HSP: P35225; 3ITR.
DR MGI: MGI:96541; IL13.
DR InterPro: IPR001325; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 131 INTERLEUKIN-13.
FT DISULFID 51 79 BY SIMILARITY.
FT DISULFID 67 93 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 131 AA; 14107 MW; 954F93F105713FED CRC64;

Query Match 57.1%; Score 378.5; DB 1; Length 131;
Best Local Similarity 59.0%; Pred. No. 2.8e-31;
Matches 79; Conservative 19; Mismatches 29; Indels 7; Gaps 3;

Qy 1 MALWLVVIALTCLGLGLASPPVTPSP----TLKELIEELVNITQNASICNGSMWVSN 56
Db 1 MALWVAVLALACGLGLAAGPVPVRSVSLPLTLKELIEELVNITQDQTPLCNGSMWVSD 60

Qy 57 LTAGMYCALESILNVDCSAIQRTQRMKALCSOKPAAGQISSERSRDTKIEVTQVKN 116
Db 61 LAAGFCVVALDSLNTNISNCNAYIRQRIHLGLCNRK-APTTVSS--LPDTKIEVAHFITK 117

Qy 117 LLYVYRGVYRHGNF 130
Db 118 LLSYTKQLFRHGPF 131

RESULT 4
IL13_RAT
ID IL13_RAT STANDARD; PRT; 131 AA.
AC P42203;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Rattus norvegicus (Rat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=101116;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=SPRAGUE-DAWLEY; TISSUE=Kidney cortex;
RX MEDLINE=94092138; PubMed=7916615;
RA Lakkis F.G., Cruet E.N.;
RT "Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13
RT gene expression in experimental glomerulonephritis.";
RL Biochem. Biophys. Res. Commun. 197:612-618(1993).
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES
CC (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L26913; AAA16478.1; -
DR HSP: P35225; 3ITR.
DR InterPro: IPR001325; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 21 BY SIMILARITY.
FT CHAIN 22 131 INTERLEUKIN-13.
FT DISULFID 52 80 BY SIMILARITY.
FT DISULFID 68 94 BY SIMILARITY.
FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 131 AA; 14093 MW; E5008CAB8D8C201 CRC64;

Query Match 57.0%; Score 378; DB 1; Length 131;
Best Local Similarity 59.0%; Pred. No. 3.1e-31;
Matches 79; Conservative 20; Mismatches 27; Indels 8; Gaps 4;

Qy 1 MALWLVVIALTCLGLGLASPPV----TPSPTLKELIEELVNITQNASICNGSMWVSV 55
Db 1 MALWVAVLALACGLGLAAGPVPVRSVSPVVALRELIEELVNITQDQKTSICNGSMWVSV 60

Qy 56 NLTAGMYCALESILNVDCSAIQRTQRMKALCSOKPAAGQISSERSRDTKIEVTQVKN 115
Db 61 DLTAGFYCALESILNVDCSAIQRTQRMKALCSOKPAAGQISSERSRDTKIEVTQVKN 117

Qy 116 NLLTYVYRGVYRHGN 129
Db 118 KLLNYSKQLFRYGH 131

RESULT 5
TYPH_HUMAN
ID TYPH_HUMAN STANDARD; PRT; 482 AA.
AC P19971; Q13390;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE THYMIDINE PHOSPHORYLASE PRECURSOR (EC 2.4.2.4) (TDRPASE) (TP)
DE (PLATELET-DERIVED ENDOTHELIAL CELL GROWTH FACTOR) (PD-ECGF)
DE (GLOSTATIN).
GN ECGF1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.


```

NCBI_TaxID=11148;
[1]
SEQUENCE FROM N.A. PubMed=8905231;
MEDLINE=97061201;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RX Miyajima N., Hirotsawa M., Sugitara M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpou S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synechocystis sp. strain PCC6803. II. Sequence determination of the
RL entire genome and assignment of potential protein-coding regions.";
CC DNA Res. 3:109-136(1996).
CC
CC -1- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
CC ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF
CC THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
CC AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
CC BEGIN. BINDS TO AND HYDROLYZES GTP (BY SIMILARITY).
CC -1- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
CC OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; D90906; BAAL7496.1; -
CC HSP; Q57816; 1FSZ.
CC InterPro; IPR000158; -
CC Pfam; PF00091; tubulin.1
CC PRINTS; PR00423; CELLDVIFTS2.
CC PROSITE; PS01134; FTSZ_1; 1.
CC PROSITE; PS01135; FTSZ_2; 1.
CC Cell division; Septation; GTP-binding.
CC NP_BIND 159 167
CC GTP (POTENTIAL).
CC SEQUENCE 430 AA; 44773 MW; E3C7DD554983FF44 CRC64;
CC
CC
CC Query Match 11.3%; Score 75; DB 1; Length 430;
CC Best Local Similarity 26.4%; Pred. No. 3.5;
CC Matches 28; Conservative 19; Mismatches 31; Indels 28; Gaps 5;
CC
CC QY 19 SPSPVTPSPTLKELEELY--NITQ-----ASLCNGSMVSVNLTAG 60
CC Db TPTFASPNLKR--DQIVPSNIAKIVGVGGGCGNAVNRMIASGVTGDFWINTDS- 102
CC
CC QY 61 MYCAALESINVSQSAIQTQRMKAL-CSQKPAAGQISSERSRD 105
CC Db -----QALTNTNPDICIQIGKLRGLGAGNPAIGQKAAEESRD 142
CC
CC RESULT 7
CC SPRE_MOUSE STANDARD; PRT; 261 AA.
CC ID Q64105; Q63996;
CC AC Q64105; Q63996;
CC DT 01-NOV-1997 (Rel. 35, Created)
CC DT 01-NOV-1997 (Rel. 35, Last sequence update)
CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
CC DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
CC GN SPR.
CC OS Mus musculus (Mouse).
CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
CC OX NCBI_TaxID=10090;
CC RN [1]
CC RP SEQUENCE FROM N.A.
CC RX MEDLINE=95178553; PubMed=7873607;
Ota A., Ichinose H., Nagatsu T.;
"Mouse sepiapterin reductase: an enzyme involved in the final step of
tetrahydrobiopterin biosynthesis. Primary structure deduced from the
cDNA sequence.";
Biochim. Biophys. Acta 1260:320-322(1995).
[2]
SEQUENCE FROM N.A.
STRAIN=129;
RX MEDLINE=99227131; PubMed=10209270;
RA Lee S.W., Park I.Y., Hahn Y., Lee J.E., Seong C.S., Chung J.H.,
RA Park Y.S.;
"Cloning of mouse sepiapterin reductase gene and characterization of
its promoter region.";
Biochim. Biophys. Acta 1445:165-171(1999).
[3]
SEQUENCE OF 209-261 FROM N.A.
RX MEDLINE=94136218; PubMed=8304109;
Raier J., Schott K., Werner T., Bacher A., Ziegler I.;
"Northern blot analysis of sepiapterin reductase mRNA in mammalian
cell lines and tissues.";
Adv. Exp. Med. Biol. 338:195-198(1993).
[4]
X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS).
RX MEDLINE=98070299; PubMed=9405351;
Auerbach G., Herrmann A., Gutlich M., Fischer M., Jacob U., Bacher A.,
Huber R.;
"The 1.25-A crystal structure of sepiapterin reductase reveals its
binding mode to pterins and brain neurotransmitters.";
EMBO J. 16:7219-7230(1997).
CC
CC -1- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIPTERIN.
CC -1- CATALYTIC ACTIVITY: 7,8-DIHYDROBIPTERIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC
CC EMBL; S77493; AAB33611.1; -
CC EMBL; U78077; AAC69364.1; -
CC EMBL; U78076; AAC69364.1; JOINED.
CC EMBL; S71375; -; NOT_ANNOTATED_CDS.
CC PDB; 1SEP; 13-JAN-99.
CC PDB; 1OAA; 16-FEB-99.
CC PDB; 1NAS; 30-MAR-99.
CC MGD; MGI:103078; Spr.
CC InterPro; IPR002198; -
CC Pfam; PF00106; adh_short; 1.
CC Oxidoreductase; NADP; 3D-structure.
CC NP_BIND 14 40 NADP (BY SIMILARITY).
CC DOMAIN 29 33 PTERIN BINDING (POTENTIAL).
CC CONFLICT 29 4 D -> G (IN REF. 2).
CC SEQUENCE 261 AA; 27883 MW; 102294E439CB8AEC CRC64;
CC
CC
CC Query Match 11.2%; Score 74; DB 1; Length 261;
CC Best Local Similarity 22.2%; Pred. No. 2.5;
CC Matches 32; Conservative 27; Mismatches 55; Indels 30; Gaps 6;
CC
CC QY 5 LTVVIALTCGLGLAS-----PSP-----VTPSPTLKELEELVNITQNAS 45
CC Db LKVVLAADLGTAGVQRLLSAYRELPRPEGLRLLLNNAATLGVDVSKGLNVN----D 117
CC
CC QY 46 LCNGSMVSVNLTAGMYCAALESINVSQSAIQTQRMKALCSQKPAAG---QISSER 102
CC Db LAEVNNYVALNLTAS-MLCLTSGTLNAPQDSPGLSKTVVNTISSLCALQPYKGLWCYAGKA 176

```

```

Db      177 ARDMLYQVLAVEEPSVRVLSYAPG 200
      :||  :|:  :  :  :|:|  |

```

```

RESULT 9
UBF2_XENLA
ID UBF2_XENLA STANDARD; PRT; 701 AA.
AC F25980;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NUCLEOLAR TRANSCRIPTION FACTOR 2 (UPSTREAM BINDING FACTOR-2) (UBF-2).
GN XUBF-2.
OS Xubus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
[1]
SEQUENCE FROM N.A.
RP MEDLINE=91293106; PubMed=2065665;
RX MEDLINE=91293106; PubMed=2065665;
RT McStay B., Hu C.H., Pikaard C.S., Reeder R.H.;
RA "XUBF and Rib 1 are both required for formation of a stable
RT polymerase I promoter complex in X. laevis.";
RL EMBO J. 10:2297-2303(1991).
[2]
SEQUENCE FROM N.A.
RP MEDLINE=91348289; PubMed=1879565;
RX MEDLINE=91348289; PubMed=1879565;
RA Bachvarov D., Normandeau M., Moss T.;
RT "Heterogeneity in the Xenopus ribosomal transcription factor xUBF has
RT a molecular basis distinct from that in mammals.";
RL FEBS Lett. 288:55-59(1991).
[3]
DOMAINS
RP MEDLINE=92038986; PubMed=1936987;
RX MEDLINE=92038986; PubMed=1936987;
RA McStay B., Frazier M.W., Reeder R.H.;
RT "XUBF contains a novel dimerization domain essential for RNA
RT polymerase I transcription.";
RL Genes Dev. 5:1957-1968(1991).
CC -!- FUNCTION: UBF RECOGNIZES THE RIBOSOMAL RNA GENE PROMOTOR AND
CC ACTIVATES TRANSCRIPTION MEDIATED BY RNA POLYMERASE I THROUGH
CC COOPERATIVE INTERACTIONS WITH THE SPECIES-SPECIFIC FACTOR SL1.
CC IT BINDS SPECIFICALLY TO THE UPSTREAM CONTROL ELEMENT.
CC -!- SUBUNIT: XUBF CONSISTS OF 2 POLYPEPTIDES OF 82 AND 85 KDA,
CC ENCODED BY THE SAME OR CLOSELY RELATED GENES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- SIMILARITY: CONTAINS 5 HMGB BOXES.
CC
CC
CC

```

CC	CC	This SWISS-PROT entry is copyright. It is produced through a collaboration
CC	CC	between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC	CC	the European Bioinformatics Institute. There are no restrictions on its
CC	CC	use by non-profit institutions as long as its content is in no way
CC	CC	modified and this statement is not removed. Usage by and for commercial
CC	CC	entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC	CC	or send an email to license@isb-sib.ch).
CC	CC	-----
CC	EMBL; X57561; CAA40794.1; -;	
DR	EMBL; X59863; CAA42523.1; -;	
DR	PIR; S16329; S16329.	
DR	PIR; S17196; S17196.	
DR	PIR; S17977; S17977.	
DR	InterPro; IPR000910; -;	
DR	Pfam; PF00505; HMC_box; 3.	
DR	Transcription regulation; DNA-binding; Activator; Nuclear protein;	
KW	Multigene family; Repeat.	
FT	DNA_BIND 113 180	HMG BOX 1.
FT	DNA_BIND 199 264	HMG BOX 2.
FT	DNA_BIND 298 362	HMG BOX 3.
FT	DNA_BIND 422 489	HMG BOX 4.
FT	DNA_BIND 508 574	HMG BOX 5.
FT	DOMAIN 615 701	ASP/GLU-RICH (ACIDIC).
FT	CONFLICT 32 32	Q -> H (IN REF. 2).
FT	CONFLICT 538 538	V -> A (IN REF. 2).
FT	FT	

DB 768 LMTLASIGGLAARLQLWAFKLDYDSMEREIAEPLFDLKVGMELV---QNATFRCILATL 824

RP SEQUE

SEQUENCE FROM N.A.

QY 72 VSDCSAIOITORMLKALCSQKPAAGQISSERSRDTKIEVIQVLKNTLYVGRVYRHGN 129
DB 324 -----EEQLISASSQAEASQVSKEASQATN-----QLIQKLLNIIDSINQSKN 370

RESULT 14
SPRE_HUMAN STANDARD; PRT; 261 AA.
AC P35270;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
GN SPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=91354248; PubMed=1883349;
RA Ichinose H., Kato S., Sueoka T., Titani K., Fujita K., Nagatsu T.;
RT "Cloning and sequencing of cDNA encoding human sepiapterin
RT reductase -- an enzyme involved in tetrahydrobiopterin biosynthesis.";
RL Biochem. Biophys. Res. Commun. 179:183-189(1991).
CC -!- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIOPTEIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOPTEIN.
CC -!- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOPTEIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- DISEASE: DEPRESSED SYNTHESIS OF TETRAHYDROBIOPTEIN MAY PLAY A
CC ROLE IN A VARIETY OF HUMAN DISEASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M76231; AAA60314.1; -
DR PIR; JQ1176; JQ1176.
DR MIM; 182125; -
DR InterPro; IPR002198; -
DR Pfam; PF00106; adh_short; 1.
KW Oxidoreductase; NADP; Acetylation.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT NP_BIND 13 39 NADP (BY SIMILARITY).
FT DOMAIN 28 32 PTERIN BINDING (POTENTIAL).
SQ SEQUENCE 261 AA; 28048 MW; 9C9BF76212826F47 CRC64;

Query Match 10.7%; Score 71; DB 1; Length 261;
Best Local Similarity 24.7%; Pred. No. 4.9;
Matches 24; Conservative 21; Mismatches 42; Indels 10; Gaps 4;

QY 36 LVNITONQASLNGSKV---WSVNLTAGMYCAALESILNVSDCSAIOITORMLKALCSQK 92
DB 104 LGDVKSGFVLDSDSTQVNNYWNALNLS-MLCLTSSVLKAPFDPSPGLNRTVVNIISSLCALQ 162

QY 93 PAAG--QISSERSRDTKIEVIQVLK---NLLTYVRG 123
DB 163 PPKGWALYCAAGRAARDMLFQVLALEEPNVRVLYNAPG 199

RESULT 15
FLHC_SALTY STANDARD; PRT; 192 AA.
ID FLHC_SALTY
AC OS2222;
DT 30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC.
GN FLHC.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Tsuchi A., Harshey R.M.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC PubMed=1058519;
RA Yanagihara S., Iyoda S., Ohnishi K., Iino T., Kutsukake K.;
RT "Structure and transcriptional control of the flagellar master operon
RT of Salmonella typhimurium.";
RL Genes Genet. Syst. 74:105-111(1999).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. TOGETHER WITH FLHD IT ACTS AS
CC A COMPOUND SIGMA FACTOR THAT ACTIVATES CLASS 2 FLAGELLAR GENES (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FLHC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF029300; AAB96640.1; -
DR EMBL; D43640; BAA85315.1; -
DR StyGene; SG10643; flhc.
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; Flagella.
SQ SEQUENCE 192 AA; 21579 MW; C7334C691ECE3F8D CRC64;

Query Match 10.6%; Score 70.5; DB 1; Length 192;
Best Local Similarity 28.6%; Pred. No. 3.9;
Matches 16; Conservative 10; Mismatches 27; Indels 3; Gaps 1;

QY 51 MWVSVNLTAGMYCAALESILNVSDCS---AIOITORMLKALCSQKPAAGQISSERS 103
DB 65 MTWEQNHASMFCAWQFLKTLGLCSGVDAVIKAYRLYLEQCQPPEGLALTRA 120

Search completed: May 14, 2001, 06:02:04
Job time: 43361 sec

Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	663	100.0	131	6	Q9N0W9		Q9n0w9 canis famil
2	398.5	60.1	114	6	Q9TV84		Q9tv84 bos taurus
3	157.5	23.8	49	4	Q9UDC7		Q9udc7 homo sapien
4	82.5	12.4	275	6	Q28609		Q28609 oryctolagus
5	78.5	11.8	1183	4	Q94918		Q94918 homo sapien
6	78.5	11.8	1230	4	Q9P0H7		Q9p0h7 homo sapien
7	78.5	11.8	1230	11	P97536		p97536 rattus norv
8	76	11.5	1448	5	Q9N946		Q9n946 trypanosoma
9	75	11.3	1448	5	Q9N949		Q9n949 trypanosoma
10	74	11.2	415	8	Q9MUM4		Q9mum4 mesostigma
11	73.5	11.1	336	10	Q9SMD4		Q9smd4 lycopersico
12	73.5	11.1	586	3	Q9P3A1		Q9p3a1 neurospora
13	73	11.0	150	14	Q98779		Q98779 vesicular s
14	73	11.0	350	14	Q9Q8P4		Q9q8p4 myxoma viru
15	73	11.0	1164	4	Q9Y613		Q9y613 homo sapien
16	73	11.0	1806	5	Q45657		Q45657 caenorhabdi
17	72.5	10.9	425	3	Q9P712		Q9p712 schizosacch
18	72.5	10.9	670	5	Q9N9C4		Q9n9c4 leishmania
19	72	10.9	150	14	Q98791		Q98791 vesicular s

```

AC Q9TVB4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (FRAGMENT).
GN IL-13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Triglona W.T., Hirano A., Brown W.;
RT "Biological activities of interleukin-13 (IL-13) on bovine
RT lymphocytes: Implications for signaling through IL-13ral.";
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF072807; AAD22748.1; -.
DR HSSP: P35225; 31TR.
DR INTERPRO: IPR001325; -.
DR PROSITE: PS00838; INTERLEUKIN_4_13; UNKNOWN_1.
FT NON_TER 114
SQ SEQUENCE 114 AA; 12355 MW; D8CC56E5627D030A CRC64;

Query Match 50.1%; Score 398.5; DB 6; Length 114;
Best Local Similarity 71.7%; Pred. No. 4e-34;
Matches 81; Conservative 10; Mismatches 21; Indels 1; Gaps 1;

QY 1 MALWLTVVIALTCGGIASPVPPTLKEIIEELVNITONQ-ASLCNGSMVSVNLTA 59
Db 1 MALLTAVIVLCFGGTSFSPVSAFKALKEIIEELVNITONQKVPICNGSMVSVNLTS 60

QY 60 GMYCAALESINVSDCSAIQRTQRLKALCSQKPAAGQISSERSRDRTKIEVIQ 112
Db 61 SMYCAALDSLISISNCVSIQRTKRLNALCPKPSAKQVSSEYVYRDKIEVAQ 113

RESULT 3
ID Q9UDC7 PRELIMINARY; PRT; 49 AA.
AC Q9UDC7;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE P600 HOMOLOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93027259; PubMed=1408833;
RA Morgan J.G., Dolganov G.M., Robbins S.E., Hinton L.M., Lovett M.;
RT "The selective isolation of novel cDNAs encoded by the regions
RT surrounding the human interleukin 4 and 5 genes.";
RL Nucleic Acids Res. 20:5173-5179(1992).
DR HSSP: P35225; 31TR.
SQ SEQUENCE 49 AA; 5109 MW; 679CD23A190C778E CRC64;

Query Match 23.8%; Score 157.5; DB 4; Length 49;
Best Local Similarity 71.4%; Pred. No. 2e-09;
Matches 35; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

QY 1 MALWLTVVIALTCGGIASPVPPTLKEIIEELVNITONQ-ASLCN 48
Db 1 MALLTAVIVLCFGGTSFSPVSAFKALKEIIEELVNITOTQKAPLCN 49

RESULT 4
ID Q28609 PRELIMINARY; PRT; 275 AA.

```

```

AC Q28609;
DT 01-NOV-1996 (TrEMBLrel. 01, Created)
DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
DE PUTATIVE PREPROSPERMINGEN PRECURSOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=TESTIS;
RX MEDLINE=94368861; PubMed=8086468;
RA Richardson R.T., O'Rand M.G.;
RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
RT preproacrosin-related cDNA.";
RL Biochim. Biophys. Acta 1219:215-218(1994).
DR EMBL: U05203; AAA61629.1; -.
DR HSSP: P00734; 2HNT.
DR INTERPRO: IPR001254; -.
DR PFAM: PF00089; trypsin; 1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW Signal.
FT CHAIN 1 16 POTENTIAL.
FT CHAIN 17 275 PROSPERMINGEN.
SQ SEQUENCE 275 AA; 29965 MW; 8FC2467414069C61 CRC64;

Query Match 12.4%; Score 82.5; DB 6; Length 275;
Best Local Similarity 30.0%; Pred. No. 0.91;
Matches 24; Conservative 12; Mismatches 35; Indels 9; Gaps 3;

QY 10 ALTCL---GGLASPSVPPTLKEIIEELVNITONQASLCNGSMVSVNLTAGMYCAAL 66
Db 172 AQTCVAGGVYKKNAPRSPPTLMEARVDLINL-----ELCNSQWYNGRITASNLGAGY 226

QY 67 ESLINVSDCSAIQRTQRLK 86
Db 227 PS-GRKIDTCRLQLVEVLK 245

RESULT 5
ID Q94918 PRELIMINARY; PRT; 1183 AA.
AC Q94918;
DT 01-MAY-1999 (TrEMBLrel. 10, Created)
DT 01-MAY-1999 (TrEMBLrel. 10, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE KIAA0829 PROTEIN (FRAGMENT).
GN KIAA0829.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=BRIN;
RC MEDLINE=99156230; PubMed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirose M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.;
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL: AB020636; BAA74852.1; -.
FT NON_TER 1
SQ SEQUENCE 1183 AA; 130962 MW; 1FE0EE56C0DFFE3A CRC64;

Query Match 11.8%; Score 78.5; DB 4; Length 1183;
Best Local Similarity 31.0%; Pred. No. 12;
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;

```

QY 5 LTVVIALTCGLGLASPSVPTPTLKELIEELVN-ITQNASLCSNGSMV-----WSV 55
DB 579 LTTVKALTLIAG--SPLKIDLRPVLCGEGVPILASFIRKNQORALKGLTSLDILIKNYS 636
QY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 112
DB 637 SLTAAMIDAVLDLPLISESDMHVSQMAISFTLTAKVYPSS---LSKISGSILNELIG 693
QY 113 LVKNLL 118
DB 694 LVRSP 699

RESULT 6
Q9POH7 PRELIMINARY; PRT; 1230 AA.
AC Q9POH7;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE TIPI20 PROTEIN.
GN TIPI20.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RC TISSUE=ADRENAL GLAND;
RA Fu S., Li Y., Wu T., Peng Y., Gu Y., Zhang L., Jiang C., Huang C.,
RA Han Z., Fu G., Chen Z., Wang Y.;
RT "A novel gene expressed in the human adrenal gland."
RL Submitted (MAY-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RC TISSUE=ADRENAL GLAND;
RA Ren S., Shi J., Huang C., Jiang C., Li Y., Zhou J., Yu Y., Xu S.,
RA Wang Y., Fu G., Chen Z., Han Z.;
RL Submitted (JUN-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF157326; AAF67492.1;
SQ SEQUENCE 1230 AA; 136360 MW; A3ACF0E99B99A1D7 CRC64;

Query Match 11.8%; Score 78.5; DB 4; Length 1230;
Best Local Similarity 31.0%; Pred. No. 13;
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;
QY 5 LTVVIALTCGLGLASPSVPTPTLKELIEELVN-ITQNASLCSNGSMV-----WSV 55
DB 626 LTTVKALTLIAG--SPLKIDLRPVLCGEGVPILASFIRKNQORALKGLTSLDILIKNYS 683
QY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 112
DB 684 SLTAAMIDAVLDLPLISESDMHVSQMAISFTLTAKVYPSS---LSKISGSILNELIG 740
QY 113 LVKNLL 118
DB 741 LVRSP 746

RESULT 7
P97536 PRELIMINARY; PRT; 1230 AA.
AC P97536;
DT 01-MAY-1997 (TremBLrel. 03, Created)
DT 01-MAY-1997 (TremBLrel. 03, Last sequence update)
DT 01-MAY-2000 (TremBLrel. 13, Last annotation update)
DE TIPI20.
GN TIPI20.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
OX NCBI_TaxID=10116;

RP SEQUENCE FROM N.A.
RX MEDLINE=97127450; Pubmed=8954946;
RA Yogosawa S., Makino Y., Yoshida T., Kishimoto T., Muramatsu M.,
RA Tamura T.;
RT "Molecular cloning of a novel 120-kDa TBP-interacting protein.";
RL Biochem Biophys Res Commun. 229:612-617(1996).
DR EMBL; D87671; BAA13432.1;
SQ SEQUENCE 1230 AA; 136360 MW; A3ACF0E99B99A1D7 CRC64;

Query Match 11.8%; Score 78.5; DB 11; Length 1230;
Best Local Similarity 31.0%; Pred. No. 13;
Matches 39; Conservative 19; Mismatches 51; Indels 17; Gaps 5;
QY 5 LTVVIALTCGLGLASPSVPTPTLKELIEELVN-ITQNASLCSNGSMV-----WSV 55
DB 626 LTTVKALTLIAG--SPLKIDLRPVLCGEGVPILASFIRKNQORALKGLTSLDILIKNYS 683
QY 56 NLTAGMYCAALES---LINVSDCSAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 112
DB 684 SLTAAMIDAVLDLPLISESDMHVSQMAISFTLTAKVYPSS---LSKISGSILNELIG 740
QY 113 LVKNLL 118
DB 741 LVRSP 746

RESULT 8
Q9N946 PRELIMINARY; PRT; 1448 AA.
ID Q9N946;
AC Q9N946;
DT 01-OCT-2000 (TremBLrel. 15, Created)
DT 01-OCT-2000 (TremBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TremBLrel. 15, Last annotation update)
DE POSSIBLE PUTATIVE ADENYLATE CYCLASE REGULATORY PROTEIN.
GN CHRI.19.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RC TISSUE=CYTOPLASM;
RA Hall N., Bowman S., Quail M., Ivens A.C., Kay M.P., Bray-Allen S.,
RA Leonard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajadream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL359782; CAB95333.1;
SQ SEQUENCE 1448 AA; 160479 MW; 688B26228AD2046B CRC64;

Query Match 11.5%; Score 76; DB 5; Length 1448;
Best Local Similarity 29.0%; Pred. No. 28;
Matches 36; Conservative 18; Mismatches 34; Indels 36; Gaps 7;
QY 13 CLGGLASPSVPTPTLKELIEELVNITQNA--SLCSNGSMVSVNL-----TAGMYCA 64
DB 557 CLGNL-----POLKMLDLSGTN-TDNESLSLCLLSQFVSLNLSHCWMTNVSHIS 606
QY 65 ALES--INVSDC-----SAIQRTQRMKALCSQKPAAGQISSERSRDTKIEVIQ 115
DB 607 SLEALNELNSNCIRINAGWEAIEKLOOLHVAI-----LSNTHITDRDISHFSCK 657
QY 116 NLIT 119
DB 658 NLVT 661

RESULT 9
Q9N949 PRELIMINARY; PRT; 1448 AA.
ID Q9N949;
AC Q9N949;
DT 01-OCT-2000 (TremBLrel. 15, Created)

QY 4 WLTWIAL-TCLG-GLASPS-----PVTSPPTLKEELVNITQ 43
DB 9 WUTVATAGICGAALUSTSTEDIKLPKENCPLTNVLPVPCGSKF--LEE-ATIDDMQ 65
QY 44 ASLCNGSMVSNLTAGMYCAALESINVSDCSAIQTORMLKALCSKP-----AAGQIS 99
DB 66 AAMNGSLT-SVOLVG--CYVLRTE-----QTDLYINSLOYNPDALSIAQMD 111
QY 100 SERS 103
DB 112 AERA 115

RESULT 13
Q98779 ID Q98779 PRELIMINARY; PRT; 150 AA.
AC Q98779; 01-FEB-1997 (TReMBLrel. 02, Created)
DT 01-FEB-1997 (TReMBLrel. 02, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0888CRB;
RX MEDLINE=97075113; PubMed=8917539;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the
evolution of vesicular stomatitis virus";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL; U39211; AAB50939.1; -;
DR INTERPRO: IPR000224; -;
DR PFAM: PF00922; Phosphoprotein; 1.
FT NON_TER 1
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16711 MW; 16D11C4E8E8A65E7 CRC64;

Query Match 11.0%; Score 73; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 4.5;
Matches 29; Conservative 19; Mismatches 42; Indels 30; Gaps 6;
QY 22 PVTSPPTLKEEL-----VNITQNA-----SLCNGSMVSN-----LTAGMY 62
DB 14 PSWTPVINKGERSLSLFPVGLTQVTEQWKKTIVTVCSSKYWNUSECOIVTSG-N 72
QY 63 CALESINVSDCSAIQTORMLKALCSQKPAAGQISSRSR-----DTKIEVIQV 114
DB 73 CLILRGQVMTSDCSSSAKSONRSQ--SESPSPNSPEHASRASASPNLWDFKTEVQLI 130

RESULT 14
Q908P4 ID Q908P4 PRELIMINARY; PRT; 350 AA.
AC Q908P4; 01-MAY-2000 (TReMBLrel. 13, Created)
DT 01-MAY-2000 (TReMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TReMBLrel. 13, Last annotation update)
DE M52L.
GN M052L.
OS Myxoma virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
OX NCBI_TaxID=10273;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LAUSANNE;
RX MEDLINE=20032073; PubMed=10562494;
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,

RA Macaulay C., Willer D., Evans D., McFadden G.;
RT "The complete DNA sequence of myxoma virus";
RL Virology 264:298-318(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=LAUSANNE;
RA Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macaulay C., Willer D., Evans D., McFadden G.;
RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF170726; AAF14940.1; -;
SQ SEQUENCE 350 AA; 39157 MW; 4D9CC2B04ACFCB7F CRC64;

Query Match 11.0%; Score 73; DB 14; Length 350;
Best Local Similarity 22.3%; Pred. No. 12;
Matches 29; Conservative 22; Mismatches 37; Indels 42; Gaps 5;
QY 26 SPTLKE-----LIEELVNITQNASLCNGSMVSN----- 56
DB 45 APTIKENVINGISFCENNIVRDIPHILVEILNKLHNSVYVCNNEFWRLYNSLSRFT 104
QY 57 ----LTAGMY--CAALESINVSDCSAIQTORMLKAL-----CSQKPAAGQISSRSR 105
DB 105 CKSFTACMYTIATLTSLTLVLSNKLHHAADMIESTIESYLFRAQKPPAQELSD--LLE 162
QY 106 TKIEVIQV 115
DB 163 MKYGLINLVQ 172

RESULT 15
Q9Y613 ID Q9Y613 PRELIMINARY; PRT; 1164 AA.
AC Q9Y613;
DT 01-NOV-1999 (TReMBLrel. 12, Created)
DT 01-NOV-1999 (TReMBLrel. 12, Last sequence update)
DT 01-JUN-2000 (TReMBLrel. 14, Last annotation update)
DE FH1/FH2 DOMAIN-CONTAINING PROTEIN FHOS.
GN FHOS.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=99282522; PubMed=10352228;
RA Westendorf J.J., Mernaugh R., Hiebert S.W.;
RT "Identification and characterization of a protein containing formin
homology (FH1/FH2) domains";
RL Gene 232:173-182(1999).
DR EMBL; AF113615; AAD39906.1; -;
SQ SEQUENCE 1164 AA; 126496 MW; 1BC6ABE3E2E70CB2 CRC64;

Query Match 11.0%; Score 73; DB 4; Length 1164;
Best Local Similarity 26.4%; Pred. No. 45;
Matches 38; Conservative 18; Mismatches 42; Indels 46; Gaps 7;
QY 8 VIALTCGLGLASPSV-----TPSPTLKEELVNITQNASLC----- 47
DB 768 LMTLASIGGLAARLQWLAFKLDYDSMERIEAEPLFDLVKGMEQLV---QNATFCILATL 824
QY 48 -----NGSMVSNLTAGMYCAALESINVSDCSAIQTORMLKALCS-----QKPAAG 96
DB 825 LAVGNFLNGSO-----SSGFELSTYLE---KVSQDKVTVRRSLLHLHLCSLVLTQRPSS 875
QY 97 QISSE---RSRDTKIEVIQV 117
DB 876 DLYSEIPALTFCAKVDFEQLTENL 899

Job time: 43951 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:47:33 ; Search time 79.9 Seconds

(without alignments)
79.413 Million cell updates/sec

Title: US-09-451-527-97

Perfect score: 561

Sequence: 1 SPVTPSPPTKLKELIELVNIT.....QLVKNLLTYRGVYRHGNGR 111

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A.Geneseq_0401.*

- 1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT.*
- 2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT.*
- 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT.*
- 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT.*
- 5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
- 6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
- 7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT.*
- 8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
- 9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT.*
- 10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT.*
- 11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT.*
- 12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT.*
- 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT.*
- 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT.*
- 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT.*
- 16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT.*
- 17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT.*
- 18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT.*
- 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT.*
- 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT.*
- 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*
- 22: /cgnl_8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Query	Score	Match	Length	ID	Description
1	561	100.0	111	21	Y58222	Canine mature inte
2	561	100.0	131	21	Y58221	Canine interleukin
3	545.5	97.2	110	21	Y58224	Canine mature inte
4	545.5	97.2	130	21	Y58223	Canine interleukin
5	382.5	68.2	112	13	R27347	Protein with cytok
6	382.5	68.2	112	17	R92793	Human interleukin-
7	382.5	68.2	132	15	R48624	Sequence of human
8	375.5	66.9	112	13	R27346	Protein with cytok
9	375.5	66.9	146	13	R27348	Cytokine NC30. R
10	367	65.4	111	17	R92794	Human interleukin-
11	295.5	52.7	131	15	R48625	Sequence of mouse

12	292.5	52.1	111	17	R92795	Murine P600. Mus
13	71.5	12.7	382	21	Y84919	Amino acid sequenc
14	67	11.9	21	20	Y49702	Human interleukin
15	65.5	11.7	279	21	B44998	Human secreted pro
16	65.5	11.7	286	21	Y58998	Wheat sulfite redu
17	65.5	11.7	330	21	G06262	Arabidopsis thalia
18	65.5	11.7	407	21	G06261	Arabidopsis thalia
19	65	11.6	482	19	W62025	Recombinantly prod
20	65	11.6	240	20	W30640	HIV-1-NC7 envelope
21	64.5	11.5	267	22	Y71919	Alternative versio
22	64.5	11.5	268	16	R78388	Tobacco mosaic vir
23	64.5	11.5	268	19	W71250	Protein sequence o
24	64.5	11.5	268	22	Y71917	Wild type viral mo
25	64.5	11.5	268	22	Y71920	Alternative versio
26	64.5	11.5	472	15	R56447	TMV replicon-encod
27	64.5	11.5	485	19	Y71249	Protein encoded by
28	64.5	11.5	634	20	Y21548	Human heparin-bind
29	63.5	11.3	229	22	B63822	Human prostate can
30	63.5	11.3	299	21	G30635	Arabidopsis thalia
31	63.5	11.3	299	21	G45468	Arabidopsis thalia
32	63.5	11.3	312	21	G30634	Arabidopsis thalia
33	63.5	11.3	357	21	G30633	Arabidopsis thalia
34	63.5	11.3	514	21	G55503	Arabidopsis thalia
35	63.5	11.3	602	21	G55502	Arabidopsis thalia
36	63.5	11.3	620	21	G55501	Arabidopsis thalia
37	63.5	11.3	673	21	Y58996	Arabidopsis thalia
38	63.5	11.3	889	21	Y95988	Rice sulfite reduc
39	63.5	11.3	919	21	Y95987	Moraxella catarrha
40	63.5	11.3	1032	21	G45673	Moraxella catarrha
41	63.5	11.3	1045	21	G45672	Arabidopsis thalia
42	63.5	11.3	1090	21	G45671	Arabidopsis thalia
43	63.5	11.3	1461	19	W64468	Human secreted pro
44	63	11.2	101	21	B53687	Human colon cancer
45	63	11.2	168	21	B35513	Baculovirus RNA ba

ALIGNMENTS

RESULT 1
Y58222
ID Y58222 standard; Protein; 111 AA.
XX
AC Y58222;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 80.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PS (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX WPI; 2000-072623/06.
XX N-PSDB; Z55559, Z55560.
XX
XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
XX Claim 31; Page 234; 264pp; English.
PS


```

CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 111 AA:

Query Match 100.0%; Score 561; DB 21; Length 111;
Best Local Similarity 100.0%; Pred. No. 1.1e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTPSTLKEIEELVNTQNASLNGSMVSNLTAGMYCAALESINVSDCSAIQR 60
   |||||
DB 1 sptpsptlkeieelvnitqnaslncngsmvsnltagmycaalesinvsdcsaigr 60
   |||||

QY 61 TQMLKALCSQKPAAGQISSERSRDTKIEVTLVKNLLTYVRGVYRHGNFR 111
   |||||
DB 61 tqrmkalcsgkpaagqissersrdtkievqlvknlltyvrgvyrhgnfr 111
   |||||

RESULT 2
Y58221
ID Y58221 standard; Protein; 131 AA.
XX
AC Y58221;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 80.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999;
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
XX
DR N-PSDB; 255555, 255556, 255557, 255558.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 31; Page 231; 264pp; English.
XX
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature

```

```

CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 131 AA:

Query Match 100.0%; Score 561; DB 21; Length 131;
Best Local Similarity 100.0%; Pred. No. 1.4e-60;
Matches 111; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 SPVTPSTLKEIEELVNTQNASLNGSMVSNLTAGMYCAALESINVSDCSAIQR 60
   |||||
DB 21 sptpsptlkeieelvnitqnaslncngsmvsnltagmycaalesinvsdcsaigr 80
   |||||

QY 61 TQMLKALCSQKPAAGQISSERSRDTKIEVTLVKNLLTYVRGVYRHGNFR 111
   |||||
DB 81 tqrmkalcsgkpaagqissersrdtkievqlvknlltyvrgvyrhgnfr 131
   |||||

RESULT 3
Y58224
ID Y58224 standard; Protein; 110 AA.
XX
AC Y58224;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 78.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
XX
DR N-PSDB; 255565, 255566.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
PS Claim 3i; Page 240; 264pp; English.
XX
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,

```

AA	Sequence	130 AA:
SQ		

1:

08

CC and some infection
CC See Q28941-Q28947.

||||| | :||| || ||||| | ||:| | :| | |
Db 82 tqrmisgfcphkvsagqfsslhvrdtkievagfvkdlhlhklkifregfr 131

RESULT 8
R27346
ID R27346 standard; Protein; 112 AA.
XX
AC R27346;
XX
DT 24-FEB-1993 (first entry)
XX
DE Protein with cytokine activity encoded by Nal.
XX
KW Interleukin; chemotaxis; immunomodulation; inflammation.
XX
PN EP506574-A.
XX
PD 30-SEP-1992.
XX
PF 27-MAR-1992; 92EP-0400858.
XX
PR 29-MAR-1991; 91FR-0003904.
PR 08-JAN-1992; 92FR-0000137.
XX
PA (SNFI) ELF SANOFI.
XX
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
PI Leplatols P, Magazin M, Minty A;
XX
DR WPI; 1992-325841/40.
DR N-PSDB; Q28943.
XX
PT New cytokine having immunomodulatory activity - useful for
PT treating tumours and infectious or inflammatory conditions
XX
PS Claim 1; Page 60; 78pp; French.
XX
CC This protein is one of two possible forms of a new cytokine
CC produced by T lymphocytes induced by phorbol-2-myristate-3-acetate
CC and phytohaemagglutinin. The proteins differ only in the amino acid
CC at position 41 which is either Asp or Gly. The cytokine acts on
CC monocytes and B lymphocytes and is useful in treatment of tumours
CC and some infections and inflammatory conditions.
CC See Q28941-Q28947.
XX
SQ Sequence 112 AA;

Query Match 66.9%; Score 375.5; DB 13; Length 112;
Best Local Similarity 69.1%; Pred. No. 4.5e-38;
Matches 76; Conservative 11; Mismatches 22; Indels 1; Gaps 1;
QY 2 PVTSPPTLKELIEELVNTQNO-ASLNGSMVSWNLTAGMYCAALESINVSDCSAIOR 60
Db 2 pvpstairelieelivntqndkaplcnqngsmvswsintadmycaaleslinvsgcsaiek 61
QY 61 TORMLKALCSOKPAAGQISSERSRDTKIEVIOLVKNLLTYVRGVYRHGNF 110
Db 62 tqrmisgfcphkvsagqfsslhvrdtkievagfvkdlhlhklkifregfr 111

RESULT 9
R27348
ID R27348 standard; Protein; 146 AA.
XX
AC R27348;
XX
DT 24-FEB-1993 (first entry)
XX
DE Cytokine NC30.
XX
KW Interleukin; chemotaxis; immunomodulation; inflammation.

XX
FH cleavage_site 20..21 Location/Qualifiers
FT /note= "putative signal peptide cleavage site"
FT cleavage_site 24..25
FT /note= "putative signal peptide cleavage site"
FT cleavage_site 32..33
FT /note= "putative signal peptide cleavage site"
FT cleavage_site 34..35
FT /note= "putative signal peptide cleavage site"
FT protein 35..146
FT /label= NC30
XX
PN EP506574-A.
XX
PD 30-SEP-1992.
XX
PF 27-MAR-1992; 92EP-0400858.
XX
PR 29-MAR-1991; 91FR-0003904.
PR 08-JAN-1992; 92FR-0000137.
XX
PA (SNFI) ELF SANOFI.
XX
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
PI Leplatols P, Magazin M, Minty A;
XX
DR WPI; 1992-325841/40.
DR N-PSDB; Q28947.
XX
PT New cytokine having immunomodulatory activity - useful for
PT treating tumours and infectious or inflammatory conditions
XX
PS Claim 1; Page 52-53; 78pp; French.
XX
CC A novel cytokine produced by T lymphocytes induced by phorbol-2-
CC myristate-3-acetate and phytohaemagglutinin was coded for by the
CC sequence in clone pSEI-NC30. A second clone was also identified
CC (pSEI-NC30bis) which differed only in the identity of codon 41.
CC The corresponding proteins differ in the amino acid at position 41
CC which is either Asp (in NC30) or Gly (in NC30bis). The cytokine
CC acts on monocytes and B lymphocytes and is useful in treatment of
CC tumours and some infections and inflammatory conditions.
CC See Q28941-Q28947.
XX
SQ Sequence 146 AA;

Query Match 66.9%; Score 375.5; DB 13; Length 146;
Best Local Similarity 69.1%; Pred. No. 6.5e-38;
Matches 76; Conservative 11; Mismatches 22; Indels 1; Gaps 1;
QY 2 PVTSPPTLKELIEELVNTQNO-ASLNGSMVSWNLTAGMYCAALESINVSDCSAIOR 60
Db 36 pvpstairelieelivntqndkaplcnqngsmvswsintadmycaaleslinvsgcsaiek 95
QY 61 TORMLKALCSOKPAAGQISSERSRDTKIEVIOLVKNLLTYVRGVYRHGNF 110
Db 96 tqrmisgfcphkvsagqfsslhvrdtkievagfvkdlhlhklkifregfr 145

RESULT 10
R27794
ID R27794 standard; Protein; 111 AA.
XX
AC R27794;
XX
DT 24-MAY-1996 (first entry)
XX
DE Human interleukin-13 mutein 2.
XX
KW Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;
KW diagnosis; therapy; cancer; inflammation; degenerative disease.

```

XX OS Synthetic.
XX FH Key Location/Qualifiers
XX FT Misc-difference 11
XX FT /note= "Glu at position 11 may be replaced by an
XX FT amidated amino acid, including Lys"
XX FT Misc-difference 64
XX FT /note= "Arg at position 64 may be replaced by an
XX FT acidic amino acid, including Asp"
XX PN WO9604306-A2.
XX PD 15-FEB-1996.
XX PF 31-JUL-1995; 95WO-US08950.
XX PR 01-AUG-1994; 94US-0284393.
XX PA (SCHE ) SCHERING CORP.
XX PI Zurawski G, Zurawski SM;
XX WPI; 1996-129335/13.
XX PT Mutin(s) of human and murine cytokine(s), esp. interleukin(s) and
XX murine P600 contg. amino acid substitutions. - useful for the
XX diagnosis and treatment of cancer, inflammation, etc.
XX PS Claim 12; Page 46; 52pp; English.
XX CC Mutins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain
XX amino acid substitutions at amino acid position 11 in helix A and/or
XX at position 64 in helix C. They are obtd. by site-directed
XX mutagenesis of natural IL-13 sequences. The mutins antagonise the
XX activity of IL-13 or IL-4. They have partial cytokine agonist
XX activity, exhibit less than 80% maximal agonist activity of natural
XX IL-2, and/or antagonize cytokine activity by least about 50% when
XX present at a 100-fold excess. They and other cytokine mutins
XX (see also R92790-92, R92795-802) are useful in the screening of
XX cytokine and cytokine receptor levels, and in the diagnosis or
XX treatment of e.g. inflammation, cancer, and degenerative disorders.
XX SQ Sequence 111 AA;

Query Match 65.4%; Score 367; DB 17; Length 111;
Best Local Similarity 69.1%; Pred. No. 4.9e-37;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PVTPSPTLKELIELVNITNQ-ASLCNGSMVSNLTAGMYCAALESINVSDCSAIQR 60
DB 2 pvpstalrelieelvnitnqkplcngsmvsnltagmycaalesinvsqcsaiek 61

QY 61 TQRLKALCSQKPAAGQISSERSRDTKIEVIQLKMLLTYYVRGVRHGNT 110
DB 62 tqrlmgfcphkvksag-fsslhvrdtkievagfvkdlhlhklkifregf 110

RESULT 11
R48625
ID R48625 standard; Protein; 131 AA.
XX AC R48625;
XX DT 14-SEP-1994 (first entry)
XX DE Sequence of mouse P600.
XX KW Interleukin-13; lymphokine; P600; Immunological disorder; therapy;
XX diagnostic.
XX OS Mus musculus.

```

```

XX PN WO9404680-A.
XX PD 03-MAR-1994.
XX PF 18-AUG-1993; 93WO-US07645.
XX PR 21-AUG-1992; 92US-0933416.
XX PR 29-JAN-1993; 93US-0010977.
XX PR 01-FEB-1993; 93US-0012543.
XX PA (SCHE ) SCHERING CORP.
XX PI Aversa G, Banchereau J, Briere F, Coffman RL, Cooks BG;
XX PI Culpepper, Dang W, De Vries J, De Waal Malefyt R;
XX PI Doherty TM, Heath A, McKenzie A, Punnonen J, Zurawski G;
XX WPI; 1994-083197/10.
XX DR N-PSDB; Q56693.
XX PT Purified interleukin-13 proteins and antibodies - obtd. using
XX mouse gene encoding related protein P600
XX PS Disclosure; Page 128-129; 135pp; English.
XX CC An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction
XX digest of the mouse P600 cDNA clone was isolated. This fragment,
XX which encompasses most of the coding region of the mouse P600 cDNA,
XX was radioactively labelled and hybridised with filter lifts pred.
XX from a cDNA library made from a clone of an A10 T cell line. One
XX clone, designated PA 10.66, was subcloned into M13 and sequenced.
XX CC This sequence encodes human IL-13.
XX SQ Sequence 131 AA;

Query Match 52.7%; Score 295.5; DB 15; Length 131;
Best Local Similarity 59.2%; Pred. No. 3.1e-28;
Matches 61; Conservative 16; Mismatches 23; Indels 3; Gaps 2;

QY 8 TLKELIELVNITNQASLCNGSMVSNLTAGMYCAALESINVSDCSAIQRTORMLKA 67
DB 32 tlkelielvnitnqdtplcngsmvsnltagmycaaleslnsnclnalyrtgrilng 91

QY 68 LCSQKPAAGQISSERSRDTKIEVIQLKMLLTYYVRGVRHGNT 110
DB 92 lcnrk-apttvs--lpdkievahfittklsytkqlfrhgp 131

RESULT 12
R92795
ID R92795 standard; Protein; 111 AA.
XX AC R92795;
XX DT 24-MAY-1996 (first entry)
XX DE Murine P600.
XX KW Cytokine; mutin; P600; interleukin-13; IL-13; agonist; antagonist;
XX diagnosis; therapy; cancer; inflammation; degenerative disease.
XX OS Mus musculus.
XX FH Key Location/Qualifiers
XX FT Misc-difference 67
XX FT /note= "Arg at position 67 may be replaced by an
XX FT acid amino acid, including Asp"
XX PN WO9604306-A2.
XX PD 15-FEB-1996.
XX OS

```

```

PF 31-JUL-1995; 95WO-US08950.
XX
PR 01-AUG-1994; 94US-0284393.
XX
PA (SCHE ) SCHERING CORP.
XX
XX Zurawski G, Zurawski SM;
XX PI
XX WPI; 1996-129335/13.
XX
XX Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
PT murine p600 contg. amino acid substitutions. - useful for the
PT diagnosis and treatment of cancer, inflammation, etc.
XX
XX Claim 12; Page 46; 52pp; English.
XX
XX Muteins of mouse p600 (R92795) contain amino acid substitutions at
CC amino acid position 67 in helix C. They are obtd. by site-directed
CC mutagenesis of natural p600 sequences. The muteins antagonise the
CC activity of IL-13 or IL-4. They have partial cytokine agonist
CC activity, exhibit less than 80% maximal agonist activity of natural
CC IL-2, and/or antagonize cytokine activity by least about 50% when
CC present at a 100-fold excess. They and other cytokine muteins
CC (see also R92790-94, R92796-802) are useful in the screening of
CC cytokine and cytokine receptor levels, and in the diagnosis or
CC treatment of e.g. inflammation, cancer, and degenerative disorders.
XX
XX Sequence 111 AA;
SQ

Query Match 52.1%; Score 292.5; DB 17; Length 111;
Best Local Similarity 58.3%; Pred. No. 5.8e-28;
Matches 60; Conservative 17; Mismatches 23; Indels 3; Gaps 2;

QY 8 TLKELIELVNITQNOASLCNGSMWVSNLTAGMYCAALESINVSDCSAIORTORMLKA 67
DB 12 tlkelielsnitqetpplngsmwsvdlaaggfcvaldslnsnchnaiyrtqrlhng 71

QY 68 LCSQKPAAGQISSRSRDTKIEVIOLVKNLLTYVRGVYRHGNF 110
DB 72 lcnrk-apttvss--lptdkievahfiktllsytkqlfrhpgf 111

RESULT 13
Y84919
ID Y84919 standard; protein; 382 AA.
XX
AC Y84919;
XX
XX 21-AUG-2000 (first entry)
XX
XX Amino acid sequence of the Shigella invasin protein SipC.
XX
XX Invasin protein; SipC; mucosal immune response; vaccine; adjuvant;
KW shigellosis; salmonellosis; enteroinvasive E. coli; immune system;
KW immuno-compromised; intracellular delivery; antigen.
XX
XX Shigella flexneri.
OS
XX
XX WO200023462-A1.
XX
XX 27-APR-2000.
XX
XX 21-OCT-1999; 99WO-US24931.
XX
XX 21-OCT-1998; 98US-0105085.
XX
XX 01-JUN-1999; 99US-0136754.
XX
XX (UYSL-) UNIV ST LOUIS.
XX
XX Picking WD, Picking WD, Oaks EV;
XX
XX WPI; 2000-339646/29.
DR

XX
PT New purified recombinant invasin proteins IpaC and SipC useful as an
PT adjuvant and vaccine against shigellosis, salmonellosis and
PT enteroinvasive Escherichia coli
XX
XX Claim 4; Page 3-5; 78pp; English.
XX
XX The present sequence represents the invasin protein SipC. The
CC specification describes a method for the production of recombinant
CC invasin proteins which are superior to presently approved adjuvants due
CC to their low toxicity, their ability to stimulate both peripherals and
CC mucosal immune response, and ease of production. The invasin protein
CC may be used as a vaccine and as an adjuvant for the prevention of
CC diseases such as shigellosis, salmonellosis and diseases caused by
CC enteroinvasive E. coli, and in stimulating the immune system of
CC immuno-compromised individuals. The invasin protein is also useful for
CC intracellular delivery of therapeutic and diagnostic agents, and to
CC stimulate immune response by cells in vitro. The invasin protein
CC can be mixed with antigens of biological or chemical origins to elicit
CC an immune response to the antigen.
XX
XX Sequence 382 AA;
SQ

Query Match 12.7%; Score 71.5; DB 21; Length 382;
Best Local Similarity 22.0%; Pred. No. 2.6;
Matches 26; Conservative 26; Mismatches 39; Indels 27; Gaps 4;

QY 4 TPSPTLKELIE-----ELVNITQNO-----ASLCNGSMWVSNLTAGMYCAALESIN 51
DB 268 spdisiqdkidrtqrtyelntlsagqkqngnatmetsavagnistsgryasale---- 323

QY 52 VSDCSAIORTQRMKALCSQKPAAGQISSRSRDTKIEVIOLVKNLLTYVRGVYRHGN 109
DB 324 -----eeeqllsqasskqaeasqvskasqatn----qliqkllniidsingskn 370

RESULT 14
Y49702
ID Y49702 standard; peptide; 21 AA.
XX
AC Y49702;
XX
XX 18-JAN-2000 (first entry)
XX
XX Human interleukin 13 N-terminal peptide #2.
DE
XX
XX Pseudomonas exotoxin; PE; mutagenised; IL-13; chimeric; interleukin;
KW cytotoxin; fusion protein; cancer; glioma; neoplasia.
XX
XX Homo sapiens.
OS
XX
XX WO9951643-A1.
XX
XX 14-OCT-1999.
XX
XX 31-MAR-1999; 99WO-US07188.
XX
XX 03-APR-1998; 98US-0054711.
XX
XX (PENN-) PENN STATE RES FOUND.
XX
XX Debinski W;
XX
XX WPI; 1999-633731/54.
XX
XX New mutagenized interleukin 13 molecules for delivery of cytotoxins to
PT cells over expressing IL13 receptors
XX
XX Disclosure; Fig 3; 57pp; English.
XX
XX The present invention describes targeting ligands which are mutagenized
CC IL13 (interleukin 13) molecules having one or more mutations in the

```

CC domain that interacts with the hIL14 receptor subunit designated the
CC 140 kDa hIL4RBeta subunit. A cytotoxic molecule covalently attached to
CC a mutagenized hIL13 can be used for delivering an effector molecule to
CC a cell bearing an IL13 receptor. Where the effector molecule is a
CC cytotoxin, neoplastic cells (e.g. a glioma) can be killed or inhibited.
CC The methods are used to target effector molecules to kidney cancers, to
CC skin cancers (Kaposi's sarcoma) and to brain cancers (gliomas and
CC medulloblastomas). When the mutagenized cell is attached to a detectable
CC label the chimeric label can be used to detect the presence or absence
CC of tumour cells, or localize and/or quantify a cell or cells expressing
CC an IL13 receptor. The label localizes at the site of overexpression and
CC indicates the presence, absence, quantity or location of such cells. If
CC the effector molecule is an antibody the chimeric molecule may act to
CC enhance and direct an immune response toward target cancer cells. The
CC mutagenized IL13s may be conjugated to a drug such as vinblastine,
CC doxorubicin, genistein, an antisense molecule, ribozymes or any other
CC pharmacological agent to specifically target target cells over
CC expressing IL13 receptors. The targeting ligands have increased
CC specificity for cancer cells as compared to normal cells and are
CC therefore very effective for specifically delivering effector molecules
CC to various neoplasias. The present sequence is used in the
CC exemplification of the present invention.
XX
SQ Sequence 21 AA;

Query Match 11.9%; Score 67; DB 20; Length 21;
Best Local Similarity 77.9%; Pred. No. 0.18;
Matches 14; Conservative 1; Mismatches 3; Indels 0; Gaps 0;

QY 2 PVTPSPPTLKEILELVNI 19
DB 4 PVPPTALRELIEELVNI 21

RESULT 15
ID B44998 standard; Protein: 279 AA.
XX
AC B44998;
XX
DT 12-FEB-2001 (first entry)
XX
DE Human secreted protein encoded by gene 28 homologue.
XX
KW Secreted protein; human; immunosuppressive; antiarthritic; antirheumatic;
KW antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective;
KW neurologic; neuroprotective; antibacterial; virucide; fungicide;
KW ophthalmological; gene therapy; treatment; autoimmune disease; infection;
KW cardiovascular disorder; nervous system disorder; ocular disorder;
KW wound healing; epithelial cell proliferation; skin aging; mental state;
KW transplantation; metabolism modulation.
XX
OS Homo sapiens.
XX
PN WO200055200-A1.
XX
PD 21-SEP-2000.
XX
PF 09-MAR-2000; 2000WO-US06042.
XX
PR 12-MAR-1999; 99US-0124143.
PR 03-DEC-1999; 99US-0168663.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM, Komatsoulis G;
XX
DR WPI; 2000-656008/63.
XX
PT Isolated human secretory proteins, nucleic acids encoding them and
PT antibodies directed against them, useful for diagnosing and treating
PT disorders related to the proteins such as cancer, Alzheimer's disease

PT and Parkinsons -
XX Disclosure; Page 434-435; 453pp; English.
PS
XX
CC This invention describes a novel isolated polypeptide (I) and its
CC encoding nucleic acid molecule (II) which have immunosuppressive,
CC antiarthritic, antirheumatic, antiproliferative, cytostatic, cardiant,
CC vasotropic, cerebroprotective, neurotropic, neuroprotective, antibacterial,
CC virucide, fungicide and ophthalmological activity and which can be used
CC for gene therapy. (I) and (II) are used to prevent, treat or ameliorate
CC a medical condition in e.g. humans, mice, rabbits, goats, horses, cats,
CC dogs, chickens or sheep. (I) and (II) are also used in diagnosing a
CC pathological condition or susceptibility to a pathological condition. The
CC antibodies to (II) can also be used in alleviating symptoms associated
CC with the disorders and in diagnostic immunoassays e.g. radioimmunoassays
CC or enzyme linked immunosorbent assays (ELISA). Disorders which are
CC diagnosed or treated include autoimmune diseases e.g. rheumatoid
CC arthritis, hyperproliferative disorders e.g. neoplasms of the breast or
CC liver, cardiovascular disorders e.g. cardiac arrest, cerebrovascular
CC disorders e.g. cerebral ischemia, angiogenesis, nervous system disorders
CC e.g. Alzheimer's disease, infections caused by bacteria, viruses and
CC fungi and ocular disorders e.g. corneal infection. The polypeptides can
CC also be used to aid wound healing and epithelial cell proliferation, to
CC prevent skin aging due to sunburn, to maintain organs before
CC transplantation, for supporting cell culture of primary tissues, to
CC regenerate tissues and in chemotaxis. The polypeptides are used to
CC modulate mammalian metabolism, to change mammal's mental state or
CC physical state by influencing biorhythms circadian rhythms, depression
CC tendency for violence tolerance for pain, reproductive capabilities,
CC hormonal or endocrine levels, appetite, libido, memory, stress or other
CC cognitive qualities, as a food additive or preservative, such as to
CC increase or decrease storage capabilities, fat content, lipid, protein,
CC carbohydrates, vitamins, minerals, cofactors or other nutritional
CC components.
XX
SQ Sequence 279 AA;

Query Match 11.7%; Score 65.5; DB 21; Length 279;
Best Local Similarity 28.7%; Pred. No. 9.1;
Matches 31; Conservative 14; Mismatches 32; Indels 31; Gaps 6;

QY 9 LKELIEELVNITQNASLC-----NGSMVSVNLTAGMYCAALESLINVSDCS 56
DB 184 lkvmeqiv---qnatfrcllatllavgnflngsq-----ssgfxlsylekvsxvkd-- 232
QY 57 AIQRTQRMUKALCS---QKPAAGQISSE---RSRDTKIEVIQLVKNL 97
DB 233 -tvrrqslhlhslsvlqtrpessdyseipaltrcakvdfqqlenl 279

Search completed: May 13, 2001, 17:47:35
Job time: 12335 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:48:30 ; Search time 42.06 seconds
(without alignments)
50.699 Million cell updates/sec

Title: US-09-451-527-97
Perfect score: 561
Sequence: 1 SPVTPSPTLKELIEELVNIT.....QLVKNLLTYVRGVYRHGNFR 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn1_7/ptodata/1/iaa/5A-COMB.pep:*
2: /cgn1_7/ptodata/1/iaa/5B-COMB.pep:*
3: /cgn1_7/ptodata/1/iaa/6A-COMB.pep:*
4: /cgn1_7/ptodata/1/iaa/6B-COMB.pep:*
5: /cgn1_7/ptodata/1/iaa/PCTUS-COMB.pep:*
6: /cgn1_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	382.5	68.2	112	1 US-08-284-393B-4	Sequence 4, Appli
2	382.5	68.2	112	5 PCT-US95-08950-4	Sequence 4, Appli
3	382.5	68.2	132	1 US-08-012-543-2	Sequence 2, Appli
4	382.5	68.2	132	5 PCT-US93-07645A-2	Sequence 2, Appli
5	382.5	68.2	132	5 PCT-US93-07645-2	Sequence 2, Appli
6	375.5	66.9	112	1 US-08-371-121-1	Sequence 1, Appli
7	375.5	66.9	146	1 US-08-371-121-16	Sequence 16, Appli
8	371.5	66.2	112	1 US-08-284-393B-14	Sequence 14, Appli
9	367	65.4	111	1 US-08-284-393B-5	Sequence 5, Appli
10	367	65.4	111	5 PCT-US95-08950-5	Sequence 5, Appli
11	356	63.5	111	1 US-08-284-393B-15	Sequence 15, Appli
12	295.5	52.7	131	1 US-08-012-543-4	Sequence 4, Appli
13	295.5	52.7	131	1 US-08-371-121-25	Sequence 25, Appli
14	295.5	52.7	131	5 PCT-US93-07645A-4	Sequence 4, Appli
15	295.5	52.7	131	5 PCT-US93-07645-4	Sequence 4, Appli
16	292.5	52.1	111	1 US-08-284-393B-6	Sequence 6, Appli
17	292.5	52.1	111	5 PCT-US95-08950-6	Sequence 6, Appli
18	285.5	50.9	111	1 US-08-284-393B-16	Sequence 16, Appli
19	64.5	11.5	268	2 US-08-176-414B-2	Sequence 2, Appli
20	64.5	11.5	268	2 US-08-687-559-25	Sequence 25, Appli
21	63.5	11.3	1461	2 US-08-993-228-10	Sequence 10, Appli
22	63	11.2	168	3 US-09-188-579-85	Sequence 85, Appli
23	63	11.2	599	1 US-08-222-619-2	Sequence 2, Appli
24	63	11.2	599	5 PCT-US95-04075-2	Sequence 2, Appli
25	63	11.2	731	1 US-08-731-716-2	Sequence 2, Appli
26	63	11.2	871	2 US-08-775-009-35	Sequence 35, Appli
27	60.5	10.8	2629	2 US-08-751-189-4	Sequence 4, Appli

28	60.5	10.8	2629	2	US-09-060-836-4	Sequence 4, Appli
29	60.5	10.8	2629	4	US-09-184-445-4	Sequence 4, Appli
30	60	10.7	2004	1	US-08-375-709-15	Sequence 15, Appli
31	60	10.7	2004	1	US-08-732-929-15	Sequence 15, Appli
32	60	10.7	2004	4	US-09-090-793-9	Sequence 9, Appli
33	59.5	10.6	735	3	US-09-191-647-9	Sequence 9, Appli
34	59	10.5	119	2	US-08-318-157B-57	Sequence 57, Appli
35	59	10.5	1130	2	US-08-519-547A-6	Sequence 6, Appli
36	58.5	10.4	232	1	US-07-990-301A-4	Sequence 4, Appli
37	58.5	10.4	649	4	US-09-188-930-305	Sequence 305, Appli
38	58	10.3	529	1	US-08-484-105-8	Sequence 8, Appli
39	58	10.3	529	1	US-08-484-106-8	Sequence 8, Appli
40	58	10.3	832	3	US-08-630-820-7	Sequence 7, Appli
41	58	10.3	2595	4	US-09-036-987A-2	Sequence 2, Appli
42	57.5	10.2	477	2	US-08-770-544-16	Sequence 16, Appli
43	57	10.2	353	3	US-08-803-603-3	Sequence 3, Appli
44	57	10.2	414	1	US-08-002-202-13	Sequence 13, Appli
45	57	10.2	414	1	US-08-002-202-17	Sequence 17, Appli

ALIGNMENTS

RESULT 1
US-08-284-393B-4
; Sequence 4, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-4

Query Match 68.2%; Score 382.5; DB 1; Length 112;
Best Local Similarity 70.0%; Pred. No. 3.2e-41;
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
QY 2 PVTSPTLKELIEELVNITQNO-ASLCNGSMVWSNLTAGMYCALESINVSQCSATOR 60
||| :||||| :||||| :||||| :||||| :||||| :||||| :||||| :
DB 2 PVPSTALRELIEELVNITQNOKAPLCNGSMVWSNLTAGMYCALESINVSQCSATOR 61


```

RESULT      6
US-08-371-121-1
; Sequence 1, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascal
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTEILLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 41
; OTHER INFORMATION: /label= Xaa
; OTHER INFORMATION: /note= "amino acid is Asp or Gly"
US-08-371-121-1

```

QY 61 TQRLKALCSOKPAAGQISSRSRDTKTEIVLVKNLLTYVRGVVRHGNF 110
db 62 TQRLSGFCPHKVSAGOFSSLHVVRTKTEVAGFVKDILLHLKAKLFGREFR 111

```

RESULT 7
US-08-371-121-16
; Sequence 16, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLIER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC Compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 16:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-371-121-16

```

```
Query Match      66.9%; Score 375.5; DB 1; Length 146;
Best Local Similarity 69.1%; Pred. No. 3.7e-40;
Matches 76; Conservative 11; Mismatches 22; Indels 1; Gaps 1;
```

Db	36	PVPPSTALRELIEELVNTQNKAPLCNGSMVWSINTADMYCAALESLLINSGCSAIEK	95
Qy	61	TQRLMKALCSQPAAGQISSERSRDTKIEVLQVKNLLTVYRGHGNF	110
Db	96	TQRLSGFCPHKVSAGQSFSLHVRDTKEVAFQVKDLLLLHLKKLFREGF	145

```

RESULT      8
US-08-284-393B-14
; Sequence 14, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 112 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-14

```

		Query Match	66.2%;	Score	371.5;	DB	1;	Length	112;
		Best Local Similarity	68.2%;	Pred. No.	8,1e-40;				
		Matches	75;	Conservative	12;	Mismatches	22;	Indels	1;
		Gaps	1;						
Qy	2	PVTPSPILKEELVNITQNQ-A	SLCNGSMWVS	VNLTAGMYCAALES	LINVS	DGCSA	IQR	60	
		: :							
Db	2	PVPSTALRLKEELVNITQNQ	KAPLCNGSMWVS	INTAGMYCAALES	LINVS	DGCSA	IEK	61	
		: :							
Qy	61	TQRMKLKALCKOKPAAGQIS	SRSRDTKIEVTQLVKNNL	TYVRGVYRHGNF	110				
		: :							
Db	62	TODMLSGFCPHKVAGOFSS	LHVHSDTKTEVAO	FVKDLLLLHLKKLFREGR	111				
		: :							

RESULT 9
US-08-284-393B-5
; Sequence 5, Application US/08284393B.
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: zurawski, Sandra M.
; APPLICANT: zurawski, Gerard
; TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute

STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX031
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-5

	Query Match	65.4%	Score 367;	DB 1;	Length 111;
	Best Local Similarity	69.1%;	Pred. No. 3e-39;		
	Matches	76;	Conservative 11;	Mismatches 21;	Indels
y	2	PVTPPTLKEELVNIQTQK-ASLCNGSMVWSVNLTAGMYCAALESINVS			
		:			
b	2	PVPPSTALRELIEELVNIQTQKAPLCNGSMVWSINLTAGMYCAALESINVS			
		:			
y	61	TQRLMKALCSQRPAGQIISERSRDTKIEVIQVKNLLTYVRGVYRHGF	110		
		: :			
	62	TQRLMSGFCPHKVSAG-FSSLHVRTDKIEVAFQVDLLHLKLLKPEGRF	110		
		: :			

RESULT 10
PCT-US95-08950-5
; Sequence 5, Application PC/TUS9508950
; GENERAL INFORMATION:
; APPLICANT: zurawski, Sandra M.
; APPLICANT: zurawski, Gerard
; TITLE OF INVENTION: MUTINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.

```

; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08950-5

```

Query Match 65.4%; Score 367; DB 5; Length 111;
Best Local Similarity 69.1%; Pred. NO. 3e-39;
Matches 76; Conservative 11; Mismatches 21; Indels

Qy	2	PVTSPTLKELIBELVNITQ-NQ-ASLNCNGSMWVSNLTAGMYCAALESINVDCSATOR	60
	1		
Db	2	PVPSTALRELIEBELVNITQKAPLNCNGSMWVSNLTAGMYCAALESINVSGSAIEK	61
	1		
Qy	61	TQRMALCSOKPAAGQTSSRSRDTKTETVLQKNLLTYRVGVYRHGNE	110
	1		
Db	62	TQRMLSGFCPHKVSAG-FSSLVHRDTEKIEVAOFVKDILLHLKLFREGRE	110
	1		

RESULT 11
 US-08-284-393B-15
 ; Sequence 15, Application US/08284393B
 ; Patent No. 5696234
 ; GENERAL INFORMATION:
 ; APPLICANT: Zurawski, Sandra M.
 ; APPLICANT: Zurawski, Gerard
 ; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
 ; NUMBER OF SEQUENCES: 16
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: DNAX Research Institute
 ; STREET: 901 California Avenue
 ; CITY: Palo Alto
 ; STATE: California
 ; COUNTRY: USA

```

1  ZIP: 94304-1104
2
3  COMPUTER READABLE FORM:
4
5  MEDIUM TYPE: Floppy disk
6
7  COMPUTER: IBM PC compatible
8
9  OPERATING SYSTEM: PC-DOS/MS-DOS
10
11 SOFTWARE: PatentIn Release #1.0, Version #1.30
12
13 CURRENT APPLICATION DATA:
14
15 APPLICATION NUMBER: US/08/284,393B
16
17 FILING DATE: 01-AUG-1994
18
19 CLASSIFICATION: 435
20
21 ATTORNEY/AGENT INFORMATION:
22
23 NAME: Ching, Edwin P.
24
25 REGISTRATION NUMBER: 34,090
26
27 REFERENCE/DOCKET NUMBER: DX0389
28
29 TELECOMMUNICATION INFORMATION:
30
31 TELEPHONE: 415-852-9196
32
33 TELEFAX: 415-496-1200
34
35 INFORMATION FOR SEQ ID NO: 15:
36
37 SEQUENCE CHARACTERISTICS:
38
39 LENGTH: 111 amino acids
40
41 TYPE: amino acid
42
43 STRANDEDNESS: single
44
45 TOPOLOGY: linear
46
47 MOLECULE TYPE: peptide
48
49 PS-08-284-393B-15

```

Query Match 63.5%; Score 356; DB 1; Length 111;
Best Local Similarity 67.3%; Pred. No. 7.5e-38;
Matches 74; Conservative 12; Mismatches 22; Indels

QY 2 PVTSPITKELIEELVNITQ-ASLNCNGSMVSNLTAGMYCAALESINVDSCSATOR 60
Db 2 PVPSTALRKELIEELVNITQKAPLNCNGSMVSNLTAGMYCAALESINVDSCSATOR 61
QY 61 TQMLKALCSOKPAAGQISSERSRDTKTEVQLVKNLLTYRGVYRHGNF 110
Db 62 TODMLSGCPKHKVAG-FSSLHVRDTKIEVAQFVADLLHLKLFRRGRF 110

RESULT 12
US-08-012-543-4
; Sequence 4, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-543-4

Query Match 52.7%; Score 295.5; DB 1; Length 131;
Best Local Similarity 59.2%; Pred. No. 4.7e-30;
Matches 61; Conservative 16; Mismatches 23; Indels 3; Gaps 2;
QY 8 TLKELIEELVNITQNASLNCNGSMVSNLTAGMYCAALESINVDSCSATOR 67
Db 32 TLKELIEELVNITQDTPLCNGSMVSNLTAGMYCAALESINVDSCSATOR 67
QY 68 LCSOKPAAGQISSERSRDTKTEVQLVKNLLTYRGVYRHGNF 110
Db 92 LCNRRK-APTTVSS--LPDTKIEVAHFITKLLSYTKQLFRHGP 131

RESULT 13
US-08-371-121-25
; Sequence 25, Application US/08371121
; Patent No. 5652123
; GENERAL INFORMATION:
; APPLICANT: CAPUT, Daniel
; APPLICANT: FERRARA, Pascual
; APPLICANT: GUILLEMOT, Jean-Claude
; APPLICANT: LEPLATOIS, Pascal
; APPLICANT: MINTY, Adrian
; APPLICANT: KAGHAD, Mourad
; APPLICANT: LABIT-LE BOUTELLER, Christine
; APPLICANT: MAGAZIN, Marilyn
; TITLE OF INVENTION: Protein having a cytokine type
; TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
; TITLE OF INVENTION: transformed cells and microorganisms.
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W., Suite 500
; CITY: Washington, D.C.
; COUNTRY: USA
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/371,121
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/938,161
; FILING DATE: 30-NOV-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/FR92/00280
; FILING DATE: 27-MAR-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 00137
; FILING DATE: 08-JAN-1992
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: FR 91 03904
; FILING DATE: 29-MAR-1991
; ATTORNEY/AGENT INFORMATION:
; NAME: SAXE, Bernhard D.
; REGISTRATION NUMBER: 28,665
; REFERENCE/DOCKET NUMBER: 16781/383
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; TELEX: 904136
; INFORMATION FOR SEQ ID NO: 25:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-371-121-25

Query Match 52.7%; Score 295.5; DB 1; Length 131;
Best Local Similarity 59.2%; Pred. No. 4.7e-30;
Matches 61; Conservative 16; Mismatches 23; Indels 3; Gaps 2;
QY 8 TLKELIEELVNITQNASLNCNGSMVSNLTAGMYCAALESINVDSCSATOR 67
Db 32 TLKELIEELVNITQDTPLCNGSMVSNLTAGMYCAALESINVDSCSATOR 67
QY 68 LCSOKPAAGQISSERSRDTKTEVQLVKNLLTYRGVYRHGNF 110
Db 92 LCNRRK-APTTVSS--LPDTKIEVAHFITKLLSYTKQLFRHGP 131

Result No.	Query			DB	ID	Description
	Score	Match	Length			
1	382.5	68.2	146	1	A47481	interleukin-13 pre
2	295.5	52.7	131	2	E30552	T-cell activation
3	234	52.4	131	2	I52290	interleukin-13 - r
4	73	13.0	701	2	S17196	transcription fact
5	71.5	12.7	382	1	A60112	42K membrane anti
6	71	12.7	261	2	JQ1176	sepiapterin reduct
7	70.5	12.6	262	2	A36024	sepiapterin reduct
8	70	12.5	382	2	S15578	ipac protein - Shi
9	70	12.5	430	2	S77393	cell division prot
10	70	12.5	677	2	S15667	transcription fact
11	69.5	12.4	267	2	JC1339	movement protein -
12	69.5	12.4	431	2	S47538	acrosin (EC 3.4.21
13	68.5	12.2	494	2	S52110	sepiapterin reduct
14	68.5	12.2	494	2	F82660	penicillin binding
15	68.5	12.2	559	2	T00714	hypothetical prote
16	68.5	12.2	2606	2	T03159	large tegument pro
17	68	12.1	1004	2	S53939	probable membrane
18	67	11.9	481	2	S62423	ATP-dependent RNA
19	67	11.9	516	2	H72427	DNA mismatch repai
20	66.5	11.9	323	1	GHRB	Ig gamma chain C r
21	66	11.8	1234	2	G70622	probable transcrip
22	65.5	11.7	325	2	T16995	probable cinnamyl-
23	65.5	11.7	326	2	S49937	hypothetical prote
24	65.5	11.7	1681	2	S42369	Clathrin heavy cha
25	65	11.6	268	2	S26359	30K protein - toba
26	65	11.6	451	2	T15000	hypothetical prote
27	65	11.6	2149	2	T47655	hypothetical prote
28	65	11.6	2626	2	T31099	myosin-RhoGAP prot
29	64.5	11.5	336	2	H82396	conserved hypothet

C;Comment: This enzyme catalyzes the NADPH-dependent reduction of sepiapterin to pro
C;Genetics:
A;Gene: GDB:SPR
A;Cross-references: GDB:128778
A;Map position: 2p14-2p12
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: NADP; oxidoreductase
F;8-199/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;28-32/Region: pterin binding #status predicted

Query Match 12.7%; Score 71; DB 2; Length 261;
Best Local Similarity 24.7%; Pred. No. 5.1;
Matches 24; Conservative 21; Mismatches 42; Indels 10; Gaps 4;

QY 16 LVNITQNASILCNGSMV---WSVNLTAGMCAALLESILNVSDCSAIQTORTMLKALCSQK 72
Db 104 LGDSVSGFVLDSDTQNNVWALNTS-MLCLTSVLKAPFDSPLNRTVVNIISSLCALQ 162
QY 73 PAAG---QISERSRDTKIEVIQLVK---NLLTVVRG 103
Db 163 PFKGALYCACKARDMLFQVLALEENVRVLYAPG 199

RESULT 7
A36024
sepiapterin reductase (EC 1.1.1.153) - rat
C;Species: Rattus norvegicus (Norway rat)
C;Date: 11-Jan-1991 #sequence.revision 07-Jul-1995 #text_change 01-Dec-2000
C;Accession: A36024; A36400; PH1577; I64799; A49174
R;Citron, B.A.; Mills, S.; Gutierrez, J.C.; Levine, R.A.; Yanak, B.L.; Kaufman, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 6436-6440, 1990
A;Title: Isolation and expression of rat liver sepiapterin reductase cDNA.
A;Reference number: A36024; MUID:90349631
A;Accession: A36024
A;Molecule type: mRNA
A;Residues: 4-262 <CIT>
R;Oyama, R.; Katoh, S.; Sueoka, T.; Suzuki, M.; Ichinose, H.; Nagatsu, T.; Titani, K.
Biochem. Biophys. Res. Commun. 173, 627-631, 1990
A;Title: The complete amino acid sequence of the mature form of rat sepiapterin reductase
A;Reference number: A36400; MUID:91083647
A;Accession: A36400
A;Molecule type: protein
A;Residues: 1-32;34;41-92,'I',96-124;126-262 <OYA>
R;Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Exp. Cell Res. 204, 217-222, 1993
A;Title: Detection of a novel sepiapterin reductase mRNA: Assay of mRNA in various ce
A;Reference number: A49174; MUID:93178546
A;Accession: PH1577
A;Molecule type: mRNA
A;Residues: 209-255 <MAI>
R;Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Adv. Exp. Med. Biol. 338, 195-198, 1993
A;Title: Northern blot analysis of sepiapterin reductase mRNA in mammalian cell lines
A;Reference number: I51849; MUID:94136218
A;Accession: I64799
A;Status: preliminary; translated from GB/EMBL/DDBJ--
A;Molecule type: mRNA
A;Residues: 209-255 <RES>
A;Cross-references: GB:S71374; NID:g557901
C;Function:
A;Description: catalyzes the NADPH-dependent reduction of sepiapterin to produce 7,8-
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: acetylated amino end; homodimer; oxidoreductase
F;9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 12.6%; Score 70.5; DB 2; Length 262;
Best Local Similarity 23.5%; Pred. No. 5.8;
Matches 24; Conservative 25; Mismatches 42; Indels 11; Gaps 4;

QY 8 TLKELIEELVNITONQASLNCNGSMWVSVNTAGMYCAALESINVSDCSAIQRTORMLKA 67
|| : : ||| | : : ||| | : : ||| | : : ||| | : :
Db 104 TLDGSKVGFLNIN---DLAEVNNYALNLTIS-MLCLTGTGLNAPNSPLSKTVVNISS 158

QY 68 LCSOKPAAG---QISSERSDTEKIEVIOLVK---NLITYVRG 103
|| : : ||| | : : ||| | : : ||| | : : ||| | : :
Db 159 LCALQPFKGWGLYCAGKAARDMLYQVLAVEEPSRVLSYAPG 200

RESULT 8
S15378
ipac protein - Shigella dysenteriae
C:Species: Shigella dysenteriae
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 26-Aug-1999
C:Accession: S15578
R;Yao, R.; Palchaudhuri, S.
submitted to the EMBL Data Library, June 1991
A:Description: Nucleotide sequence of the ipaBCD structure genes of Shigella dysenteriae
A:Reference number: S15575
A:Accession: S15578
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-382 <X>
A:Cross-references: EMBL:X60777; NID:g46932; PIDN:CAA43191.1; PID:g46936
C:Superfamily: 42K membrane antigen ipac

Query Match 12.5%; Score 70; DB 2; Length 382;
Best Local Similarity 21.7%; Pred. No. 10;
Matches 28; Conservative 26; Mismatches 39; Indels 36; Gaps 5;

QY 4 TPSPTLKELIE-----ELVNITQNQ-----ASLCNGSMWVSVNLTAGMYCAALESLIN 51
|| : : ||| | : : ||| | : : ||| | : : ||| | : :
Db 268 SPDISLODKIDITRRYYELNLTSLAQKQGNIGRAMETSAVAGNISTSGRYASALE---- 323

QY 52 VSDCSAIQTORMKLKALCSOKPAGQISSERSDTEKIEVIOLVKLLTYVRGVYRH---- 107
|| : : ||| | : : ||| | : : ||| | : : ||| | : :
Db 324 -----EEQLITSASSKOAEASQVSKASQATN-----QLIQKLLNIIDNINGSRST 372

QY 108 ----CNER 111
||| |
Db 373 ASQIAGNIR 381

RESULT 9
S77393
cell division protein ftsZ - Synechocystis sp. (strain PCC 6803)
C:Species: Synechocystis sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 20-Jun-2000
C:Accession: S77393
R;Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.;
O., K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda,
DNA Res. 3, 109-136, 1996
A:Title: Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis
s.
A:Reference number: S74322; MUID:97061201
A:Accession: S77393
A>Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-430 <KAN>
A:Cross-references: EMBL:D90906; GB:AB001339; NID:g1652492; PIDN:BAA17496.1; PID:g165251
A>Note: The nucleotide sequence was submitted to the EMBL Data Library, June 1996.
C:Genetics:
A:Gene: ftsZ
C:Superfamily: cell division protein ftsZ
C:Keywords: cell division; GTP binding
F:161-167/Region: tubulin/FtsZ GRP/GDP-binding (G-G-G-T-G-[ST]-G) motif
F:262-269/Region: GTP hydrolyzing

Query Match 12.5%; Score 70; DB 2; Length 430;

```
QY 3 VTPSPTLKELIELVNI--TONQASLNCNGSM-----VMSVNLTAGMYCAALESNLVS 53
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 127 IITQDVKNVQVVLNIRNVKMSAGFCPLSLERFVAVCIIVSNIKLGL-----REKTIINR 182
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 54 DCSAQTQRMKALCSQKPAAGQISSERSRDTKIEVIQLVKN 96
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 183 DGGPMELTEEVDFMEDVPMISRLAKFRSRTCKKSDVRKGN 225
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 12
S47538
acrosin (EC 3.4.21.10) precursor - rabbit
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S47538
R:Richardson, R.T.; O'Rand, M.G.
Biochim. Biophys. Acta 1219, 215-218, 1994
A:Title: Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin
A:Reference number: S47538; MUID:94368861
A:Accession: S47538
A:Molecule type: mRNA
A:Residues: 1-431 <RIC>
A:Cross-references: EMBL:U05204; NID:9451841; PIDN:AAA61630.1; PID:9451842
C:Superfamily: acrosin; trypsin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:40-283/Domain: trypsin homology <TRY>

Query Match 12.4%; Score 69.5; DB 2; Length 431;
Best Local Similarity 36.4%; Pred. No. 13;
Matches 16; Conservative 7; Mismatches 16; Indels 5; Gaps 1;

QY 5 PSPTLKEIEELVNITQNASLNCNGSMVSNLTAGMYCAALES 48
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 190 PSPTLMEARVDLNL-----ELCNSTQWYNGRITASLNCAGYPS 228
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 13
S52110
sepiapterin reductase (EC 1.1.1.153) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 18-Feb-2000
C:Accession: S52110; PH1578
R:Ota, A.; Ichinose, H.; Nagatsu, T.
Biochim. Biophys. Acta 1260, 320-322, 1995
A:Title: Mouse sepiapterin reductase: an enzyme involved in the final step of tetrahydrobiopterin synthesis
A:Reference number: S52110; MUID:95178553
A:Accession: S52110
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <OTA>
A:Cross-references: GB:S77493; NID:957229; PIDN:AAB33611.1; PID:957230
R:Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Exp. Cell Res. 204, 217-222, 1993
A:Title: Detection of a novel sepiapterin reductase mRNA: Assay of mRNA in various cells
A:Reference number: A49174; MUID:93178546
A:Accession: PH1578
A:Molecule type: mRNA
A:Residues: 209-255 <MAI>
C:Comment: This enzyme catalyzes the reduction of both C1' and C2' oxo group.
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 12.2%; Score 68.5; DB 2; Length 261;
Best Local Similarity 21.5%; Pred. No. 9.4;
Matches 23; Conservative 26; Mismatches 47; Indels 11; Gaps 4;

QY 3 VTPSPTLKELIELVNIITQNASLNCNGSMVSNLTAGMYCAALESNLVSQDSATQRTQ 62
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 99 INNAATLGDVGKFLNVN----DLAEVNNYVALNLTSLMCLTSGTLNAPQDSPGLSKTV 153
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
```

```
QY 63 RMLKALCSQKPAAG--QISSERSRDTKIEVIQLVK---NLLTYVRG 103
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 154 WNISLALQPYKGLGYCAGKAARDMLYQVLAABEPSRVLSYAPG 200
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 14
F82660
penicillin binding protein XF1614 [imported] - Xylella fastidiosa (strain 9a5c)
C:Species: Xylella fastidiosa
C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 20-Aug-2000
C:Accession: F82660
R:anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Seq
Nature 406, 151-157, 2000
A:Title: The genome sequence of the plant pathogen Xylella fastidiosa.
A:Reference number: A82515; MUID:20365717
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: F82660
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-494 <SIM>
A:Cross-references: GB:AE003988; GB:AE003849; NID:99106653; PIDN:AAF84423.1; GSPDB:GN
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer
as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Fr
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; La
chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins
A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.
, F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri,
Rodrigues, V.; Rosa, A.J.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawa
M.; Tshuko, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovski-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: XF1614

Query Match 12.2%; Score 68.5; DB 2; Length 494;
Best Local Similarity 30.0%; Pred. No. 20;
Matches 21; Conservative 11; Mismatches 35; Indels 3; Gaps 1;

QY 30 SMVSVNLTAGMYCAALESNLVNSDCSAIORT---QRMKALCSQKPAAGQISSERSRDT 86
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 7 SMVVFVFGCGTFCHIKDQTSKKSASSRSLSASLRLDKILSNKSTVGSVALTVRDG 66
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

QY 87 KIEVIQLVKN 96
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|
Db 67 KIGDVLVARN 76
      :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :| :|

RESULT 15
T00714
hypothetical protein F22013.9 - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 22-Oct-1999
C:Accession: T00714
R:Shinn, P.; Buehler, E.; Dewar, K.; Feng, J.; Kim, C.; Li, Y.; Sun, H.; Conway, A.;
eologis, A.; Ecker, J.R.
submitted to the EMBL Data Library, April 1998
A:Description: Genomic sequence for Arabidopsis thaliana BAC F22013.
A:Reference number: Z14200
A:Accession: T00714
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-559 <SHI>
A:Cross-references: EMBL:AC003981; NID:93063438; PID:93063447; GSPDB:GN00059; ATSP:F2
C:Genetics:
A:Gene: ATSP:F22013.9
A:Map position: 1
```

```

Query Match      12.2%; Score 68.5; DB 2; Length 559;
Best Local Similarity 28.2%; Pred. No. 23;
Matches 31; Conservative 19; Mismatches 37; Indels 23; Gaps 6;

Qy 13 IEELVNITQNASLCSMVWSVNI:TAGMYCAALESLINVSDCSAIQRTQRLKALC--- 69
    :||:| | | | | : : : | | | | | : | | : | | : | | : | | : |
Db 333 VEEILNI-MYQTSYCPTVITYNI-LINGLCKARLLS-----RAIDFFYQMLEQKCLPD 383

Qy 70 --SOKPAAGQISSERSRDTKIEVIOLVKN-----LLTY---VRGVYRHG 108
    : | | | | | | | | | | | | | | | | | | | | | | | | | | | |
Db 384 IVTYNTVLGAMSKEGMVDDAIELLGLLKNTCCPPGLITYNSVIDGLAKKG 433

```

Search completed: May 13, 2001, 21:48:39
Job time: 26248 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2001, 06:02:04 ; Search time 44.64 Seconds
(without alignments)
85.178 Million cell updates/sec

Title: US-09-451-527-97

Perfect score: 561

Sequence: 1 SPVTPSPTLKELIELVNIT.....QLVKNLLTYRGVYRHNGNR 111

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	382.5	68.2	132	1 IL13_HUMAN	P35225 homo sapien
2	360.5	64.3	132	1 IL13_BOVIN	Q9XSV9 bos taurus
3	295.5	52.7	131	1 IL13_MOUSE	P20109 mus musculus
4	294	52.4	131	1 IL13_RAT	P42203 rattus norv
5	73	13.0	701	1 UBFL_MOUSE	P25976 mus musculus
6	71.5	12.7	382	1 IPAC_XENLA	P18012 shigella fl
7	71	12.7	261	1 SPRE_HUMAN	P35270 homo sapien
8	70.5	12.6	192	1 FLHC_SALTY	O52222 salmonella
9	70.5	12.6	262	1 SPRE_RAT	P18297 rattus norv
10	70	12.5	382	1 IPAC_SHIDY	P03946 shigella dy
11	70	12.5	430	1 FTSZ_SYNY3	Q03946 synchocyst
12	70	12.5	677	1 UBFL_XENLA	P25979 xenopus lae
13	69.5	12.4	431	1 ACRO_RABIT	P48038 oryctolagus
14	68.5	12.2	261	1 SPRE_MOUSE	Q64105 mus musculus
15	68	12.0	1004	1 YGZ1_YEAST	P53067 saccharomyc
16	67.5	12.0	1164	1 FHOS_HUMAN	Q9Y613 homo sapien
17	67	11.9	481	1 YAB8_SCHPO	Q09775 schizosacch
18	67	11.9	510	1 MUTL1_THEMA	P74925 thermotoga
19	66.5	11.9	323	1 GC_RABIT	P01870 oryctolagus
20	66	11.8	1234	1 MED_MYCTU	P96380 mycobacteri
21	65.5	11.7	326	1 YEL1_YEAST	P40531 saccharomyc
22	65.5	11.7	1681	1 CLH_CAEEL	P34574 caenorhabdi
23	65	11.6	268	1 MOVPTMVKR	P30737 tabacco mos
24	64.5	11.5	268	1 MOVPTTMV	Q91275 tabacco mos
25	64.5	11.5	268	1 MOVPTTMVB	Q91275 tabacco mos
26	64.5	11.5	268	1 MOVPTTMVRA	Q98746 tabacco mos
27	64	11.4	1164	1 KEL1_YEAST	P38853 saccharomyc
28	64	11.4	1167	1 ITAE_MOUSE	Q60677 mus musculus
29	63.5	11.3	725	1 VR2A_BPT4	P30690 bacterioph
30	63.5	11.3	1477	1 AL13_RAT	P14046 rattus norv
31	63.5	11.3	1539	1 Y373_HUMAN	O15078 homo sapien
32	63	11.2	168	1 PTP_NPVAC	P24656 autographa
33	63	11.2	211	1 HIT_PIG	P06348 sus scrofa

ALIGNMENTS

RESULT 1	IL13_HUMAN	STANDARD;	PRT;	132 AA.
ID	IL13_HUMAN	AC P35225; O43644;		
DT	01-FEB-1994 (Rel. 28, Created)			
DT	01-FEB-1994 (Rel. 28, Last sequence update)			
DT	01-OCT-2000 (Rel. 40, Last annotation update)			
DE	INTERLEUKIN-13 PRECURSOR (IL-13).			
GN	IL13 OR NC30.			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93211479; PubMed=8096327;			
RA	Minty A.J., Chalton P., Derocq J.M., Dumont X., Guillemot J.C.,			
RA	Kaghad M., Labit C., Lepitolois P., Liauzun P., Miloux B.,			
RA	Caput D.,			
RT	"Interleukin-13 is a new human lymphokine regulating inflammatory and			
RT	immune responses."			
RL	Nature 362:248-250(1993).			
RN	[2]			
RP	SEQUENCE FROM N.A.			
RX	MEDLINE=93234572; PubMed=8097324;			
RA	McKenzie A.N., Culpepper J.A., Waal Malefyt R., Briere F.,			
RA	Punnonen J., Aversa G., Sato A., Dang W., Cocks B.G., Menon S.,			
RA	de Vries J.E., Banchereau J., Zurawski G.R.;			
RT	"Interleukin 13, a T-cell-derived cytokine that regulates human			
RT	monocyte and B-cell function."			
RL	Proc. Natl. Acad. Sci. U.S.A. 90:3735-3739(1993).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	Dolganov G., Lewis D.B., Lovett M., Burr J., Bort S., Short D.,			
RA	McGurn M., Gibson C.;			
RL	Submitted (JUL-1995) to the EMBL/GenBank/DBSJ databases.			
RN	[4]			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RA	MEDLINE=95237624; PubMed=7721105;			
RA	Smirnov D.V., Smirnova M.G., Korobko V.G., Frolova E.I.;			
RT	"Tandem arrangement of human genes for interleukin-4 and			
RT	interleukin-13: resemblance in their organization."			
Gene	155:277-281(1995).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Jang J.S., Kim B.E.;			
RL	Submitted (JAN-1997) to the EMBL/GenBank/DBSJ databases.			
RN	[6]			
RP	3D-STRUCTURE MODELING.			
RA	MEDLINE=95132583; PubMed=7530359;			
RA	Bamorough P., Duncan D., Richards W.G.;			
RT	"Predictive modelling of the 3-D structure of interleukin-13."			
RL	Protein Eng. 7:1077-1082(1994).			
RN	[7]			

34	63	11.2	482	1	TYPH_HUMAN	P19971 homo sapien
35	63	11.2	599	1	AFAM_HUMAN	P43652 homo sapien
36	63	11.2	764	1	UBFL_HUMAN	P17480 homo sapien
37	63	11.2	764	1	UBFL_RAT	P25977 rattus norv
38	63	11.2	765	1	UBFL_MOUSE	P25976 mus musculus
39	63	11.2	1675	1	CLHL_HUMAN	Q00610 homo sapien
40	63	11.2	1675	1	CLHL_BOVIN	P49951 bos taurus
41	63	11.2	1675	1	CLHL_RAT	P14442 rattus norv
42	63	11.2	1934	1	MYSB_MESAU	P13540 mesocricetu
43	63	11.2	1935	1	MYSB_HUMAN	P12883 homo sapien
44	63	11.2	1935	1	MYSB_PIG	P79293 sus scrofa
45	63	11.2	2875	1	MRPL_TSWV1	P28976 tomato spot

RP VARIANT GLN-130.
RX MEDLINE=20164293; PubMed=10699178;
RA Heinzmann A., Mao X.-O., Akaiwa M., Kremer R.T., Gao P.-S.,
RA Ohshima K., Umehita R., Abe Y., Braun S., Yamashita T., Roberts M.H.,
RA Sugimoto K., Arima K., Arinobu Y., Yu B., Kruse S., Enomoto T.,
RA Dake Y., Kawai M., Shimazu S., Sasaki S., Adra C.N., Kitaichi M.,
RA Inoue H., Yamauchi K., Tomichi N., Kurimoto F., Hamasaki N.,
RA Hopkin J.M., Izuwara K., Shirakawa T., Deichmann K.A.;
RT "Genetic variants of IL-13 signalling and human asthma and atopy";
RL Hum. Mol. Genet. 9:549-559(2000).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- POLYMORPHISM: GLN AT POSITION 130 IS A SIGNIFICANT RISK FACTOR FOR
CC ASTHMA DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: L06801; AAA36107.1; -;
DR EMBL: X59079; CAA48824.1; -;
DR EMBL: X59079; CAA48823.1; ALT_INIT.
DR EMBL: U31120; AAB01681.1; -;
DR EMBL: U10307; AAB83738.1; -;
DR EMBL: AF043334; AAC03535.1; -;
DR PIR: A47481; A47481.
DR PDB: 3ITR; 15-JAN-95.
DR PDB: 3ITS; 26-JAN-95.
DR MIM: 147683; -;
DR InterPro: IPR001325; -;
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.
FT SIGNAL 1 20 INTERLEUKIN-13.
FT CHAIN 21 132
FT DISULFID 48 76
FT DISULFID 64 90
FT CARBOHYD 38 38
FT CARBOHYD 49 49
FT CARBOHYD 57 57
FT CARBOHYD 72 72
FT VARIANT 130 130
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT N-LINKED (GLCNAC. . .) (POTENTIAL).
FT R -> Q.
FT /FTIG-VAR_010037.
FT CONFLICT 45 45 A -> R (IN REF. 4).
FT CONFLICT 87 87 S -> G (IN REF. 5).
FT CONFLICT 98 98 MISSING (IN REF. 4).
SQ SEQUENCE 132 AA; 14319 MW; 123FIDCAB87FD78B CRC64;

Query Match 68.2%; Score 382.5; DB 1; Length 132;
Best Local Similarity 70.0%; Pred. No. 3.1e-34;
Matches 77; Conservative 11; Mismatches 21; Indels 1; Gaps 1;

QY 2 PVPSTPLKELIELVNIQNO-ASLCNGSMVWSVNLTAGMYCALESILNVSDCSAIO 60
DB 22 PVPSTALRELIELVNIQNOAKPLCNGSMVWSVNLTAGMYCALESILNVSDCSAIEK 81
QY 61 TQRMKALCSQKPAAGQISSERSRDTKIEVQLVKNLLTYVRVYRHGNE 110
DB 82 TQRMKALCSQKPAAGQISSERSRDTKIEVQLVKNLLTYVRVYRHGNE 110

RESULT 2
ID IL13_BOVIN STANDARD; PRT; 132 AA.
AC Q9XSV9;
DT -30-MAY-2000 (Rel. 39, Created)

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
GN INTERLEUKIN-13 PRECURSOR (IL-13).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Buickamp J., Jann O., Fries R.;
RT "The bovine interleukin-13 gene: genomic organization, chromosomal
RT location and evolution of the promoter".
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS. MAY
CC BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: AJ132441; CAB46636.1; -;
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 132 INTERLEUKIN-13.
FT DISULFID 48 76 BY SIMILARITY.
FT DISULFID 64 90 BY SIMILARITY.
FT CARBOHYD 38 38 BY SIMILARITY.
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 132 AA; 14623 MW; 723BD42375C161F3 CRC64;

Query Match 64.3%; Score 360.5; DB 1; Length 132;
Best Local Similarity 65.8%; Pred. No. 7.1e-32;
Matches 73; Conservative 16; Mismatches 21; Indels 1; Gaps 1;

QY 1 SPVTPSTPLKELIELVNIQNO-ASLCNGSMVWSVNLTAGMYCALESILNVSDCSAIO 59
DB 21 SPVPSATALKELIELVNIQNOQKPLCNGSMVWSVNLTAGMYCALESILNVSDCSAIO 80
QY 60 TQRMKALCSQKPAAGQISSERSRDTKIEVQLVKNLLTYVRVYRHGNE 110
DB 81 RTKMLNALCPKPSAKQVSSEYVRDTEKIEVAQFLKLLRHRSIVRNERF 131

RESULT 3
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;

Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
 "A family of small inducible proteins secreted by leukocytes are members of a small superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.";
 J. Immunol. 142:679-687(1989).
 CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
 CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
 CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; M23504; AAA0149.1; -;
 DR PIR; E30552; E30552.
 DR HSP; P35225; 3ITR.
 DR MGI; 96541; IL13.
 DR InterPro; IPR001325; -;
 DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 131 INTERLEUKIN-13.
 FT DISULFID 51 79 BY SIMILARITY.
 FT DISULFID 67 93 BY SIMILARITY.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 131 AA; 14107 MW; 954F93F105713FED CRC64;
 Query Match 52.7%; Score 285.5; DB 1; Length 131;
 Best Local Similarity 59.2%; Pred. No. 6.6e-25;
 Matches 61; Conservative 16; Mismatches 23; Indels 3; Gaps 2;
 Qy 8 TLKELIEELVNTQASLCNGSMVSNLTAGMYCAALESINVSDCSAIQTQRLKA 67
 Db 32 TLKELIEELSNITQDTPLCNGSMVSNLTAGMYCAALESINVSDCSAIQTQRLHG 91
 Qy 68 LCSOKPAAGQISSRSRDKIEVQLVKNLLTYVRGVYRHGNF 110
 Db 92 LCNRK-APTVSS--LPDTKIEVAHFITKLLSYTKOLFRHGPF 131
 RESULT 4
 ID IL13_RAT STANDARD; PRT; 131 AA.
 AC P42203;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
 GN IL13 OR IL-13.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE-Kidney cortex;
 RX MEDLINE=94092138; PubMed=7916615;
 RA Lakis F.G., Cruet E.N.;
 RT "Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expression in experimental glomerulonephritis.";
 RL Biochem. Biophys. Res. Commun. 197:612-618(1993).
 CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.

CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
 CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: SECRETED.
 CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
 CC This SWISS-PROT entry is copyrighted. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL Outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC EMBL; L26913; AAA16478.1; -;
 DR HSP; P35225; 3ITR.
 DR InterPro; IPR001325; -;
 DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
 KW Cytokine; Glycoprotein; Signal.
 FT SIGNAL 1 21 BY SIMILARITY.
 FT CHAIN 22 131 INTERLEUKIN-13.
 FT DISULFID 52 80 BY SIMILARITY.
 FT DISULFID 68 94 BY SIMILARITY.
 FT CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 121 121 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 131 AA; 14093 MW; E508CAB8DE8C201 CRC64;
 Query Match 52.4%; Score 294; DB 1; Length 131;
 Best Local Similarity 57.9%; Pred. No. 9.5e-25;
 Matches 62; Conservative 17; Mismatches 24; Indels 4; Gaps 3;
 Qy 4 TPSPFLKELIEELVNTQASLCNGSMVSNLTAGMYCAALESINVSDCSAIQTQ 62
 Db 28 SPVALRELIEELSNITQDTPLCNSMWSVDLTAGGFCALLESINSSCAIHRQTQ 87
 Qy 63 RMLKALCSQKPAAGQISSRSRDKIEVQLVKNLLTYVRGVYRHGN 109
 Db 88 RILNGLCNQK--ASDVASS--PPDKIEVAQFISKLLNYSKQLFRYGH 131
 RESULT 5
 ID UBF2_XENLA STANDARD; PRT; 701 AA.
 AC P25980;
 DT 01-MAY-1992 (Rel. 22, Created)
 DT 01-MAY-1992 (Rel. 22, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE NUCLEOLAR TRANSCRIPTION FACTOR 2 (UPSTREAM BINDING FACTOR-2) (UBF-2).
 GN UBF-2.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 OX NCBI_TaxID=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91293106; PubMed=2065665;
 RA McStay B., Hu C.H., Pikaard C.S., Reeder R.H.;
 RT "UBF and Rib 1 are both required for formation of a stable polymerase I promoter complex in X. laevis.";
 RL EMBO J. 10:2297-2303(1991).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=91348289; PubMed=1879565;
 RA Bachvarov D., Normandeau M., Moss T.;
 RT "Heterogeneity in the Xenopus ribosomal transcription factor xUBF has a molecular basis distinct from that in mammals.";
 RL FEBS Lett. 288:55-59(1991).
 RN [3]
 RP DOMAINS.


```
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
GN SPR.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=91354248; PubMed=1883349;
RX Ichinose H., Katoh S., Sueoka T., Titani K., Fujita K., Nagatsu T.;
RA "Cloning and sequencing of cDNA encoding human sepiapterin
RT reductase -- an enzyme involved in tetrahydrobiopterin biosynthesis.";
RL Biochem. Biophys. Res. Commun. 179:183-189(1991).
CC -!- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIOPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOPTERIN.
CC -!- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOPTERIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
CC -!- SUBUNIT: HOMODIMER.
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -!- DISEASE: DEPRESSED SYNTHESIS OF TETRAHYDROBIOPTERIN MAY PLAY A
CC ROLE IN A VARIETY OF HUMAN DISEASES.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M76231; AAA60314.1; -
DR PIR; JQ1176; JQ1176.
DR MIM; 182125; -
DR InterPro; IPR002198; -
DR Pfam; PF00106; adh_short; 1.
DR Oxidoreductase; NADP; Acetylation.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT NP_BIND 13 39 NADP (BY SIMILARITY).
FT DOMAIN 28 32 PTERIN BINDING (POTENTIAL).
FT SEQUENCE 261 AA; 28048 MW; 9C9BF76212826F47 CRC64;
SQ
Query Match 12.7%; Score 71; DB 1; Length 261;
Best Local Similarity 24.7%; Pred. No. 1.8;
Matches 24; Conservative 21; Mismatches 42; Indels 10; Gaps 4;
QY 16 LVNITONQASLNGSMV---WSVNLTAGMYCALESILNVSDCSAQTORTMLKALCSQK.72
DB 104 LGDVSKGFDLSDSQVNNYWNALNLS-MLCLTSSVLKAFPPDSPGLNRTVVNLSICALQ.162
QY 73 PAAG---QISSERSRDTKTEVLQV---NLLTYVRG.103
DB 163 PPKGALYACAGKAARDMLFQVLALEPNVRLNYPG.199
RESULT 8
FLHC_SALTY
ID FLHC_SALTY STANDARD; PRT; 192 AA.
AC 052222;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 01-OCT-2000 (Rel. 40, Last annotation update)
DE FLAGELLAR TRANSCRIPTIONAL ACTIVATOR FLHC.
GN FLHC.
OS Salmonella typhimurium.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Salmonella.
OX NCBI_TaxID=602;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LT2;
RA Toguchi A., Harshey R.M.;
RL Submitted (OCT-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX PubMed=10586519;
RA Yanagihara S., Iyoda S., Ohnishi K., Iino T., Kutsukake K.;
RT "Structure and transcriptional control of the flagellar master operon
of Salmonella typhimurium.";
RL Genes Genet. Syst. 74:105-111(1999).
CC -!- FUNCTION: TRANSCRIPTIONAL ACTIVATOR. TOGETHER WITH FLHD IT ACTS AS
CC A COMPOUND SIGMA FACTOR THAT ACTIVATES CLASS 2 FLAGELLAR GENES (BY
CC SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FLHC FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AF029300; AAB96640.1; -
DR EMBL; D43640; BAA83315.1; -
DR StyGene; SG10643; FLHC.
KW Transcription regulation; Sigma factor; DNA-directed RNA polymerase;
KW DNA-binding; Flagella.
SQ SEQUENCE 192 AA; 21579 MW; C7334C691ECE3F8D CRC64;
Query Match 12.6%; Score 70.5; DB 1; Length 192;
Best Local Similarity 28.6%; Pred. No. 1.4;
Matches 16; Conservative 10; Mismatches 27; Indels 3; Gaps 1;
QY 31 MWVSNLTAGMYCALESILNVSDCS---ATQRTOMLKALCSQKPAAGQISSERS.83
DB 65 MTWEQNTIHSMFCNAQWFLKLTGLCSGDVAVIKAYRLYLEQCPQPEGLALTRA.120
RESULT 9
SPRE_RAT
ID SPRE_RAT STANDARD; PRT; 262 AA.
AC P18297;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
GN SPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90349631; PubMed=2201030;
RA Citron B.A., Milstien S., Gutierrez J.C., Levine R.A., Yanak B.L.,
RA Kaufman S.;
RT "Isolation and expression of rat liver sepiapterin reductase cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6436-6440(1990).
RN [2]
RP SEQUENCE.
RX MEDLINE=91083647; PubMed=2260974;
RA Oyama R., Katoh S., Sueoka T., Suzuki M., Ichinose H., Nagatsu T.,
RA Titani K.;
RT "The complete amino acid sequence of the mature form of rat
sepiapterin reductase.";
RL Biochem. Biophys. Res. Commun. 173:627-631(1990).
CC -!- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIOPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOPTERIN.
CC -!- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOPTERIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
```

```
CC -!- SUBUNIT: HOMODIMER
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M36410; AAA42130.1; -
DR PIR: A36400; A36400; -
DR InterPro: IPR002198; -
DR Pfam: PF00106; adh_short; 1.
KW Oxidoreductase; NADP; Acetylation.
FT MOD_RES 1 1 ACETYLATION.
FT NP_BIND 14 40 NADP (BY SIMILARITY).
FT DOMAIN 29 33 PTERIN BINDING (POTENTIAL).
SQ SEQUENCE 262 AA; 28128 MW; EC992564A0334C61 CRC64;
-----
Query Match 12.6%; Score 70.5; DB 1; Length 262;
Best Local Similarity 23.5%; Pred. No. 2.1;
Matches 24; Conservative 25; Mismatches 42; Indels 11; Gaps 4;
QY 8 TLKELIELVNITONQASLNGSMVSNLTAGMYCAALESINVSDCSAIQRTORMLKA 67
DB 104 TLGDVSKGFLNIN---DLAEVNNYVALNLT'S-MLCLTGTGLNAFNSPGLSKTVVNISS 158
QY 68 LCSOKPAAG---QISSRSRDTKIEVLQVVK---NLLTYVRG 103
DB 159 LCAQLQPKGMLGKAGCAARDMLYQVLAVEEPSVRVLSYAPG 200
-----
RESULT 10
IPAC_SHIDY STANDARD; PRT; 382 AA.
AC Q03946;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE 42 KDA MEMBRANE ANTIGEN PRECURSOR.
GN IPAC.
OS Shigella dysenteriae.
OG Plasmid Invasion.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Shigella
OX NCBI_TaxID=622;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CG097;
RX MEDLINE=92114800; PubMed=1766387;
RA Yao R., Palchaudhuri S.;
RT "Nucleotide sequence of the ipaBCD structural genes of Shigella
RT dysenteriae.";
RL Mol. Microbiol. 5:2217-2221(1991).
CC -!- FUNCTION: ASSOCIATED WITH THE ENTRY OF THE BACTERIA INTO COLONIC
CC EPITHELIAL CELLS.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: X60777; CAA43191.1; -
DR PIR: S15578; S15578
KW Antigen; Plasmid; Virulence; Membrane; Signal.
FT SIGNAL 1 19 BY SIMILARITY.
FT CHAIN 20 382 42 KDA MEMBRANE ANTIGEN.
SQ SEQUENCE 382 AA; 41098 MW; A22E1D6399EC90BF CRC64;
```

```
QY 4 TSPSTPLKELIE-----ELVNITONQ-----ASLNGSMVSNLTAGMYCAALESIN 51
DB 268 SPDISLQDRITQRTYELNTLSAQCKQKIGRATMETSAVAGNISTGGRYASALE---- 323
QY 52 VSDCSAIQRTORMLKA LCSOKPAAGQISSRSRDTKIEVLQVVKLLTYVRGVYRH---- 107
DB 324 -----EEEQLISQASSQKAEASQVKEASQATN-----QLIQKLLNIIDINQSRSS 372
QY 108 -----GNFR 111
DB 373 ASQIAGNIR 381
-----
RESULT 11
FTSZ_SYNY3 STANDARD; PRT; 430 AA.
AC P73456;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE CELL DIVISION PROTEIN FTSZ.
GN FTSZ OR SLL1633.
OS Synecocystis sp. (strain PCC 6803).
OC Bacteria; Cyanobacteria; Chroococcales; Synecocystis.
OX NCBI_TaxID=11448;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=97061201; PubMed=8905231;
RA Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu E., Nakamura Y.,
RA Miyajima N., Hirose M., Sugita M., Sasamoto S., Kimura T.,
RA Hosouchi T., Matsuno A., Muraki A., Nakazaki N., Naruo K.,
RA Okumura S., Shimpo S., Takeuchi C., Wada T., Watanabe A.,
RA Yamada M., Yasuda M., Tabata S.;
RT "Sequence analysis of the genome of the unicellular cyanobacterium
RT Synecocystis sp. strain PCC6803. II. Sequence determination of the
RT entire genome and assignment of potential protein-coding regions.";
RL DNA Res. 3:109-136(1996).
CC -!- FUNCTION: THIS PROTEIN IS ESSENTIAL TO THE CELL-DIVISION PROCESS.
CC ITS SEEMS TO ASSEMBLE INTO A DYNAMIC RING ON THE INNER SURFACE OF
CC THE CYTOPLASMIC MEMBRANE AT THE PLACE WHERE DIVISION WILL OCCUR,
CC AND THE FORMATION OF THE RING IS THE SIGNAL FOR SEPTATION TO
CC BEGIN. BINDS TO AND HYDROLYSES GTP (BY SIMILARITY).
CC -!- SUBUNIT: AGGREGATE TO FORM A RING-LIKE STRUCTURE (BY SIMILARITY).
CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC. ASSEMBLE AT THE INNER SURFACE
CC OF THE CYTOPLASMIC MEMBRANE (BY SIMILARITY).
CC -!- SIMILARITY: BELONGS TO THE FTSZ FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D90906; BAA17496.1; -
DR HSSP: Q57816; 1FSZ.
DR InterPro: IPR000158; -
DR InterPro: IPR003008; -
DR Pfam: PF00091; tubulin; 1.
DR PRINTS: PR00423; CELLDIVISFTSZ.
DR PROSITE: PS01134; FTSZ_1; 1.
DR PROSITE: PS01135; FTSZ_2; 1.
KW Cell division; Septation; GTP-binding.
FT NP_BIND 159 167 GTP (POTENTIAL).
SQ SEQUENCE 430 AA; 44773 MW; E3C7DD554983FF44 CRC64;
```

Query Match 12.5%; Score 70; DB 1; Length 430;
Best Local Similarity 26.7%; Pred. No. 4.3;
Matches 27; Conservative 17; Mismatches 29; Indels 28; Gaps 5;

QY 4 TPSPTLKELIELV--NITONO-----ASLNGSMVSVNLTAGMYCAA 45
DB 51 SPSPNLKR--DQIVPSNTAKIKVIGGGGCVNVRMIASGVTDGFWAINTDS----- 102
QY 46 LESLNVDCSAIORTMLKAL-CSQKPAAGQISSERSRD 85
DB 103 -QALTNTNAPDCIOIGQKLTGRLGAGGNPAIGKAAEESRD 142

RESULT 12
UBF1_XENLA
ID UBF1_XENLA STANDARD; PRT; 677 AA.
AC P25979;
DT 01-MAY-1992 (Rel. 22, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE NUCLEAR TRANSCRIPTION FACTOR 1 (UPSTREAM BINDING FACTOR-1) (UBF-1).
GN XUBF-1.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidea; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91252272; PubMed=20411774;
RA Bachvarov D.R., Moss T.;
RT "The RNA polymerase I transcription factor XUBF contains 5 tandemly repeated HMG homology boxes".
RL Nucleic Acids Res. 19:2331-2335(1991).
CC -1- FUNCTION: UBF RECOGNIZES THE RIBOSOMAL RNA GENE PROMOTOR AND ACTIVATES TRANSCRIPTION MEDIATED BY RNA POLYMERASE I THROUGH COOPERATIVE INTERACTIONS WITH THE SPECIES-SPECIFIC FACTOR SL1. IT BINDS SPECIFICALLY TO THE UPSTREAM CONTROL ELEMENT.
CC -1- SUBUNIT: XUBF CONSISTS OF 2 POLYPEPTIDES OF 82 AND 85 KDA, ENCODED BY THE SAME OR CLOSELY RELATED GENES.
CC -1- SUBCELLULAR LOCATION: NUCLEAR.
CC -1- SIMILARITY: CONTAINS 5 HMG BOXES.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; X57201; CAA04087.1; -
DR PIR; S15667; S15667.
DR InterPro; IPR000910; -
DR PFAM; PF00505; HMG_box; 3.
DR PROSITE; PS00090; MYB_3; 1.
KW Transcription regulation; DNA-binding; Activator; Nuclear protein;
KW Multigene family; Repeat.
FT DNA_BIND 113 180 HMG BOX 1.
FT DNA_BIND 199 264 HMG BOX 2.
FT DNA_BIND 298 362 HMG BOX 3.
FT DNA_BIND 400 467 HMG BOX 4.
FT DNA_BIND 486 552 HMG BOX 5.
FT DOMAIN 593 677 ASP/GLU-RICH (ACIDIC).
SQ SEQUENCE 677 AA; 79168 MW; 91340A46AFE7A702 CRC64;

Query Match 12.5%; Score 70; DB 1; Length 677;
Best Local Similarity 30.3%; Pred. No. 7.3;
Matches 20; Conservative 16; Mismatches 14; Indels 16; Gaps 4;

QY 41 MYCAALSLNVDCSAIORTMLKALCSQ-----KPAAGQISSERSRDTKIEVI 91
DB 307 MYCA--ELMANMKD---VPSTERMV--LCSQRWLLSQKEDAYNKCEQRKKDYVELM 359
QY 92 QLVKNL 97
DB 360 RELESL 365
RESULT 13
ACRO_RABIT
ID ACRO_RABIT STANDARD; PRT; 431 AA.
AC P48038;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ACROSIN PRECURSOR (EC 3.4.21.10).
GN ACR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RX STRAIN=NEW ZEALAND WHITE; TISSUE=Testis;
RX MEDLINE=94368861; PubMed=8086468;
RA Richardson R.T., O'Rand M.G.;
RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproacrosin-related cDNA".
RL Biochim. Biophys. Acta 1219:215-218(1994).
CC -1- FUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAMMALIAN SPERMATOZOEA. IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY, IT IS SYNTHESIZED IN A ZYMOGEN FORM, PROACROSIN AND STORED IN THE ACROSOME.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
CC -1- SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE TRYPSIN FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
DR EMBL; U05204; AAA61630.1; -
DR MEROPS; S01.223; -
DR InterPro; IPR001254; -
DR InterPro; IPR001314; -
DR PFAM; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
FT SIGNAL 1 16
FT CHAIN 17 431 ACROSIN.
FT CHAIN 17 39 ACROSIN LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 40 ? ACROSIN HEAVY CHAIN (BY SIMILARITY).
FT PROPEP 2 431 PRO-RICH.
FT DISULFID 22 152 INTERCHAIN (BY SIMILARITY).
FT DISULFID 26 160 INTERCHAIN (BY SIMILARITY).
FT DISULFID 71 87 BY SIMILARITY.
FT DISULFID 175 244 BY SIMILARITY.
FT DISULFID 207 223 BY SIMILARITY.
FT DISULFID 234 264 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC...) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC...) (POTENTIAL).
FT ACT_SITE 86 86 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 140 140 CHARGE RELAY SYSTEM (BY SIMILARITY).

```

DR EMBL; S77493; AAB33611.1; -.
DR EMBL; U78077; AAC69364.1; -.
DR EMBL; U78076; AAC69364.1; JOINED.
DR EMBL; S71375; -. NOT_ANNOTATED_CDS.
DR PDB; LSEP; 13-JAN-99.
DR PDB; LOAA; 16-FEB-99.
DR PDB; LNAS; 30-MAR-99.
DR MGD; MGI:103078; Spr.
DR InterPro; IPR002198; -.
DR Pfam; PF0106; adh_short; 1.
KW Oxidoreductase; NADP; 3D-structure.
FT NP_BIND 14 40
FT DOMAIN 29 33
FT CONFLICT 4 4
FT SEQUENCE 261 AA; 27883 MW; 102294E439CB8AEC CRC64;

Query Match 12.2%; Score 68.5; DB 1; Length 261;
Best Local Similarity 21.5%; Pred. No. 3.4;
Matches 23; Conservative 26; Mismatches 47; Indels 11; Gaps 4;

QY 3 VTPSPTLKELLEELVNITQNOASLCNGSMWVSNLTAGMYCAALESNLINSDCSAIQRTQ 62
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 99 INNAATLGDVSKGFLNVN----DLAEVNNYALNLTSLMLCLTSGTLNFAQDPSGLSKTV 153
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
QY 63 RMLKALCSQKPAAG---QISSERSDRTKIEVIQLVK---NLLTVRG 103
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 154 VNIISSLCALQPKWGLYCAGKAARDMLQVLAEEPSRVLSVAPG 200
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

RESULT 15
YG21 YEAST STANDARD; PRT; 1004 AA.
ID YG21 YEAST
AC P53067;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE HYPOTHEICAL 113.9 KDA PROTEIN IN TAD1-CSE1 INTERGENIC REGION.
GN YGL241W OR HRC1004.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RA Vandenbol M., Durand P., Portetelle D., Hilger F.;
RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z49149; CAA89014.1; -.
DR EMBL; Z72763; CAA96960.1; -.
DR SGD; S0003210; KAP114.
KW Hypothetical protein.
SQ SEQUENCE 1004 AA; 113920 MW; 1F4C02AA6AB2FF39 CRC64;

Query Match 12.1%; Score 68; DB 1; Length 1004;
Best Local Similarity 22.7%; Pred. No. 19;
Matches 22; Conservative 25; Mismatches 38; Indels 12; Gaps 4;

QY 7 PTLKELLEELVNITQNOASLCNGSMWVSNLTAGMYC--AALESNLINSDCSAIQRTQ 63
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :
Db 475 PDKPLTSAFLAKSLNALKSDKELIKSATLIAFTYCYCPAELDSVLGPEVCSSTQ--EK 532
   : : : : : : : : : : : : : : : : : : : : : : : : : : : :

```

Search completed: May 14, 2001, 06:02:05
Job time: 43362 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2001, 06:01:08 ; Search time 133.94 Seconds
(without alignments)
97.134 Million cell updates/sec

Title: US-09-451-527-97
Perfect score: 561
Sequence: 1 SPVTPSPFLKELIELVNIT.....QLVKNLLTYVRGVYRHGNFR 111

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SPTREMBL_15.*

- 1: sp_archaea.*
- 2: sp_bacteria.*
- 3: sp_fungi.*
- 4: sp_human.*
- 5: sp_invertebrate.*
- 6: sp_mammal.*
- 7: sp_mhc.*
- 8: sp_organelle.*
- 9: sp_phage.*
- 10: sp_plant.*
- 11: sp_rodent.*
- 12: sp_unclassified.*
- 13: sp_vertebrate.*
- 14: sp_virus.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	561	100.0	131	Q9N0W9	Q9N0W9 canis famil
2	331.5	59.1	114	Q9TV84	Q9TV84 bos taurus
3	87.5	15.6	49	Q9UDC7	Q9UDC7 homo sapien
4	80	14.3	275	Q28609	Q28609 oryctolagus
5	74	13.2	415	Q9NUM4	Q9NUM4 mesostigma
6	73	13.0	150	Q98779	Q98779 vesicular s
7	73	13.0	350	Q9Q8P4	Q9Q8P4 myxoma viru
8	72	12.8	150	Q98791	Q98791 vesicular s
9	72	12.8	438	Q9M3H8	Q9M3H8 cicor ariet
10	71	12.7	150	Q98780	Q98780 vesicular s
11	71	12.7	150	Q98787	Q98787 vesicular s
12	71	12.7	150	Q98789	Q98789 vesicular s
13	70.5	12.6	1510	Q9VX92	Q9VX92 drosophila
14	70	12.5	274	Q89048	Q89048 vesicular s
15	69	12.3	670	Q9N9C4	Q9N9C4 leishmania
16	68.5	12.2	494	Q9PCZ0	Q9PCZ0 xyella fas
17	68.5	12.2	2606	Q36414	Q36414 aicelaphine
18	68	12.1	150	Q98778	Q98778 vesicular s
19	67.5	12.0	198	Q9UBB1	Q9UBB1 homo sapien

20	67.5	12.0	284	2	Q9XBM2	Q9XBM2 acidaminoco
21	67.5	12.0	1164	4	Q9Y613	Q9Y613 homo sapien
22	67.5	12.0	1448	5	Q9N946	Q9N946 trypanosoma
23	67	11.9	486	13	Q9YH07	Q9YH07 scyllorhinu
24	67	11.9	651	11	Q9JI78	Q9JI78 mus musculu
25	66.5	11.9	1102	11	Q9JHG7	Q9JHG7 mus musculu
26	66.5	11.9	1344	10	Q9SN94	Q9SN94 oryza sativ
27	66.5	11.9	1448	5	Q9N949	Q9N949 trypanosoma
28	66	11.8	150	14	Q98790	Q98790 vesicular s
29	66	11.8	421	5	Q9TXL7	Q9TXL7 caenorhabdi
30	66	11.8	478	2	Q9KXF0	Q9KXF0 escherichia
31	66	11.8	478	9	Q9MCT4	Q9MCT4 bacterioph
32	66	11.8	483	9	Q9TIM4	Q9TIM4 bacterioph
33	66	11.8	607	10	Q9SI43	Q9SI43 arabidopsis
34	65.5	11.7	325	10	Q65152	Q65152 malus domes
35	65.5	11.7	393	5	O44600	O44600 caenorhabdi
36	65.5	11.7	1763	11	Q9JKX5	Q9JKX5 mus musculu
37	65	11.6	431	4	Q9NV02	Q9NV02 homo sapien
38	65	11.6	451	5	Q19260	Q19260 caenorhabdi
39	65	11.6	732	2	Q9RH03	Q9RH03 azospirillu
40	65	11.6	2149	10	Q9M3D3	Q9M3D3 arabidopsis
41	65	11.6	2626	11	Q9Z1N3	Q9Z1N3 rattus norv
42	64.5	11.5	156	14	Q9IWI4	Q9IWI4 crimean-con
43	64.5	11.5	268	14	Q98746	Q98746 tobacco mos
44	64.5	11.5	268	14	Q91275	Q91275 tobacco mos
45	64.5	11.5	268	14	Q9QPN6	Q9QPN6 tobacco mos

ALIGNMENTS

RESULT 1					
Q9N0W9	PRELIMINARY;	PRT;	131 AA.		
AC	Q9N0W9				
DT	01-OCT-2000 (TREMBlrel. 15, Created)				
DT	01-OCT-2000 (TREMBlrel. 15, Last sequence update)				
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)				
DE	INTERLEUKIN-13.				
OS	Canis familiaris (Dog).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.				
OX	NCBI_TaxID=9615;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Yang S., Borroughs K.L., McDermott M.J.;				
RT	"Canine Interleukin-13: Molecular Cloning of Full-Length cDNA and				
RT	Expression of Biologically Active Recombinant Protein.";				
RL	Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.				
DR	EMBL; AF244915; AAF63204.1; -.				
SQ	SEQUENCE 131 AA; 14268 MW; 9A142B4D0F80370F CRC64;				

Query Match	100.0%;	Score 561;	DB 6;	Length 131;
Best Local Similarity	100.0%;	Pred. No. 1.7e-54;		
Matches 111;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
QY	1	SPVTPSPFLKELIELVNITQNASLCSNGSMVWSVNLTAGMYCAALESINVS	QY	60
Db	21	SPVTPSPFLKELIELVNITQNASLCSNGSMVWSVNLTAGMYCAALESINVS	Db	80

QY	61	TORMLKALCSQKPAAGQISSRSRDTKTEVIQLVKNLLTYVRGVYRHGNFR	111
Db	81	TORMLKALCSQKPAAGQISSRSRDTKTEVIQLVKNLLTYVRGVYRHGNFR	131

RESULT 2					
ID	Q9TV84	PRELIMINARY;	PRT;	114 AA.	
AC	Q9TV84				
DT	01-MAY-2000 (TREMBlrel. 13, Created)				
DT	01-MAY-2000 (TREMBlrel. 13, Last sequence update)				
DT	01-OCT-2000 (TREMBlrel. 15, Last annotation update)				

[illegible]

```

Db      188 LIQNPLSTSLC-GAITLWVALFAGIHWFYINLSIGAVTALISIGSQEYQRIISFL 244
QY      69 CSOKPAAGQISSERSRDTKIEVQLVKNLITYVRG 103
Db      247 --NPWANPTSIG-----YQLVQSLLAVGSG 269

RESULT 6
Q98779 Q98779 PRELIMINARY; PRT; 150 AA.
AC Q98779;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
ON NCBI_TaxID=11276;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=0888CRB;
RC MEDLINE=97075113; PubMed=8917539;
RX Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the
RL evolution of vesicular stomatitis virus.";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL: U39211; AAB50939.1;
DR INTERPRO: IPR000224;
DR PFAM: PF00922; Phosphoprotein; 1.
DR FT NON_TER 1
FT NON_TER 150
FT SEQUENCE 150 AA; 16711 MW; 16D11C4E8E8A65E7 CRC64;

Query Match 13.0%; Score 73; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 1.7;
Matches 29; Conservative 19; Mismatches 42; Indels 30; Gaps

QY 2 PVTPSPTLKELIEL-----VNITQNA-----SICNGSMWSVN----LTAGMY 42
Db 14 PWTQPVIRKNGGERSLSLPPVGLTVQVTEQWKKTETVCSSKYNNLSLSECOIVTSG-N 72
QY 43 CAALESILNYSDCSAIQRTQRMKALCSQKPAAGQISSERSR-----DTKIEVQLV 94
Db 73 CLILRGVMTSDCSSSAKSONSRQS--SESPSPSNSPEHASRASASPNLWDFKTFEVL 130

RESULT 7
Q908P4 Q908P4 PRELIMINARY; PRT; 350 AA.
AC Q908P4;
DT 01-MAY-2000 (TrEMBLrel. 13, Created)
DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE M52L.
GN M052L.
OS Myxoma virus.
OC Viruses; dsDNA viruses, no RNA stage; Poxviridae; Chordopoxvirinae;
OC Leporipoxvirus.
ON NCBI_TaxID=10273;
RX [1]
RN SEQUENCE FROM N.A.
RP STRAIN=LAUSANNE;
RC MEDLINE=20032073; PubMed=10562494;
RX Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.X.,
RA Macaulay C., Willer D., Evans D., McFadden G.;
RT "The complete DNA sequence of myxoma virus.";
RL Virology 264:298-318(1999).
RN [2]
RN SEQUENCE FROM N.A.
RP STRAIN=LAUSANNE;
RC Cameron C., Hota-Mitchell S., Chen L., Barrett J., Cao J.-X.,

```

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Cicer.
OX NCBI_TaxID=3627;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
RA Dopico B., Munoz F.J., Labrador E.;
RT "A putative UDP-Glycose: Flavonoid glycosyltransferase is expressed in
RT chickpea epicotyls";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL; AJ400861; CAB88666.1; -;
FT NON_TER 1
SQ SEQUENCE 438 AA; 48662 MW; 0BB7B805BD66E27C CRC64;

Query Match 12.8%; Score 72; DB 10; Length 438;
Best Local Similarity 26.7%; Pred. No. 7.7;
Matches 36; Conservative 21; Mismatches 46; Indels 32; Gaps 7;
QY 2 PVTSPPTLKELIEELVN-----ITONQASL-----CNGSMVWSVNLTAGMYC 43
Db 136 PIKSPGFARLTPLVEAKGSHGVIVNSFAELDEGYEYVENLTGRKVVHVGPTSLMIK 195
QY 44 AALESILNVDCSAIORTQRMKALCSOKPAA-----GOISSERSRDTKIEV---ITAGMY 94
Db 196 TTLETNINISGSKT--HKCLTWLDTKPSVSVISFGSLCS-LSNDOLLELAKGIEAS 252
QY 95 KNLTYVRGVYRHGN 109
Db 253 KHQFLWV--VHRKGD 265

RESULT 10
QY 98780 ID Q98780 PRELIMINARY; PRT; 150 AA.
AC Q98780;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=0986CRB2;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the
RT evolution of vesicular stomatitis virus";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL; U39212; AAB50940.1; -;
DR INTERPRO; IPR000224; -;
DR PFAM; PF00922; Phosphoprotein; 1.
FT NON_TER 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16611 MW; E3D1095B8E8A65FD CRC64;

Query Match 12.7%; Score 71; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 2.9;
Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;
QY 2 PVTSPPTLKELIEEL-----VNITQNA-----SLCNGSMVWSVN-----ITAGMY 42
Db 14 PSWTQPVIKENGGRSLFPVGLTQVTEQWKKTITVCESSKYWNLSCEQIVTSG-N 72
QY 43 CAALESILNVDCSAIORTQRMKALCSOKPAAAGQISSERSR-----DTKIEVQLV 94
Db 73 CLILRGQVMTSDCSSAKSQN--SQGSESPSPNSPEHASRASPMLWDFKFTFVQLI 130

RESULT 11
QY 98787 ID Q98787 PRELIMINARY; PRT; 150 AA.
AC Q98787;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=1187CRB2;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the
RT evolution of vesicular stomatitis virus";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL; U39219; AAB50947.1; -;
DR INTERPRO; IPR000224; -;
DR PFAM; PF00922; Phosphoprotein; 1.
FT NON_TER 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16625 MW; D8BCBF97FF435477 CRC64;

Query Match 12.7%; Score 71; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 2.9;
Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;
QY 2 PVTSPPTLKELIEEL-----VNITQNA-----SLCNGSMVWSVN-----ITAGMY 42
Db 14 PSWTQPVIKENGGRSLFPVGLTQVTEQWKKTITVCESSKYWNLSCEQIVTSG-N 72
QY 43 CAALESILNVDCSAIORTQRMKALCSOKPAAAGQISSERSR-----DTKIEVQLV 94
Db 73 CLILRGQVMTSDCSSAKSQN--SQGSESPSPNSPEHASRASPMLWDFKFTFVQLI 130

RESULT 12
QY 98789 ID Q98789 PRELIMINARY; PRT; 150 AA.
AC Q98789;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RN SEQUENCE FROM N.A.
RC STRAIN=1187CRB4;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the
RT evolution of vesicular stomatitis virus";
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL; U39221; AAB50949.1; -;
DR INTERPRO; IPR000224; -;
DR PFAM; PF00922; Phosphoprotein; 1.
FT NON_TER 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16625 MW; D8BCBF97FF435477 CRC64;

Query Match 12.7%; Score 71; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 2.9;
Matches 29; Conservative 17; Mismatches 44; Indels 30; Gaps 6;

QY 2 PVTSPPTLKELIEEL-----VNITONQA-----SLCNGSMVWSVN-----LTAGMY 42
 Db 14 PSWTQPVIRENGERSLSLPPVGLTQIQTEQWKKTIVTCESSKYWNLSQCIIVTSG-N 72
 QY 43 CAALESINVSDCSATQRTQRMKALCSQKPAAGQISSRSR-----DTRKIEVIQLV 94
 Db 73 CLILRGQVMTSDCSSANSKON--SQSSPSPSNPEHASRASASPNLWDFKTEVOLI 130

RESULT 13
 Q9VX92
 ID Q9VX92 PRELIMINARY; PRT; 1510 AA.
 AC Q9VX92
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-JUN-2000 (Tremblrel. 14, Last annotation update)
 DE CG4937 PROTEIN.
 GN CG4937
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.-H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
 RA Abril J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Bertram P.P., Blandari D., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Foslter C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskaas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zhong X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster."
 RL Science 287:2185-2195(2000).
 DR EMBL: AE003504; AAF48686.1;
 DR FLYBASE; FBgn0030808; CG4937.
 DR INTERPRO; IPR000159;
 DR INTERPRO; IPR000198;
 DR PFAM; PF00620; RhoGAP; 1.
 SQ SEQUENCE 1510 AA; 169935 MW; E2C0AEC7945B9714 CRC64;

Query Match 12.6%; Score 70.5; DB 5; Length 1510;
 Best Local Similarity 31.4%; Pred. No. 47;
 Matches 32; Conservative 14; Mismatches 35; Indels 21; Gaps 6;

QY 8 TLKELIEELVNITONQA-----SLCNGSMVWSVNLTAG-----MY-----CAALESIL----- 50
 Db 1177 TLRIVGHLVFIISQQAQKMSVONLTWIGPTLLAKKSDLEIYSQKADVLSDLVLYK 1236

QY 51 NVSDCSA--IQRTQRMKALCSQKPAAGQISS--ERSRDTKI 88
 Db 1237 NLFPCSADETKREQACLAQLQKYAAAEATLKDAVKQSDIKI 1278

RESULT 14
 Q89048
 ID Q89048 PRELIMINARY; PRT; 274 AA.
 AC Q89048;
 DT 01-NOV-1996 (Tremblrel. 01, Created)
 DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE (STRAIN 01/85-PN-B1) PHOSPHOPROTEIN.
 OS Vesicular stomatitis virus.
 OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
 OC Rhabdoviridae; Vesiculovirus.
 OC NCBI_TaxID=11276;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90244358; PubMed=2159527;
 RA Bilsel P.A., Rowe J.E., Fitch W.M., Nichol S.;
 RT "Phosphoprotein and nucleocapsid protein evolution of vesicular
 stomatitis virus New Jersey."
 RL J. Virol. 64:2498-2504(1990).
 DR EMBL: M31878; AAA48478.1;
 DR INTERPRO: IPR000224;
 DR PFAM: PF00922; Phosphoprotein; 1.
 DR PRODOM; PD002677; -; 1.
 SQ SEQUENCE 274 AA; 31169 MW; 4D3A014211837DID CRC64;

Query Match 12.5%; Score 70; DB 14; Length 274;
 Best Local Similarity 23.3%; Pred. No. 7.4;
 Matches 28; Conservative 20; Mismatches 42; Indels 30; Gaps 6;

QY 2 PVTSPPTLKELIEEL-----VNITONQA-----SLCNGSMVWSVN-----LTAGMY 42
 Db 101 PSWTQPVIRENGERSLSLPPVGLTQIQTEQWKKTIVTCESSKYWNLSQCIIVTSG-N 159

QY 43 CAALESINVSDCSATQRTQRMKALCSQKPAAGQISSRSR-----DTRKIEVIQLV 94
 Db 160 CLILRGQVMTSDCSSANSKNSVQS--SESPSPSNPEHASRASASPNLWDFKTEVOLI 217

RESULT 15
 Q9N9C4
 ID Q9N9C4 PRELIMINARY; PRT; 670 AA.
 AC Q9N9C4;
 DT 01-OCT-2000 (Tremblrel. 15, Created)
 DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
 DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
 DE HYPOTHETICAL 73.4 KDA PROTEIN.
 GN P1408.01
 OS Leishmania major.
 OC Eukaryota; Euzlenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
 OC NCBI_TaxID=5664;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=FRIEDLIN;
 RA Bothe G., Pohl T., Ivens A.C., Quail M., Rajandream M.A.,
 RA Barrell B.G.;
 RL Submitted (JUN-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:47:35 ; Search time 79.9 Seconds.
(without alignments)
93.007 Million cell updates/sec

Title: US-09-451-527-100

Perfect score: 658

Sequence: 1 MALWLTWVIALTCGLGLASP.....QLVKNLLTYVRGVVHGNFR 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_0401.*

1: /cgnl_8/gcgdata/geneseq/geneseqp/AA1980.DAT.*
2: /cgnl_8/gcgdata/geneseq/geneseqp/AA1981.DAT.*
3: /cgnl_8/gcgdata/geneseq/geneseqp/AA1982.DAT.*
4: /cgnl_8/gcgdata/geneseq/geneseqp/AA1983.DAT.*
5: /cgnl_8/gcgdata/geneseq/geneseqp/AA1984.DAT.*
6: /cgnl_8/gcgdata/geneseq/geneseqp/AA1985.DAT.*
7: /cgnl_8/gcgdata/geneseq/geneseqp/AA1986.DAT.*
8: /cgnl_8/gcgdata/geneseq/geneseqp/AA1987.DAT.*
9: /cgnl_8/gcgdata/geneseq/geneseqp/AA1988.DAT.*
10: /cgnl_8/gcgdata/geneseq/geneseqp/AA1989.DAT.*
11: /cgnl_8/gcgdata/geneseq/geneseqp/AA1990.DAT.*
12: /cgnl_8/gcgdata/geneseq/geneseqp/AA1991.DAT.*
13: /cgnl_8/gcgdata/geneseq/geneseqp/AA1992.DAT.*
14: /cgnl_8/gcgdata/geneseq/geneseqp/AA1993.DAT.*
15: /cgnl_8/gcgdata/geneseq/geneseqp/AA1994.DAT.*
16: /cgnl_8/gcgdata/geneseq/geneseqp/AA1995.DAT.*
17: /cgnl_8/gcgdata/geneseq/geneseqp/AA1996.DAT.*
18: /cgnl_8/gcgdata/geneseq/geneseqp/AA1997.DAT.*
19: /cgnl_8/gcgdata/geneseq/geneseqp/AA1998.DAT.*
20: /cgnl_8/gcgdata/geneseq/geneseqp/AA1999.DAT.*
21: /cgnl_8/gcgdata/geneseq/geneseqp/AA2000.DAT.*
22: /cgnl_8/gcgdata/geneseq/geneseqp/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	658	100.0	130	21 Y58223	Canine interleukin
2	647.5	98.4	131	21 Y58221	Canine interleukin
3	556	84.5	110	21 Y58224	Canine mature inte
4	545.5	82.9	111	21 Y58222	Canine mature inte
5	448	68.1	132	15 R48624	Sequence of human
6	441	67.0	146	13 R27348	Cytokine NC30. R
7	385	58.5	131	15 R48625	Sequence of mouse
8	377.5	57.4	111	17 R52794	Human interleukin
9	367	55.8	112	13 R27347	Protein with cytot
10	367	55.8	112	17 R52793	Human interleukin
11	360	54.7	112	13 R27346	Protein with cytot

12	302	45.9	111	17	R92795	Murine P600. Mus
13	81	12.3	20	13	R27345	Cytokine signal pe
14	81	12.3	34	13	R27344	Cytokine signal pe
15	79	12.0	665	21	B38312	Human secreted pro
16	79	12.0	667	21	B38311	Gene 38 human secr
17	79	12.0	1230	18	W15764	TIP120. Rattus ra
18	79	12.0	1230	21	B42180	Human ORFX ORF1944
19	78	11.9	21	20	Y49702	Human interleukin
20	77.5	11.8	634	20	Y21548	Human heparin-bind
21	72.5	11.0	286	21	Y58998	Wheat sulfite redu
22	72	10.9	141	21	G35063	Arabidopsis thalia
23	72	10.9	482	13	R20841	Placental-derived
24	72	10.9	482	17	R77531	Human platelet der
25	72	10.9	482	19	W62026	Recombinantly prod
26	72	10.9	5072	12	R11510	Ryanodine receptor
27	71.5	10.9	718	20	W84067	Drosophila mitofus
28	71	10.8	482	19	W62025	Recombinantly prod
29	70	10.6	237	21	Y84892	A human proliferat
30	70	10.6	330	21	G06262	Arabidopsis thalia
31	70	10.6	407	21	G06261	Arabidopsis thalia
32	69.5	10.6	513	11	R04585	Aquaricine I. The
33	69.5	10.6	513	12	R13181	Aquaricine I. The
34	69.5	10.6	513	16	R67653	T.aquaticus Aquari
35	69.5	10.6	980	19	W69741	Aquarysin I. Ther
36	69.5	10.6	980	19	W69743	SAPAP1 protein. H
37	69	10.5	4987	12	R10834	SAPAP2 protein. H
38	68.5	10.4	221	21	Y91434	Rianodin receptor.
39	67	10.2	150	16	R85457	Human secreted pro
40	67	10.2	618	16	R85456	Flax rust resistan
41	67	10.2	673	20	Y58996	Rice sulfite reduc
42	66	10.0	387	20	Y08621	Human secreted pro
43	66	10.0	387	21	Y67312	Human secreted pro
44	66	10.0	477	18	W21643	Grapevine leafroll
45	65.5	10.0	135	21	B41418	Human ORFX ORF1182

ALIGNMENTS

RESULT 1
Y58223
ID Y58223 standard; Protein; 130 AA.
XX
AC Y58223;
XX
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 78.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine;
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR N-PSDB; 255561, 255562, 255563, 255564.
XX
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 3i; Page 237; 264pp; English.

XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
 CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
 CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
 CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 SQ Sequence 130 AA;

Query Match 100.0%; Score 658; DB 21; Length 130;
 Best Local Similarity 100.0%; Pred. No. 1.9e-68;
 Matches 130; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MALMLTVVIALTCGLGLASPSVPTSPPTLKELIEELVNITQNASLCSGSMVWSVNLTAG 60
 DB 1 MALMLTVVIALTCGLGLASPSVPTSPPTLKELIEELVNITQNASLCSGSMVWSVNLTAG 60
 QY 61 MYCAALESINVSQSAIQTORMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLITY 120
 DB 61 MYCAALESINVSQSAIQTORMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLITY 120
 QY 121 RGVYRHGNFR 130
 DB 121 RGVYRHGNFR 130

RESULT 2
 Y58221
 ID Y58221 standard; Protein; 131 AA.
 AC Y58221;
 XX
 XX
 DT 14-MAR-2000 (first entry)
 DE Canine interleukin-13 (IL-13) clone 80.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.
 XX
 OS Canis familiaris.
 XX
 PN WO961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 XX 28-MAY-1999; 99WO-US11942.
 XX
 XX 29-MAY-1998; 98US-0087306.
 PR
 XX (HESK-) HESKA CORP.
 XX
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 PI WPI: 2000-072623/06.
 XX
 DR N-PSDB; 255555, 255556, 255557, 255558.
 DR
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PT

XX Claim 31; Page 231; 264pp; English.
 XX
 CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
 CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
 CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
 CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
 CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
 CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
 CC immunoregulatory proteins. The proteins, their associated
 CC nucleic acids, specific antibodies and inhibitors may be used as
 CC vaccines for therapeutic or prophylactic regulation of an immune
 CC response in animals (particularly cats, dogs, horses and humans).
 CC They may be used to treat autoimmune or infectious diseases including
 CC allergies, tumours, inflammation and graft rejection, and to increase
 CC the response from a co-administered antigen. The nucleotide sequences
 CC can also be used for the recombinant production of a protein, while
 CC nucleotide fragments are useful as probes, as amplification primers and
 CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
 CC The proteins may be used to raise antibodies and to screen for
 CC modulators of activity, while the antibodies may be used in detection,
 CC and in drug targeting.
 XX
 SQ Sequence 131 AA;

Query Match 98.4%; Score 647.5; DB 21; Length 131;
 Best Local Similarity 99.2%; Pred. No. 3.2e-67;
 Matches 130; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MALMLTVVIALTCGLGLASPSVPTSPPTLKELIEELVNITQNASLCSGSMVWSVNLTAG 60
 DB 1 MALMLTVVIALTCGLGLASPSVPTSPPTLKELIEELVNITQNASLCSGSMVWSVNLTAG 60
 QY 61 MYCAALESINVSQSAIQTORMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLITY 119
 DB 61 MYCAALESINVSQSAIQTORMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLITY 120
 QY 120 RGVYRHGNFR 130
 DB 121 RGVYRHGNFR 131

RESULT 3
 Y58224
 ID Y58224 standard; Protein; 110 AA.
 AC Y58224;
 XX
 XX
 DT 14-MAR-2000 (first entry)
 DE Canine mature interleukin-13 (IL-13) clone 78.
 XX
 KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
 KW Immunoregulation; tumour; cancer; autoimmune disease; vaccine.
 XX
 OS Canis familiaris.
 XX
 PN WO961618-A2.
 XX
 PD 02-DEC-1999.
 XX
 XX 28-MAY-1999; 99WO-US11942.
 PF
 XX 29-MAY-1998; 98US-0087306.
 PR
 XX (HESK-) HESKA CORP.
 XX
 XX Sim G, Yang S, Dreitz MJ, Wonderling RS;
 PI WPI: 2000-072623/06.
 XX
 DR N-PSDB; 255555, 255556, 255557, 255558.
 DR
 XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
 PT useful for treating or preventing e.g. tumors or autoimmune disease
 PT

PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 3i; Page 240; 264pp; English.
XX
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
CC canine IL-4, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 110 AA;

Query Match 84.5%; Score 556; DB 21; Length 110;
Best Local Similarity 100.0%; Pred. No. 9.7e-57;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 SPVTPSPTLKEELVNIQTQASLCNGSMVSVNLTAGMYCAALSLINVSDCSAIQR 80
|||||
Db 1 spvtspptlkelieelvnitqngslcngsmvsvnltagmycaaleslinvsdcsaigr 60
|||||

QY 81 TQRLMKALCSQKPAAGISSRSRDTKIEVLQVKNLLTYVRGVYRHGNFR 130
|||||
Db 61 tqrmkalcscqkpaagissersrtdkievlqvlknlltyvrgvyrhgnfr 110
|||||

RESULT 4
Y58222
ID Y58222 standard; Protein; 111 AA.
AC
XX Y58222;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 80.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PF 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Dreitz MJ, Wonderling RS;
XX
DR WPI; 2000-072623/06.
DR N-PSDB; Z55559..Z55560.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX
XX Claim 3i; Page 234; 264pp; English.
XX
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
CC canine IL-4, canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 111 AA;

Query Match 82.9%; Score 545.5; DB 21; Length 111;
Best Local Similarity 99.1%; Pred. No. 1.6e-55;
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 21 SPVTPSPTLKEELVNIQTQASLCNGSMVSVNLTAGMYCAALSLINVSDCSAIQR 80
|||||
Db 1 spvtspptlkelieelvnitqngslcngsmvsvnltagmycaaleslinvsdcsaigr 60
|||||

QY 81 TQRLMKALCSQKPAAG-ISSRSRDTKIEVLQVKNLLTYVRGVYRHGNFR 130
|||||
Db 61 tqrmkalcscqkpaagissersrtdkievlqvlknlltyvrgvyrhgnfr 111
|||||

RESULT 5
R48624
ID R48624 standard; Protein; 132 AA.
AC
XX R48624;
XX
DT 14-SEP-1994 (first entry)
XX
DE Sequence of human interleukin-13 (IL-13).
XX
KW Interleukin-13; lymphokine; immunological disorder; therapy;
KW diagnostic.
XX
OS Homo sapiens.
XX
PN WO9404680-A.
XX
PD 03-MAR-1994.
XX
PF 18-AUG-1993; 93WO-US07645.
XX
PR 21-AUG-1992; 92US-0933416.
PR 29-JAN-1993; 93US-0010977.
PR 01-FEB-1993; 93US-0012543.
XX
PA (SCHE) SCHERING CORP.
XX
PI Aversa G, Banchemareau J, Briere F, Coffman RL, Cooks BG;
PI Culppepper, Dang W, De Vries J, De Waal Malefyt R;
PI Doherty TM, Heath A, Mckenzie A, Punnonen J, Zurawski G;
XX
DR WPI; 1994-083197/10.
DR N-PSDB; Q56692.
XX

* PS Disclosure: Page 128-129; 135pp; English.

XX An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction
CC digest of the mouse P600 cDNA clone was isolated. This fragment,
CC which encompasses most of the coding region of the mouse P600 cDNA,
CC was radioactively labelled and hybridised with filter lifts prepd.
CC from a cDNA library made from a clone of an A10 T cell line. One
CC clone, designated PA 10.66, was subcloned into M13 and sequenced.
CC This sequence encodes human IL-13.
XX
SQ Sequence 131 AA;

Query Match 58.5%; Score 385; DB 15; Length 131;
Best Local Similarity 58.8%; Pred. No. 7.8e-37;
Matches 78; Conservative 19; Mismatches 30; Indels 6; Gaps 2;
QY 1 MALWLVWIALTCIGGLASPSVPTSP- ---TLKELIEELVNITQNOASLCNGSMVWSVN 56
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
Db 1 malwvtavialac19laapppvrsvslptlkelleelsnlcqdplcngsmvwsvd 60
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
QY 57 LTAGMYCAALESINVSDCSAIQRTQRMKALCSQKPAAGISSERSRDTKIEVIQLVKNL 116
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
Db 61 laagfcvaldslnsncnalyrtgrllhglcnrkapttvs--lpdtkievahfickl 118
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
QY 117 LTYVRGVYRHGNF 129
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
Db 119 lsytkqlfrhgp 131

RESULT 8
R92794
ID R92794 standard; Protein; 111 AA.
AC
XX
AC R92794;
DT 24-MAY-1996 (first entry)
XX
DE Human Interleukin-13 mutein 2.
XX
KW Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;
KW diagnosis; therapy; cancer; inflammation; degenerative disease.
XX
OS Synthetic.
FH
XX Key Location/Qualifiers
FT Misc-difference 11
FT /note= "Glu at position 11 may be replaced by an
FT amidated amino acid, including Lys"
FT Misc-difference 64
FT /note= "Arg at position 64 may be replaced by an
FT acidic amino acid, including Asp"
XX
PN WO9604306-A2.
XX
PD 15-FEB-1996.
XX
XX 31-JUL-1995; 95WO-US08950.
XX
PR 01-AUG-1994; 94US-0284393.
XX
XX (SCHE) SCHERING CORP.
PA
XX Zurawski G, Zurawski SM;
PI
XX WPI; 1996-129335/13.
DR
XX Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
PT murine P600 contg. amino acid substitutions - useful for the
PT diagnosis and treatment of cancer, inflammation, etc.
XX
PS Claim 12; Page 46; 52pp; English.
XX

CC Muteins 1 and 2 (R92793-94) of human interleukin-13 (IL-13) contain
CC amino acid substitutions at amino acid position 11 in helix A and/or
CC at position 64 in helix C. They are obtd. by site-directed
CC mutagenesis of natural IL-13 sequences. The muteins antagonise the
CC activity of IL-13 or IL-4. They have partial cytokine agonist
CC activity, exhibit less than 80% maximal agonist activity of natural
CC IL-2, and/or antagonize cytokine activity by least about 50% when
CC present at a 100-fold excess. They and other cytokine muteins
CC (see also R92790-92, R92795-802) are useful in the screening of
CC cytokine and cytokine receptor levels, and in the diagnosis or
CC treatment of e.g. inflammation, cancer, and degenerative disorders.
XX
SQ Sequence 111 AA;

Query Match 57.4%; Score 377.5; DB 17; Length 111;
Best Local Similarity 69.7%; Pred. No. 4.6e-36;
Matches 76; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
QY 22 PVPSPSTLKEELIEELVNITQNO-ASLCNGSMVWSVNLTAGMYCAALESINVSDCSAIQR 80
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
Db 2 pvpstlrelleelvnitqndkplcngsmvwslnltagmycaaleslnvsgcsaiek 61
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
QY 81 TQRMKALCSQKPAAGISSERSRDTKIEVIQLVKNLTYVRGVYRHGNF 129
|||:| |:| |||||:| | | ||||| |||||:| ||||| |||||:
Db 62 tqrmisgfcphkvsagfsslhvrdtkievagfvkdllhikklifregfr 110

RESULT 9
R27347
ID R27347 standard; Protein; 112 AA.
XX
AC R27347;
XX
DT 24-FEB-1993 (first entry)
XX
DE Protein with cytokine activity encoded by Nal'.
XX
KW Interleukin; chemotaxis; immunomodulation; inflammation.
XX
PN EP506574-A.
XX
PD 30-SEP-1992.
XX
XX 27-MAR-1992; 92EP-0400858.
XX
PR 29-MAR-1991; 91PR-0003904.
PR 08-JAN-1992; 92FR-0000137.
XX
PA (SNFI) ELF SANOFI.
XX
PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
PI Leplatois P, Magazin M, Minty A;
XX
XX WPI; 1992-325841/40.
DR N-PSDB; Q28944.
XX
PT New cytokine having immunomodulatory activity - useful for
PT treating tumours and infectious or inflammatory conditions
XX
PS Claim 1; Page 60; 78pp; French.
XX
CC This protein is one of two possible forms of a new cytokine
CC produced by T lymphocytes induced by phorbol-2-myristate-3-acetate
CC and phytohaemagglutinin. The proteins differ only in the amino acid
CC at position 41 which is either Asp or Gly. The cytokine acts on
CC monocytes and B lymphocytes and is useful in treatment of tumours
CC and some infections and inflammatory conditions.
CC See Q28941-Q28947.
XX
SQ Sequence 112 AA;

```
Matches   76; Conservative    11; Mismatches    21; Indels      2; Gaps       2;
```

```
Oy  22 PVTSPPTLKELIELVNITQO-ASLCNGSMVWSVNLTAGMYCAALESLLNVSDCSAIOR 80  
II II :|||||:||||| |||||::||| |::||| |::||| |::|||  
Db  2 pypstalreleeivnitqkaplcnsgmvwsinltadmycaalesllnvsgcsaik 61
```

```
Oy  81 TORMMLKALCOKPAAG-ISSERSDRTKIEVIQLVKNLITYVRGVYRHGNF 129  
|||| I | :|| II ||||| ||::|| ::|| ::||  
Db  62 tqrmalsgfcphksaggfsslhvrdtkievafvkdlhlklkfregrf 111
```

```
RESULT 11  
R27346  
ID R27346 standard; Protein; 112 AA.  
XX AC R27346;  
XX XX  
DT 24-FEB-1993 (first entry)  
XX DE Protein with cytokine activity encoded by NaI.  
XX KW Interleukin; chemotaxis; immunomodulation; inflammation.  
XX PN EP506574-A.  
XX PD 30-SEP-1992.  
XX PF 27-MAR-1992; 92EP-0400858.  
XX PR 29-MAR-1991; 91FR-0003904.  
XX PS 08-JAN-1992; 92FR-0000137.  
XX PA (SNFI ) ELF SANOFI.  
XX PI Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;  
PI Lepiatcois P, Magazin M, Minty A;  
DR WPI; 1992-325841/40.  
XX DR N-PSDB; Q28943.  
XX PT New cytokine having immunomodulatory activity - useful for  
PT treating tumours and infectious or inflammatory conditions  
XX PS Claim 1; Page 60; 78pp; French.
```

```
This protein is one of two possible forms of a new cytokine  
CC produced by r lymphocytes induced by phorbol-2-myristate-3-acetate  
CC and phytohaemagglutinin. The proteins differ only in the amino acid  
CC at position 41 which is either Asp or Gly. The cytokine acts on  
CC monocytes and B lymphocytes and is useful in treatment of tumours  
CC and some infections and inflammatory conditions.  
CC See Q28941-Q28947.
```

```
XX SQ Sequence 112 AA;
```

```
Query Match          54.7%; Score 360; DB 13; Length 112;  
Best Local Similarity 68.2%; Pred. NO. 4.9e-34;  
Matches 75; Conservative 11; Mismatches 22; Indels 2; Gaps 2;
```

```
Oy  22 PVTSPPTLKELIELVNITQO-ASLCNGSMVWSVNLTAGMYCAALESLLNVSDCSAIOR 80  
II II :|||||:||||| |||||::||| |::||| |::||| |::|||  
Db  2 pypstalreleeivnitqkaplcnsgmvwsinltadmycaalesllnvsgcsaik 61
```

```
Oy  81 TORMMLKALCOKPAAG-ISSERSDRTKIEVIQLVKNLITYVRGVYRHGNF 129  
|||| I | :|| II ||||| ||::|| ::|| ::||  
Db  62 tqrmalsgfcphksaggfsslhvrdtkievafvkdlhlklkfregrf 111
```

```
RESULT 12  
R92795  
ID R92795 standard; Protein; 111 AA.  
XX XX
```

```

KW Interleukin; chemotaxis; immunomodulation; inflammation.
XX
XX EP506574-A.
XX
XX 30-SEP-1992.
XX
XX 27-MAR-1992; 92EP-0400858.
XX
XX 29-MAR-1991; 91FR-0003904.
PR 08-JAN-1992; 92FR-0000137.
XX
XX (SNFI ) ELF SANOFI.
XX
XX Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
PI Leplatols P, Magazin M, Minty A;
XX
XX WPI; 1992-325841/40.
DR N-PSDB; Q28941.
XX
XX New cytokine having immunomodulatory activity - useful for
PT treating tumours and infectious or inflammatory conditions
PT
XX Claim 12; Page 61; 78pp; French.
PS
XX The b4 peptide is a preferred signal peptide to be fused to the
CC N-terminus of the new cytokine. The last two amino acids (Ser-Pro)
CC are opt. absent; when absent the signal peptide is designated b3.
CC See Q28942-Q28947.
XX
XX Sequence 20 AA;
SQ
Query Match 12.3%; Score 81; DB 13; Length 20;
Best Local Similarity 85.9%; Pred. No. 0.0093;
Matches 17; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
QY 1 MALWLTVVIALTCILGLASP 20
DB 11111111111111111111
1 mallltvtialtcilgfpasp 20
RESULT 14
R27344
ID R27344 standard; peptide; 34 AA.
XX
XX R27344;
AC
XX
XX 21-MAY-1998 (first entry)
DT
XX
XX Cytokine signal peptide b2.
DE
XX
XX Interleukin; chemotaxis; immunomodulation; inflammation.
KW Homo sapiens.
XX
XX EP506574-A.
XX
XX 30-SEP-1992.
XX
XX 27-MAR-1992; 92EP-0400858.
XX
XX 29-MAR-1991; 91FR-0003904.
PR 08-JAN-1992; 92FR-0000137.
XX
XX (SNFI ) ELF SANOFI.
XX
XX Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteiller C;
PI Leplatols P, Magazin M, Minty A;
XX
XX WPI; 1992-325841/40.
DR N-PSDB; Q28941.
XX
XX New cytokine having immunomodulatory activity - useful for
PT

```

PT treating tumours and infectious or inflammatory conditions

PS Claim 12; Page 61; 78pp; French.

The b2 peptide is a preferred signal peptide to be fused to the N-terminus of the new cytokine. The last two amino acids (Ser-Pro) are opt. absent; when absent the signal peptide is designated b1. See Q28942-Q28947.

Sequence	34 AA;
SQ	

Query Match 12.3%; Score 81; DB 13; Length 34;
Best Local Similarity 85.0%; Pred. No. 0.019;
Matches 17; Conservative 0; Mismatches 3; Indels

Qy	1	MALWLT	VVIALTCLGLASP	20
Db	15	mallltt	vialtclqqasp	34

RESULT 1.5

B38312

ID B38312 standard; Protein; 665 AA.

AC B38312;

DT 30-JAN-2001 (first entry)

Human secreted protein sequence encoded by gene 38 SEQ ID NO:168.

Human; secreted protein; diagnosis; immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiac; vasotropic; cerebroprotective; neurotropic; neuroprotective; antibacterial; virucide; fungicide; ophthalmological; gene therapy; autoimmune disease; infection; hyperproliferative disorder; cardiovascular disorder; anglogenesis; cerebrovascular disorder; nervous system disorder; ocular disorder; wound healing; skin aging; food additive; preservative.

OS Homo sapiens.

PN WO200058469-A1.

05-OCT-2000.

23-MAR-2000; 2000WO-US07579.

PR 26-MAR-1999; 99US-0126509

PR 07-JAN-2000; 2000US-0174853.

PA (HUMA-) HUMAN GENOME SCI INC.

PI Rosen CA, Ruben SM, Komatsoulis G;

DR WPI; 2000-594642/56.

Isolated nucleic acid molecule encoding a human secreted protein is used in preventing, treating or ameliorating a medical condition -

PS Disclosure; Page 407-409; 416pp; English.

The polynucleotide sequences given in C69455 to C69502 encode the human secreted proteins given in B38203 to B38250. B38251 to B38320 represent human secreted polypeptide sequences and proteins homologous to them, which are given in the exemplification of the present invention. Human secreted proteins have activities based on the tissues and cells the genes are expressed in. Example of activities include: immunosuppressive; antiarthritic; antirheumatic; antiproliferative; cytostatic; cardiant; vasotropic; cerebroprotective; nootropic; neuroprotective; antibacterial; virucide; fungicide; and ophthalmological. The polynucleotides and polypeptides can be used to prevent, treat or ameliorate a medical condition in e.g. humans, mice, rabbits, goats, horses, cats, dogs, chickens or sheep. They are also used in diagnosing a pathological condition.

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:48:32 ; Search time 42.06 Seconds
(without alignments)
59.377 Million cell updates/sec

Title: US-09-451-527-100
Perfect score: 658
Sequence: 1 MALWLVVIALTCGLGLASP.....QLVKNLITVYRCVYRHGNER 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents.AA.*

- 1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*
- 2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*
- 3: /cgnl_7/ptodata/1/iaa/6A_COMB.pep.*
- 4: /cgnl_7/ptodata/1/iaa/6B_COMB.pep.*
- 5: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*
- 6: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	448	68.1	132	1 US-08-012-543-2	Sequence 2, Appli
2	448	68.1	132	5 PCT-US93-07645A-2	Sequence 2, Appli
3	448	68.1	132	5 PCT-US93-07645-2	Sequence 2, Appli
4	441	67.0	146	1 US-08-371-121-16	Sequence 16, Appli
5	385	58.5	131	1 US-08-012-543-4	Sequence 4, Appli
6	385	58.5	131	1 US-08-371-121-25	Sequence 25, Appli
7	385	58.5	131	5 PCT-US93-07645A-4	Sequence 4, Appli
8	385	58.5	131	5 PCT-US93-07645-4	Sequence 4, Appli
9	377.5	57.4	111	1 US-08-284-393B-5	Sequence 5, Appli
10	377.5	57.4	111	5 PCT-US95-08950-5	Sequence 5, Appli
11	367	55.8	112	1 US-08-284-393B-4	Sequence 4, Appli
12	367	55.8	112	5 PCT-US95-08950-4	Sequence 4, Appli
13	366.5	55.7	111	1 US-08-284-393B-15	Sequence 15, Appli
14	360	54.7	112	1 US-08-371-121-1	Sequence 1, Appli
15	356	54.1	112	1 US-08-284-393B-14	Sequence 14, Appli
16	302	45.9	111	1 US-08-284-393B-6	Sequence 6, Appli
17	302	45.9	111	5 PCT-US95-08950-6	Sequence 6, Appli
18	295	44.8	111	1 US-08-284-393B-16	Sequence 16, Appli
19	81	12.3	30	1 US-08-371-121-8	Sequence 8, Appli
20	81	12.3	34	1 US-08-371-121-6	Sequence 6, Appli
21	71.5	10.9	718	4 US-09-090-808-2	Sequence 2, Appli
22	70	10.6	18	1 US-08-371-121-7	Sequence 7, Appli
23	70	10.6	32	1 US-08-371-121-5	Sequence 5, Appli
24	67	10.2	1209	5 PCT-US95-04589-107	Sequence 107, App
25	67	10.2	1258	2 US-08-310-912A-107	Sequence 107, App
26	67	10.2	1294	3 US-08-930-996A-10	Sequence 10, Appl
27	66	10.0	477	2 US-08-770-544-16	Sequence 16, Appli

28	65.5	10.0	206	3 US-09-041-889-6	Sequence 6, Appli
29	65.5	10.0	206	3 US-08-837-058-6	Sequence 6, Appli
30	65.5	10.0	426	2 US-08-484-993B-12	Sequence 12, Appli
31	65.5	10.0	426	2 US-08-484-158B-12	Sequence 12, Appli
32	65.5	10.0	426	2 US-08-484-596A-12	Sequence 12, Appli
33	65.5	10.0	426	2 US-08-480-150A-12	Sequence 12, Appli
34	65.5	10.0	426	3 US-08-458-731-12	Sequence 12, Appli
35	65.5	10.0	426	3 US-08-149-223A-12	Sequence 12, Appli
36	64.5	9.8	168	3 US-09-188-579-85	Sequence 85, Appli
37	64.5	9.8	496	2 US-08-696-349-2	Sequence 2, Appli
38	64.5	9.8	496	5 PCT-US96-13156-2	Sequence 2, Appli
39	64	9.7	383	1 US-08-486-037B-2	Sequence 2, Appli
40	64	9.7	1461	2 US-08-993-228-10	Sequence 10, Appli
41	64	9.7	1754	1 US-07-745-208A-13	Sequence 13, Appli
42	64	9.7	1754	2 US-08-311-363-13	Sequence 13, Appli
43	62.5	9.5	228	4 US-08-569-221A-2	Sequence 2, Appli
44	62.5	9.5	848	4 US-08-976-255-10	Sequence 10, Appli
45	62.5	9.5	1589	3 US-08-755-587-189	Sequence 189, App

ALIGNMENTS

RESULT 1
US-08-012-543-2
; Sequence 2, Application US/08012543
; Patent No. 5596072
; GENERAL INFORMATION:
; APPLICANT: Culpepper, Janice
; APPLICANT: McKenzie, Andrew
; APPLICANT: Dang, Warren
; APPLICANT: de Waal Malefyt, Rene
; APPLICANT: Heath, Andrew
; APPLICANT: Aversa, Gregorio
; APPLICANT: Briere, Francine
; APPLICANT: Banchereau, Jacques
; APPLICANT: de Vries, Jan
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/012,543
; FILING DATE: 01-FEB-1993
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933,416
; FILING DATE: 21-AUG-1992
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0302K1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 132 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-012-543-2

Query Match 58.5%; Score 385; DB 1; Length 131;

Query Match 58.5%; Score 385; DB 1; Length 131;

Matches	78;	Conservative	19;	Mismatches	30;	Indels	6;	Gaps	2;
<p>See below Summary section, Location: 100-33)</p>									

0Y 1 MALWLTVVIALTCGGI.ASPSPVTPSP-----TKELIEELVNITONOA.SI.CNGSMWWSVN 56

Db 1 MAIWVTA V I A C I G G I A A G P V P R S V S I P I T I K E I I E E I S N I T O D O T P I L N G S M W S V D 60

57 LTAGMYCAALESLINVSDCSAIOBTORMLKALCSOKPAAGTSSERSRDTKTEVIOIVKNI. 116

61 LAAGGFCVALDSLTSNSCNATYRTORILHGLCNBKAPTIVSS--LPDTKIEVAHFITKL 11

QY 117 LTYVRGVYRHGNE 129

Db 119 LSYTKQLFRHGPF 131

RESULT 6

RESULT 6

US-08-371-121-25

; Sequence 25, Applying
: Patent No. 5652123

; GENERAL INFORMATION:

; APPLICANT: CAPUT, Daniel

APPLICANT: FERRARA, Pascual
APPLICANT: CUIJI I EMOT Icent-clauda

;; AFFILIANT: GUILLERMO, Jean-Claude
;; APPLICANT: LEPLATOIS, Pascal

APPLICANT: MINTY, Adrian

APPLICANT: KAGHAD, Mourad

APPLICANT: MAGAZIN, Marilyn

TITLE OF INVENTION: Protein having a cyto

;	TITLE OF INVENTION:	activity, recombinant
:	TITLE OF INVENTION:	transformed cells and

; NUMBER OF SEQUENCES: 27

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: EOLEY & LADNER

ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington, D.C.

COUNTRY: USA
ZIP: 20007-5109

; COMPUTER READABLE FORM:

```

; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible

```

COMPUTER: IBM PC COMPATIBLE

```

RESULT 7
PCT-US93-07645A-4
; Sequence 4, Application PC/TUS9307645A
; GENERAL INFORMATION:
;
; APPLICANT:
;
; TITLE OF INVENTION: Human Interleukin-13
;
; NUMBER OF SEQUENCES: 6
;
; COMPUTER READABLE FORM:
;
; MEDIUM TYPE: Floppy disk
;
; COMPUTER: Apple Macintosh
;
; OPERATING SYSTEM: Macintosh 6.0.5
;
; SOFTWARE: Microsoft Word 5.1a
;
; CURRENT APPLICATION DATA:
;
; APPLICATION NUMBER: PCT/US93/07645A
;
; FILING DATE:
;
; PRIORITY APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/012543
;
; FILING DATE: 01-FEB-1993
;
; PRIOR APPLICATION DATA:
;
; APPLICATION NUMBER: US 08/010977
;
; FILING DATE: 29-JAN-1993

```

```

RESULT      8
PCT-US93-07645-4
; Sequence 4, Application PC/TUS9307645
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Human Interleukin-13
; NUMBER OF SEQUENCES: 6
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: Apple Macintosh
; OPERATING SYSTEM: Macintosh 6.0.5
; SOFTWARE: Microsoft Word 5.1a
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US93/07645
; FILING DATE: 19930818
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/012543
; FILING DATE: 01-FEB-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/010977
; FILING DATE: 29-JAN-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/933416
; FILING DATE: 21-AUG-1992
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 131 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US93-07645-4

```

	Query Match	58.5%	Score 385;	DB 5;	Length 131;
	Best Local Similarity	58.6%;	Pred. No. 1.8e-39;		
	Matches	78;	Conservative 19;	Mismatches 30;	Indels 6; Gaps 2;
QY	1	MALWLTWVIALTCIGGLASPSVTPSP----	TKELIEELVNTIQNASLCSNGSMWWSVN	56	
		: : :	: :		
Db	1	MALWVTAVLACLGGLAACPVP	PRSVSLPTLTKELIEELSNITQDQPLCSNGSMWWSVD	60	
		: : :	: :		
QY	57	LTAGMYCAALESINWSDCAIQRTQRLMKALCSQKPAAGISERSRDTKIEVTLQVLKVL	116		
		: : : :	: :		
Db	61	LAAGGFCVALDSLTINISNCALRYRTORILGCLNKRKAPTAVSS--LPDTKIEVAHFITKL	118		
		: : : :	: :		

QY 117 LTVGVGRHGNF 129
Db 119 LSYTKQLFRHGP 131

RESULT 9

US-08-284-393B-5
; Sequence 5, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-5

Query Match 57.4%; Score 377.5; DB 1; Length 111;
Best Local Similarity 69.7%; Pred. No. 1.2e-38;
Matches 76; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
QY 22 PVTPSPTLKELIEELVNITQNO-ASLCNGSMVSNLTAGMYCAALESINVSDCSAIOR 80
Db 2 PVPPSTALRELIEELVNITQNKAPLCNGSMVSNLTAGMYCAALESINVSDCSAIAEK 61
QY 81 TQMLKALCSQKPAAGISSERSRDTKIEVQLVKNLLTYVGVYRHGNF 129
Db 62 TQMLSGFCPHKVSAGFSSLHVHRTKIEVAQFVKDLLLHLKLFREGRF 110

RESULT 10

PCT-US95-08950-5
; Sequence 5, Application PC/TUS9508950
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 13
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto

; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US95/08950
; FILING DATE:

; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/284,393
; FILING DATE: 01-AUG-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US95-08950-5

Query Match 57.4%; Score 377.5; DB 5; Length 111;
Best Local Similarity 69.7%; Pred. No. 1.2e-38;
Matches 76; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
QY 22 PVTPSPTLKELIEELVNITQNO-ASLCNGSMVSNLTAGMYCAALESINVSDCSAIOR 80
Db 2 PVPPSTALRELIEELVNITQNKAPLCNGSMVSNLTAGMYCAALESINVSDCSAIAEK 61
QY 81 TQMLKALCSQKPAAGISSERSRDTKIEVQLVKNLLTYVGVYRHGNF 129
Db 62 TQMLSGFCPHKVSAGFSSLHVHRTKIEVAQFVKDLLLHLKLFREGRF 110

RESULT 11

US-08-284-393B-4
; Sequence 4, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090

REFERENCE/DOCKET NUMBER: DX0389
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-4

Query Match 55.8%; Score 367; DB 1; Length 112;
Best Local Similarity 69.1%; Pred. No. 2.3e-37;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 22 PVTPSTLKLIEELVNITQNO-ASLCNGSMWVSNLTAGMYCAALESINVSDCSAIOR 80
DB 2 PVPPSTALRELIEELVNITQNO-KAPLCNGSMWVSNLTAGMYCAALESINVSDCSAIEK 61
QY 81 TQMLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 129
DB 62 TQMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKLFREGRF 111

RESULT 12

PCT-US95-08950-4
Sequence 4, Application PC/TUS9508950
GENERAL INFORMATION:
APPLICANT: Zurawski, Sandra M.
TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
NUMBER OF SEQUENCES: 13
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US95/08950
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/284,393
FILING DATE: 01-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08950-4

Query Match 55.8%; Score 367; DB 5; Length 112;
Best Local Similarity 69.1%; Pred. No. 2.3e-37;

Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;
QY 22 PVTPSTLKLIEELVNITQNO-ASLCNGSMWVSNLTAGMYCAALESINVSDCSAIOR 80
DB 2 PVPPSTALRELIEELVNITQNO-KAPLCNGSMWVSNLTAGMYCAALESINVSDCSAIEK 61
QY 81 TQMLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 129
DB 62 TQMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKLFREGRF 111

RESULT 13

US-08-284-393B-15
Sequence 15, Application US/08284393B
Patent No. 5696234
GENERAL INFORMATION:
APPLICANT: Zurawski, Sandra M.
TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,393B
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-15

Query Match 55.7%; Score 366.5; DB 1; Length 111;
Best Local Similarity 67.9%; Pred. No. 2.6e-37;
Matches 74; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 22 PVTPSTLKLIEELVNITQNO-ASLCNGSMWVSNLTAGMYCAALESINVSDCSAIOR 80
DB 2 PVPPSTALRELIEELVNITQNO-KAPLCNGSMWVSNLTAGMYCAALESINVSDCSAIEK 61
QY 81 TQMLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNLLTYVRGVYRHGNF 129
DB 62 TQMLSGFCPHKVSAGQFSSLHVRDTKIEVAQFVKDLLLHLKLFREGRF 110

RESULT 14

US-08-371-121-1
Sequence 1, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniele
ATTORNEY: FERRARA, Pascual

```

Query Match      54.1%; Score 356; DB 1; Length 112;
Best Local Similarity 67.3%; Pred. No. 5e-36;
Matches 74; Conservative 12; Mismatches 22; Indels 2; Gaps 2;

Qy 22 PVTSPTELKELIELLVNITQNQ-ASLNGSMWVSVNLTAGYCAALESLINVSDCSAIQR 80
      || | :|||:||||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| :|
Db 2 PVPSTALRKLIELLVNITQNQAPLNGSMWVSINLTAGYCAALESLINVSCCSAIEK 61

Qy 81 TQRMKLKALCSQKPAAG-ISSERSRDTKIEVIQLVKNNLLTYVRGVYRHGNF 129
      || | | :|| | ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 62 TQDMLSGFCPHKVSAGQFSSLHVRDRTKIEVAQFVKDLELLHLKKLFRGRF 111

```


Db 15 MALLTTVIALTCGGFASGPPVPPSTALRELIEELVNITQNKAPLCNGSMWWSINLTA 74
Qy 60 GMYCAALESINVDSCSAIQTORMLKALCSOKPAAG-ISSERSRDTKIEVIQLVKNLT 118
Db 75 GMYCAALESINVDSCSAIQTORMLKALCSOKPAAG-ISSERSRDTKIEVIQLVKNLT 118
Qy 119 YVGVGRHGNF 129
Db 135 HLKLFREGRF 145

RESULT 2
E30552
T-cell activation protein P600 precursor - mouse
C:Species: Mus musculus (house mouse)
C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 16-Jul-1999
C:Accession: E30552
R:Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
J. Immunol. 142, 679-687, 1989
A:Title: A family of small inducible proteins secreted by leukocytes are members of a new class of various activation processes.
A:Reference number: A30552; MUID:89093958
A:Accession: E30552
A:Molecule type: mRNA
A:Residues: 1-131 <BRO>
A:Cross-references: GB:M23504; NID:9533246; PIDN:AAA40149.1; PID:9533247
C:Superfamily: Interleukin-13

Query Match 58.5%; Score 385; DB 2; Length 131;
Best Local Similarity 58.6%; Pred. No. 2.3e-31;
Matches 78; Conservative 19; Mismatches 30; Indels 6; Gaps 2;

Qy 1 MALWTVVIALTCGGASPSPTSP-----TLKELIEELVNITQNKASLCNGSMWWSVN 56
Db 1 MALWTVVIALTCGGASPSPTSP-----TLKELIEELVNITQNKASLCNGSMWWSVN 56
Qy 57 LTAGMYCAALESINVDSCSAIQTORMLKALCSOKPAAG-ISSERSRDTKIEVIQLVKNL 116
Db 61 LAAGGFCVALDSLITNSCNALYRTQRIHLGLCNKRKAPTIVSS--LPDRTKIEVAHFITKL 118
Qy 117 LTYVGRVGRHGNF 129
Db 119 LSYTKQLFRHGPF 131

RESULT 3
I52290
Interleukin-13 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
C:Accession: I52290
R:Lakkis, F.G.; Cruet, E.N.
Biochem. Biophys. Res. Commun. 197, 612-618, 1993
A:Title: Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expression in rat thymocytes.
A:Reference number: I52290; MUID:94092138
A:Accession: I52290
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-131 <RES>
A:Cross-references: GB:L26913; NID:9438875; PIDN:AAA16478.1; PID:9438876
C:Genetics:
A:Gene: IL-13
C:Superfamily: Interleukin-13

Query Match 57.5%; Score 378.5; DB 2; Length 131;
Best Local Similarity 59.4%; Pred. No. 1e-30;
Matches 79; Conservative 21; Mismatches 26; Indels 7; Gaps 4;

Qy 1 MALWTVVIALTCGGASPSPTSP-----TPSPYLKELIEELVNITQNKASLCNGSMWWSV 55
Db 1 MALWTVVIALTCGGASPSPTSP-----TPSPYLKELIEELVNITQNKASLCNGSMWWSV 55

Qy 56 NLTAGMYCAALESINVDSCSAIQTORMLKALCSOKPAAG-ISSERSRDTKIEVIQLVKN 115
Db 61 DLTAGGCAALESITNISSCNAIHRTILNGLCNQK-ASDVASS-PPDTKIEVAQFISK 118
Qy 116 LTYVGRVGRHGN 128
Db 119 LLYNSKQLFRYGH 131

RESULT 4
T42735
TBP-interacting protein TBP120 - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 21-Jul-2000
C:Accession: T42735
R:Yogisawa, S.; Makino, Y.; Yoshida, T.; Kishimoto, T.; Muramatsu, M.; Tamura, T.
Biochem. Biophys. Res. Commun. 229, 612-617, 1996
A:Title: Molecular cloning of a novel 120-kDa TBP-interacting protein.
A:Reference number: Z22253; MUID:97127450
A:Accession: T42735
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1230 <VOG>
A:Cross-references: EMBL:D87671; NID:91799569; PIDN:BAA13432.1; PID:91799570
C:Genetics:
A:Gene: tipl20
C:Function:
A:Description: considered to participate in transcription regulation through the interaction with TBP.

Query Match 12.0%; Score 79; DB 2; Length 1230;
Best Local Similarity 31.2%; Pred. No. 11;
Matches 39; Conservative 19; Mismatches 51; Indels 16; Gaps 5;

Qy 5 LTVVIALTCGGASPSPTSPYLKELIEELVN-ITQNKASLCNGSMV-----WSV 55
Db 626 LTVVIALTCGGASPSPTSPYLKELIEELVN-ITQNKASLCNGSMV-----WSV 55
Qy 56 NLTAGMYCAALES---LINVDSCSAIQTORMLKALCSOKPAAG-ISSERSRDTKIEVIQL 112
Db 684 SLTAMIDAVDELPLPLISESDMHVSQMAISFLTTLAKVYPSS--LSKISGSILNELIGL 741
Qy 113 VKNLL 117
Db 742 VRSPL 746

RESULT 5
E83551
conserved hypothetical protein PA0752 [imported] - Pseudomonas aeruginosa (strain PAO)
C:Species: Pseudomonas aeruginosa
C:Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
C:Accession: E83551
R:Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warren, P.; Hickey, M.J.; Adam, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig, K.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
A:Title: Complete genome sequence of Pseudomonas aeruginosa PAO1, an opportunistic pathogen.
A:Reference number: AB2950; MUID:20437337
A:Accession: E83551
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-505 <STO>
A:Cross-references: GB:AE004510; GB:AE004091; NID:99946634; PIDN:AAG04141.1; GSPDB:GN000001
A:Experimental source: strain PAO1
C:Genetics:
A:Gene: PA0752

Query Match 11.7%; Score 77; DB 2; Length 505;
Best Local Similarity 24.8%; Pred. No. 6.1;
Matches 34; Conservative 25; Mismatches 42; Indels 36; Gaps 6;

F;9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 11.3%; Score 74.5; DB 2; Length 261;
Best Local Similarity 22.2%; Pred. No. 5.2;
Matches 32; Conservative 27; Mismatches 54; Indels 31; Gaps 6;

QY 5 LTVVIALTCGLGSPSPVTPPTLKELIEELVNITONQASLCNGSMWV-----SVNLT 58
DB 150 FVLMFAIVCLGSGMAGDRP-----LKTLLAALGLFLSVGDIDANSVYRFTGDSIHLA 203
QY 59 AGW-YCAALESINVSDC-----SAIQRTORMLKALCSOKPAAGISSERSRDTK 106
DB 204 DGIOFVVVLGFLFSVEIILLLEKTHHGQEAQVATGRM---LNFKAASVL-----252
QY 107 IEVILQVLKMLTYVRGV 123
DB 253 --LVNLRCLGLGFVMGV 267

RESULT 6
T34264
hypothetical protein F46C8.4 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999
C:Accession: T34264
R:Wilcox, L.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid F46C8.
A:Reference number: Z21497
A:Accession: T34264
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-2195 <WIL>
A:CROSS-references: EMBL:U41624; PIDN:AAA83316.1; CESP:F46C8.4
C:Genetics:
A:Gene: CESP:F46C8.4
A:Introns: 19/3; 61/3; 80/1; 159/1; 182/1; 208/2; 246/1; 308/1; 367/1; 422/1; 466/1; 507/629/3; 1721/3; 1767/3; 1811/1; 1874/1; 1920/1; 2011/2; 2068/3; 2117/1; 2161/1

Query Match 11.4%; Score 75; DB 2; Length 2195;
Best Local Similarity 25.9%; Pred. No. 52;
Matches 28; Conservative 17; Mismatches 43; Indels 20; Gaps 4;

QY 5 LTVVIALTCGLGSPSPVTPPTLKELIEELVNITONQASLCNGSMWVSNLTAGMYC 63
DB 1168 LPIIISMKLGTSSPSQITSPEYKRWLSKPGHMCNDKTHCTNCS-----VCVNGFC 1221
QY 64 AALESINVSDD--CSAIQRTQ-----RMLKALCSOKPAAGIS 98
DB 1222 RCEGLVHVGDKVSEIDATKCLASNCQPSGAQCVGCKRCKPGLGIT 1269

RESULT 7
S52110
sepiapterin reductase (EC 1.1.1.153) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 18-Feb-2000
C:Accession: S52110; PH1578
R:Ota, A.; Ichinose, H.; Nagatsu, T.
Biochim. Biophys. Acta 1260, 320-322, 1995
A:Title: Mouse sepiapterin reductase: an enzyme involved in the final step of tetrahydrobiopterin biosynthesis
A:Reference number: S52110; MUID:95178553
A:Accession: S52110
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <OTA>
A:CROSS-references: GB:S77493; NID:957229; PIDN:AB33611.1; PID:957230
R:Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Exp. Cell Res. 204, 217-222, 1993
A:Title: Detection of a novel sepiapterin reductase mRNA in various cells
A:Reference number: A49174; MUID:93178546
A:Accession: PH1578
A:Molecule type: mRNA
A:Residues: 209-255 <MAI>
A:Comment: This enzyme catalyzes the reduction of both C1' and C2' oxo group.
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase

F;9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match 11.3%; Score 74.5; DB 2; Length 261;
Best Local Similarity 22.2%; Pred. No. 5.2;
Matches 32; Conservative 27; Mismatches 54; Indels 31; Gaps 6;

QY 5 LTVVIALTCGLGSPSPVTPPTLKELIEELVNITONQAS 45
DB 62 LKVVLAADLGTGAGVQRLLSAVRELPRGQLQRLINNAATLGDVSKGFLNVN---D 117

QY 46 LCNQSMWVSNLTAGMYCAALESINVSDCSAIQRTORMLKALCSOKPAAG-----ISSER 101
DB 118 LAEVNMYWALNLTSLMLCLTSGTLNFAQDPSGLSKTGVNMISSCALQPYKMGLYCAGKA 176

QY 102 SRDTKIEVIQLVK---NLLTVVRG 122
DB 177 ARDMLYQVLAEEPSVRLSYAPG 200

RESULT 8
A36024
sepiapterin reductase (EC 1.1.1.153) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jan-1991 #sequence_revision 07-Jul-1995 #text_change 01-Dec-2000
C:Accession: A36024; A36400; PH1577; I64799; A49174
R:Citron, B.A.; Milstien, S.; Gutierrez, J.C.; Levine, R.A.; Yanak, B.L.; Kaufman, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 6436-6440, 1990
A:Title: Isolation and expression of rat liver sepiapterin reductase cDNA.
A:Reference number: A36024; MUID:90349631
A:Accession: A36024
A:Molecule type: mRNA
A:Residues: 4-262 <CIT>
A:CROSS-references: GB:M36410; NID:9206895; PIDN:AAA42130.1; PID:9206896
R:Oyama, R.; Katoh, S.; Sueoka, T.; Suzuki, M.; Ichinose, H.; Nagatsu, T.; Titani, K.
Biochem. Biophys. Res. Commun. 173, 627-631, 1990
A:Title: The complete amino acid sequence of the mature form of rat sepiapterin reductase
A:Reference number: A36400; MUID:91083647
A:Accession: A36400
A:Molecule type: protein
A:Residues: 1-32; 34; 41-92, 1', 96-124; 126-262 <OVA>
R:Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Exp. Cell Res. 204, 217-222, 1993
A:Title: Detection of a novel sepiapterin reductase mRNA in various cells
A:Reference number: A49174; MUID:93178546
A:Accession: PH1577
A:Molecule type: mRNA
A:Residues: 209-255 <MAI>
A:CROSS-references: GB:S55545; NID:9266077; PIDN:AB25506.1; PID:9266078
R:Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Adv. Exp. Med. Biol. 338, 195-198, 1993
A:Title: Northern blot analysis of sepiapterin reductase mRNA in mammalian cell lines
A:Reference number: I51849; MUID:94136218
A:Accession: I64799
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 209-255 <RES>
A:CROSS-references: GB:S71374; NID:9557901
C:Function:
A:Description: catalyzes the NADPH-dependent reduction of sepiapterin to produce 7,8-dihydrosepiapterin
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: acetylated amino end; homodimer; oxidoreductase
F;9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;1/Modified site: acetylated amino end (Met) #status experimental

Query Match 11.3%; Score 74.5; DB 2; Length 262;
Best Local Similarity 23.6%; Pred. No. 5.2;
Matches 34; Conservative 26; Mismatches 53; Indels 31; Gaps 6;

QY 5 LTVVIALTCGLG-----GLASPSVTPSP-----TLKELIEELVNITONQAS 45
DB 62 LOVLAADLGTGSCVQQLLSAVRELPRERLQRLINNAATLGDVSKGFLNIN---D 117

[illegible]

Qy	77	AIQ-----RTQRLKALCSQPAAGISSERSDTKIE-----VIQLVKLLTVV	120
		: : : : : : : : : : : : : : :	
Db	581	HKSIIISLDDKHGRNHKVLDVLCSVCNGVAVRNQDLITENLPGLRELLQTNLINV	640
Qy	121	RGV 123	
Db	641	TSI 643	

RESULT 14
JQ1176
sepiapterin reductase (EC 1.1.1.153) - human
C:Species: Homo sapiens (man)
C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jul-2000
C:Accession: JQ1176; PH1579; I51849
R:Ichinose, H.; Katoh, S.; Sueoka, T.; Titani, K.; Fujita, K.; Nagatsu, T.
Biochem. Biophys. Res. Commun. 179, 183-189, 1991
A:Title: Cloning and sequencing of cDNA encoding human sepiapterin reductase
A:Reference number: JQ1176; MUID:91354248
A:Accession: JQ1176

A:Cross-references: GB:M76231; NID:G338020; PIDN:AAA60314.1; PID:g338021
A:Residues: 1-261 <I>
A:Experimental source: liver
R:Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Exp. Cell Res. 204, 217-222, 1993
A:Title: Detection of a novel septaplerin reductase mRNA: Assay of mRNA in
A:Reference number: A49174; MUID:93178546
A:Accession: PH1579
A:Molecule type: mRNA
A:Residues: 208-254 <MAI>
R:Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Adv. Exp. Med. Biol. 338, 195-198, 1993
A:Title: Northern blot analysis of septaplerin reductase mRNA in mammalian
A:Reference number: I51849; MUID:94136218
A:Accession: I51849
A>Status: translated from GB/EMBL/DBDJ
A:Molecule type: mRNA
A:Residues: 208-254 <RSS>
A:Cross-references: GB:S71376; NID:q557903; PIDN:AAD14079.1; PID:q4261779
C:Comment: This enzyme catalyzes the NADPH-dependent reduction of septaple
C:Genetics:

```

Query Match          10.9% ; Score 71.5; DB 2; Length 261;
Best Local Similarity 24.7% ; Pred. No. 10;
Matches 24; Conservative 21; Mismatches 41; Indels 11; Gaps

QY 36 LVNITQNASLNCMSW---WSVNLTAGWYCAALESINVSDCSATQRTQRMKALCSOK 92
      | : : : : | : | : | : | : | : | : | : | : | : | : | : | :
Db. 104 LGDVSKFGVLDSTQVNNYWNALNVS-MLCITLSSVLKAFPPDSPGLNRTVWNIISSCALQ 162
      | : : : : | : | : | : | : | : | : | : | : | : | : | : | :
QY 93 PAAG----ISSRSRDPKIEVIOLVK---NLLTYVRG 122
      | : : : : | : | : | : | : | : | : | : | : | : | : | : | :
Db. 163 PFKGWALYCAGKAARDMLFQVLALEEFNVRVLNYPG 199
      | : : : : | : | : | : | : | : | : | : | : | : | : | : | :

```

ATP-dependent RNA helicase - fission yeast (*Schizosaccharomyces pombe*)
 S62423
 C:Species: Schizosaccharomyces pombe
 C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
 C:Accession: T38183; S62423
 R:Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
 submitted to the EMBL Data Library, October 1995

A:Accession: T38183
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-481 <LY2>
 A:Cross-references: EMBL:254285; PIDN:CAA91073.1; PID:gl008436; GSPDB:GN00066; SPDB:SPAC
 A:Experimental source: strain 972h-; cosmid c22F3
 C:Genetics:
 A:Gene: SPAC22F3.08c
 A:Map position: 1L
 C:Keywords: ATP; P-loop
 F:90-97/Region: nucleotide-binding motif A (P-loop)
 F:192-197/Region: nucleotide-binding motif B
 F:196-199/Region: DEAD motif

Query Match 10.9%; Score 71.5; DB 2; Length 481;
 Best Local Similarity 24.3%; Pred. NO. 21;
 Matches 25; Conservative 25; Mismatches 48; Indels 5; Gaps 4;
 QY 25 PSPTLKEL-IEELVNITONQASLCNGSMWVS-V-NLTAGMYCAALESLINVSDCSAIQRTQ 82
 Db 18 PPSIKEKEAKKLGQITKGAKVTCNNPVDPIEEFPEGILCENLKKQ-NITECTTIQR-- 74
 QY 83 RMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGYYR 125
 Db 75 YAIPTIGSKRDLACAPTGSCKTIAYLPFILOKLQHLHVPGGYR 117

Search completed: May 13, 2001, 21:48:44
 Job time: 26253 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2001, 06:02:05 ; Search time 44.64 Seconds
(without alignments)
99.758 Million cell updates/sec

Title: US-09-451-527-100

Perfect score: 658

Sequence: 1 MALWLVVIALTCGLGLASP.....QLVKNLLTYRGVYRHGNER 130

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 20000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	448	68.1	132	1	IL13_HUMAN
2	412	62.6	132	1	IL13_BOVIN
3	385	58.5	131	1	IL13_MOUSE
4	378.5	57.5	131	1	IL13_RAT
5	74.5	11.3	261	1	SPRE_MOUSE
6	74.5	11.3	262	1	SPRE_RAT
7	73.5	11.2	211	1	H1T_PIG
8	72	10.9	431	1	ACRO_RABIT
9	72	10.9	482	1	TYPH_HUMAN
10	72	10.9	5032	1	RYNR_HUMAN
11	71.5	10.9	261	1	SPRE_HUMAN
12	71.5	10.9	481	1	YA88_SCHPO
13	70.5	10.7	207	1	H1T_MACMU
14	70	10.6	725	1	VR2A_BPT4
15	69.5	10.6	192	1	FLHC_SALTY
16	69.5	10.6	513	1	AQLI_THEAQ
17	69.5	10.6	1037	1	ACRD_ECOLI
18	69	10.5	323	1	GC_RABIT
19	69	10.5	5035	1	RYNR_PIG
20	69	10.5	5037	1	RYNR_RABIT
21	68	10.3	805	1	UBP5_YEAST
22	68	10.3	936	1	PHL1_YEAST
23	67.5	10.3	1164	1	KEL1_YEAST
24	67	10.2	522	1	TSAW_RICTS
25	67	10.2	1221	1	TOP2_TRYBB
26	66.5	10.1	633	1	DNAA_AGRTU
27	66.5	10.1	891	1	YB33_SCHPO
28	65.5	10.0	206	1	H1T_HUMAN
29	65.5	10.0	426	1	ZP3_CANFA
30	65.5	10.0	510	1	MUTL1_THEMA
31	65.5	10.0	638	1	DNAA_RHILE
32	65.5	10.0	1164	1	PHOS_HUMAN
33	65	9.9	1477	1	ALI13_RAT

34	64.5	9.8	168	1	PTP_NPVAC	P24556 autographa
35	64.5	9.8	292	1	IBP3_RAT	P15473 rattus norv
36	64.5	9.8	475	1	ASPA_HAETN	P44324 haemophilus
37	64.5	9.8	538	1	RO60_XENLA	P42700 xenopus lae
38	64.5	9.8	701	1	UBF2_XENLA	P25980 xenopus lae
39	64.5	9.8	981	1	YM48_YEAST	Q12751 saccharomyc
40	64	9.7	382	1	ADH2_ZYMMO	P06758 zymomonas m
41	64	9.7	503	1	ZNT1_MOUSE	Q60738 mus musculu
42	64	9.7	952	1	YK15_CAEEL	P46012 caenorhabdi
43	64	9.7	1131	1	PMAL1_DUNBI	P54211 dunaliella
44	63.5	9.7	472	1	EXUT_ECOLI	P42609 escherichia
45	63.5	9.7	585	1	YM67_CAEEL	P34528 caenorhabdi

ALIGNMENTS

```
RESULT 1
IL13_HUMAN
ID IL13_HUMAN STANDARD; PRT; 132 AA.
AC P35225; O43644;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13).
GN IL13 OR NC30.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211479; PubMed=8096327;
RA Minty A.J., Chalton P., Derocq J.M., Dumont X., Guillemot J.C.,
RA Kaghad M., Labit C., Leplatois P., Liauzun P., Miloux B.,
RA Minty C., Casellas P., Loison G., Lupker J., Shire D., Ferrara P.,
RA Caput D.;
RT "Interleukin-13 is a new human lymphokine regulating inflammatory and
RT immune responses.";
RL Nature 362:248-250(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93234572; PubMed=8097324;
RA McKenzie A.N., Culpepper J.A., Waal Malefyt R., Briere F.,
RA Punnonen J., Aversa G., Sato A., Dang W., Cocks B.G., Menon S.,
RA de Vries J.E., Banchereau J., Zurawski G.R.;
RT "Interleukin 13, a T-cell-derived cytokine that regulates human
RT monocyte and B-cell function.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:3735-3739(1993).
RN [3]
RP SEQUENCE FROM N.A.
RA Dolganov G., Lewis D.B., Lovett M., Burr J., Bort S., Short D.,
RA McGurn M., Gibson C.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE=Blood;
RX MEDLINE=95237624; PubMed=7721105;
RA Smirnov D.V., Smirnova M.G., Korobko V.G., Frolova E.I.;
RT "Tandem arrangement of human genes for interleukin-4 and
RT interleukin-13: resemblance in their organization.";
RL Gene 155:277-281(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95132583; PubMed=7530359;
RA Ramborough P., Duncan D., Richards W.G.;
RT "Predictive modelling of the 3-D structure of interleukin-13.";
RL Protein Eng. 7:1077-1082(1994).
```

```
RP VARIANT GLN-130.
RX MEDLINE=20164293; PubMed=10699178;
RA Heinemann A., Mao X.-Q., Akaiwa M., Kreomer R.T., Gao P.-S.,
RA Oshima K., Umehita K., Abe Y., Braun S., Yamashita T., Roberts M.H.,
RA Sugimoto R., Arima K., Arinobu Y., Yu B., Kruse S., Enomoto T.,
RA Dake Y., Kawai M., Shimazu S., Sakaki S., Adra C.N., Kitaichi M.,
RA Inoue H., Yamauchi K., Tomichi N., Kurimoto F., Hanasaki N.,
RA Hopkin J.M., Izuhara K., Shirakawa T., Deichmann K.A.;
RT "Genetic variants of IL-13 signalling and human asthma and atopy."
RL Hum. Mol. Genet. 9:549-559(2000).
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES.
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- POLYMORPHISM: GLN AT POSITION 130 IS A SIGNIFICANT RISK FACTOR FOR
CC ASTHMA DEVELOPMENT.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; L06801; AAA36107.1; -
DR EMBL; X69079; CAA48824.1; -
DR EMBL; X69079; CAA48823.1; ALT_INIT.
DR EMBL; U11120; AAB01681.1; -
DR EMBL; U10307; AAA83738.1; -
DR EMBL; AF043334; AAC03535.1; -
DR PIR; A47481; A47481.
DR PDB; 3ITS; 26-JAN-95.
DR MIM; 147683; -
DR InterPro; IPR001325; -
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 132 INTERLEUKIN-13.
FT DISULFID 48 76
FT DISULFID 64 90
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 130 130 R -> Q.
FT /FTID=VAR_010037.
FT CONFLICT 45 45 A -> R (IN REF. 4).
FT CONFLICT 87 87 S -> G (IN REF. 5).
FT CONFLICT 98 98 MISSING (IN REF. 4).
SQ SEQUENCE 132 AA; 14319 MW; 123F1DCAB87FD78B CRC64;

Query Match 68.1%; Score 448; DB 1; Length 132;
Best Local Similarity 71.0%; Pred. No. 1.2e-38;
Matches 93; Conservative 11; Mismatches 25; Indels 2; Gaps 2;

QY 1 MALWLTVVIALTCGLGASPSVPTSPPTLKELIEELVNITNQ-ASLCNGSMVWSNLT 59
DQ 1 MALLTTVIALTCGLGASPGVPPPTALREELIEELVNITNQKAPLCNGSMVWSNLT 60
QY 60 GMYCAALESINVSQCSAQTQRMKALCSQKPAAG-ISSERSRDTKIEVQLVKNLT 118
DQ 61 GMYCAALESINVSQCSAQTQRMKALCSQKPAAG-ISSERSRDTKIEVQLVKNLT 118
QY 119 YVRGVYRHGNF 129
DQ 121 HLKLFREGFR 131

RESULT 2
IL13_MOUSE
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
```

```
IL13_BOVIN
ID IL13_BOVIN STANDARD; PRT; 132 AA.
AC Q9XSV9;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13).
GN IL13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Buikamp J., Jann O., Fries R.;
RT "The bovine interleukin-13 gene: genomic organization, chromosomal
RT location and evolution of the promoter";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS. MAY
CC BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY
CC SIMILARITY).
CC -!- SUBCELLULAR LOCATION: SECRETED.
CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AJ132441; CAB46636.1; -
DR PROSITE; PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 20 BY SIMILARITY.
FT CHAIN 21 132 INTERLEUKIN-13.
FT DISULFID 48 76 BY SIMILARITY.
FT DISULFID 64 90 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 132 AA; 14623 MW; 723BD42375C161F3 CRC64;

Query Match 62.6%; Score 412; DB 1; Length 132;
Best Local Similarity 65.6%; Pred. No. 5.3e-35;
Matches 86; Conservative 16; Mismatches 27; Indels 2; Gaps 2;

QY 1 MALWLTVVIALTCGLGASPSVPTSPPTLKELIEELVNITNQ-ASLCNGSMVWSNLT 59
DQ 1 MALLTTAVILICFGLTSPSPVPSATLREELVNITNQKVPCLNGSMVWSNLT 60
QY 60 GMYCAALESINVSQCSAQTQRMKALCSQKPAAG-ISSERSRDTKIEVQLVKNLT 118
DQ 61 GMYCAALESINVSQCSAQTQRMKALCSQKPAAG-ISSERSRDTKIEVQLVKNLT 118
QY 119 YVRGVYRHGNF 129
DQ 121 HSRIVFRNERF 131

RESULT 3
IL13_MOUSE
ID IL13_MOUSE STANDARD; PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
```



```

QY 102 SRDTKIEVIOLVK---NLLTYVRG 122
Db 177 ARDMLYQVLAVEPSVRVLSTAPG 200

RESULT 7
HIT_PIG
ID HIT_PIG STANDARD; PRT; 211 AA.
AC P06348;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-JAN-1988 (Rel. 06, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HISTONE HIT.
OS Sus scrofa (Pig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE.
RX MEDLINE=85054795; PubMed=6389534;
RA Cole K.D., York R.G., Kistler W.S.;
RT "The amino acid sequence of boar Hit, a testis-specific H1 histone
RT variant.";
RL J. Biol. Chem. 259:13695-13702(1984).
CC -!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: THIS HISTONE IS A TESTIS-SPECIFIC H1 VARIANT
CC THAT APPEARS DURING MEIOSIS IN SPERMATOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
CC PIR: A02581; HSPG1T.
DR HSP; P08287; IGHC.
DR InterPro; IPR001386; -.
DR Pfam; PF00538; linker histone; 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
KW Acetylation; Spermatogenesis; Testis.
FT MOD_RES 1 ACETYLATION.
FT DOMAIN 39 112 GLOBULAR.
FT SEQUENCE 211 AA; 22059 MW; EACA47C51A8F5364 CRC64;

Query Match 11.2%; Score 73.5; DB 1; Length 211;
Best Local Similarity 26.5%; Pred. No. 1.9;
Matches 31; Conservative 16; Mismatches 31; Indels 39; Gaps 5;

QY 16 GLASPSVPTPSPTLKEIIELVNITONQASLCNGSMWYNLTAGMYCAALESINVSDC 75
Db 30 GLTGTGRKAPSASVSLITELSVSQER-----AGMSLAALK----- 66

Query Match 11.2%; Score 73.5; DB 1; Length 211;
Best Local Similarity 26.5%; Pred. No. 1.9;
Matches 31; Conservative 16; Mismatches 31; Indels 39; Gaps 5;

QY 76 SATQRTQRMKALCSOKPAAGISSESRD-TKIEVIOLV-KNLLTYVRGVYRHGNFR 130
Db 67 -----KALA---AAGYDEKNNRKIKLGLKSLVCKGILVQTRGTGASGSFK 109

RESULT 8
ACRO_RABIT
ID ACRO_RABIT STANDARD; PRT; 431 AA.
AC P48038;
DT 01-FEB-1996 (Rel. 33, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE ACROSIN PRECURSOR (EC 3.4.21.10).
GN ACR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=NEW ZEALAND WHITE; TISSUE=Testis;
RX MEDLINE=94368861; PubMed=8086469;
RA Richardson R.T., O'Rend M.G.;

```

```

RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
RT preproacrosin-related cDNA.";
RL Biochim. Biophys. Acta 1219:215-218(1994).
CC -!- FUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAMMALIAN SPERMATOZOEA.
CC IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY. IT
CC IS SYNTHESIZED IN A ZMOGEN FORM, PROACROSIN AND STORED IN THE
CC ACROSOME.
CC -!- CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL
CC CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
CC -!- SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -!- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U05204; AAA61630.1; -.
DR MEROPS; S01_223; -.
DR InterPro; IPR001254; -.
DR InterPro; IPR001314; -.
DR Pfam; PF00089; trypsin; 1.
DR PRINTS; PR00722; CHYMOTRYPSIN.
DR PROSITE; PS00134; TRYPSIN_HIS; 1.
DR PROSITE; PS00135; TRYPSIN_SER; 1.
KW Hydrolase; Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
FT SIGNAL 1 16
FT CHAIN 17 431 ACROSIN.
FT CHAIN 17 39 ACROSIN LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 40 ? ACROSIN HEAVY CHAIN (BY SIMILARITY).
FT PROPEP ? 431 PRO-RICH.
FT DISULFID 22 152 INTERCHAIN (BY SIMILARITY).
FT DISULFID 26 160 INTERCHAIN (BY SIMILARITY).
FT DISULFID 71 87 BY SIMILARITY.
FT DISULFID 175 244 BY SIMILARITY.
FT DISULFID 207 223 BY SIMILARITY.
FT DISULFID 234 264 BY SIMILARITY.
FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT ACT_SITE 86 86 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 140 140 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT SEQUENCE 431 AA; 46422 MW; IC0154E0BC0C668 CRC64;

Query Match 10.9%; Score 72; DB 1; Length 431;
Best Local Similarity 32.3%; Pred. No. 6.3;
Matches 20; Conservative 8; Mismatches 26; Indels 8; Gaps 2;

QY 10 ALTCL---GGLASPSVPTPSPTLKEIIELVNITONQASLCNGSMWYNLTAGMYCAAL 66
Db 172 AQTCTVAGGVYKENAPRPSPTLMEARVDLINL-----ELCNSTQWYNGRIATSLCAGY 226

QY 67 ES 68
Db 227 PS 228

RESULT 9
TYPH_HUMAN
ID TYPH_HUMAN STANDARD; PRT; 482 AA.
AC P19971; Q13390;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE THYMIDINE PHOSPHORYLASE PRECURSOR (EC 2.4.2.4) (TDPase) (TP)
DE (PLATELET-DERIVED ENDOTHELIAL CELL GROWTH FACTOR) (PD-ECGF)
DE (GLIOTATIN).

```

GN EC9P1.
OS Homo sapiens (Human).
CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Placenta;
RX MEDLINE=89181955; PubMed=2467210;
RA Ishikawa F., Miyazono K., Hellman U., Drexler H., Wernstedt C.,
RA Hagihara K., Usuki K., Takaku F., Risaue W., Heidln C.-H.;
RT "Identification of angiogenic activity and the cloning and expression
RT of platelet-derived endothelial cell growth factor.";
RL Nature 338:557-562(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Flinnis C., Goodey A.R., Courtney M., Sleep D.;
RL Submitted (xxx-1991) to the EMBL/Genbank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Adams M.D., Kerlavage A.R., Fuldner R.A., Phillips C.A.,
RA Venter J.C.;
RL Submitted (JUL-1996) to the EMBL/Genbank/DBJ databases.
RN [4]
RP SEQUENCE OF 149-244 FROM N.A., AND SEQUENCE OF 125-178 AND 236-244.
RX MEDLINE=92236753; PubMed=1570012;
RA Furukawa T., Yoshimura A., Sumizawa T., Haraguchi M., Akiyama S.-I.,
RA Fukui K., Yamada Y.;
RT "Angiogenic factor.";
RL Nature 356:668-668(1992).
RN [5]
RP PARTIAL SEQUENCE.
RX MEDLINE=93015908; PubMed=1400349;
RA Asai K., Nakanishi K., Isobe I., Eksloglu Y.Z., Hirano A., Hama K.,
RA Miyamoto T., Kato T.;
RT "Neurotrophic action of gliostatin on cortical neurons. Identity of
RT gliostatin and platelet-derived endothelial cell growth factor.";
RL J. Biol. Chem. 267:20311-20316(1992).
RN [6]
RP FUNCTION.
RX MEDLINE=92272724; PubMed=1590793;
RA Usuki K., Saras J., Waltenberger J., Miyazono K., Pierce G.,
RA Thomson A., Heidln C.-H.;
RT "Platelet-derived endothelial cell growth factor has thymidine
RT phosphorylase activity.";
RL Biochem. Biophys. Res. Commun. 184:1311-1316(1992).
RN [7]
RP VARIANTS MNGIE.
RX MEDLINE=91123033; PubMed=9924029;
RA Nishino I., Spinazzola A., Hirano M.;
RT "Thymidine phosphorylase gene mutations in MNGIE, a human
RT mitochondrial disorder.";
RL Science 263:689-692(1999).
RN [8]
RP FUNCTION: MAY HAVE A ROLE IN MAINTAINING THE INTEGRITY OF THE
CC BLOOD VESSELS. HAS GROWTH PROMOTING ACTIVITY ON ENDOTHELIAL CELLS,
CC ANGIOGENIC ACTIVITY IN VIVO AND CHEMOTACTIC ACTIVITY ON
CC ENDOTHELIAL CELLS IN VITRO.
RN [9]
RP FUNCTION: CATALYZES THE REVERSIBLE PHOSPHORYLATION OF THYMIDINE.
CC THE PRODUCED MOLECULES ARE THEN UTILIZED AS CARBON AND ENERGY
CC SOURCES OR IN THE RESCUE OF PYRIMIDINE BASES FOR NUCLEOTIDE
CC SYNTHESIS.
RN [10]
RP CATALYTIC ACTIVITY: THYMIDINE + PHOSPHATE = THYMINES + 2-DEOXY-D-
CC RIBOSE 1-PHOSPHATE.
RN [11]
RP PATHWAY: NUCLEOTIDE AND DEOXYRIBONUCLEOTIDE CATABOLISM.
RN [12]
RP SUBUNIT: HOMODIMER.
RN [13]
RP DISEASE: DEFECTS IN EC9P1 ARE THE CAUSE OF MITOCHONDRIAL
CC NEUROGASTROINTESTINAL ENCEPHALOMYOPATHY (MNGIE) (ALSO KNOWN AS
CC MYONUROGASTROINTESTINAL ENCEPHALOMYOPATHY); AN AUTOSOMAL
CC RECESSIVE HUMAN DISEASE ASSOCIATED WITH MULTIPLE DELETIONS OF
CC SKELETAL MUSCLE MITOCHONDRIAL DNA (MTDNA). IT IS CLINICALLY
CC CHARACTERIZED BY ONSET BETWEEN THE SECOND AND FIFTH DECADES OF
CC LIFE, PTOSIS, PROGRESSIVE EXTERNAL OPHTHALMOPLAGIA,
CC GASTROINTESTINAL DYSMOTILITY (OFTEN PSEUDOBSTRUCTION), DIFFUSE

CC LEUCEPNEPHALOPATHY, THIN BODY HABITUS, PERIPHERAL NEUROPATHY, AND
CC MYOPATHY.
CC -1- SIMILARITY: BELONGS TO THE THYMIDINE/PYRIMIDINE-NUCLEOSIDE
CC PHOSPHORYLASES FAMILY.
CC -1- DATABASE: NAME-Rad Systems' cytokine source book;
CC WWW="http://www.rndsystems.com/cyt_cat/pdcegf.html".
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: M63193; AAA60043.1; -
CC EMBL: U62317; AAA03344.1; -
CC PIR: S03904; S03904.
CC MIM: 131222; -
CC MIM: 603041; -
CC DR InterPro: IPR000053; -
CC DR InterPro: IPR000312; -
CC Pfam: PF00591; Glycosyltransferase; Growth factor; Chemotaxis;
CC PROSITE: PS00647; THYMID_PHSOPHSORYLASE.1.
CC TRANSFERASE: Glycosyltransferase; Growth factor; Chemotaxis;
CC VASCULARIZATION; Repeat; Polymorphism; Disease mutation.
CC PROPEP 1 10
CC CHAIN 11 482
CC REPEAT 265 279
CC REPEAT 329 342
CC REPEAT 393 401
CC REPEAT 453 461
CC VARIANT 145 145
CC VARIANT 153 153
CC VARIANT 222 222
CC VARIANT 289 289
CC VARIANT 397 398
CC VARIANT 471 471
CC CONFLICT 444 444
CC CONFLICT 452 452
CC SEQUENCE 482 AA; 49981 MW; 0652FA132C3BDE28 CRC64;
Query Match 10.9%; Score 72; DB 1; Length 482;
Best Local Similarity 28.0%; Pred. No. 7.2; Matches 28; Conservative 11; Mismatches 33; Indels 28; Gaps 4;
QY 5 LTVVATCTGGLASPSVPTSLKELIELVNITONQASLQSGMWSVNLNAGYCA 64
DB 285 LEVEALLCMKG-AGP-----PDLRLVLT-----GGALWLSGHAGTQAG 326
QY 65 ALESILNVSQSAIORQRL-----KALCSKPA 94
DB 327 AARVAALDDGSLGRERMLAAGVDPGLRALCSGSPA 366
RESULT 10
ID RYNR_HUMAN STANDARD; PRT; 5032 AA.
AC P21817;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-MAY-1991 (Rel. 18, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE
DE CHANNEL).
GN RYR1 OR RYDR.
OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Skeletal muscle;
RX MEDLINE=90130482; PubMed=2298749;
RA Zorzato F., Fujii J., Otsu K., Phillips M., Green N.M., Lai F.A.,
RA Weissner G., MacLennan D.H.;
RT "Molecular cloning of cDNA encoding human and rabbit forms of the
RT Ca2+ release channel (ryanodine receptor) of skeletal muscle
RT sarcoplasmic reticulum.";
RL J. Biol. Chem. 265:2244-2256(1990).
RN [2]
RP VARIANT MH CYS-614.
RX MEDLINE=92128959; PubMed=1774074;
RA Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S.,
RA Derdemezi J., Britt B.A., Duff C.L., Worton R.G., MacLennan D.H.;
RT "A substitution of cysteine for arginine 614 in the ryanodine
RT receptor is potentially causative of human malignant hyperthermia.";
RL Genomics 11:731-755(1991).
RN [3]
RP VARIANT MH ARG-248, AND VARIANTS CYS-471; LEU-1786 AND CYS-2059.
RX MEDLINE=92372020; PubMed=1354642;
RA Gillard E.F., Otsu K., Fujii J., Duff C., de Leon S., Khanna V.K.,
RA Britt B.A., Worton R.G., MacLennan D.H.;
RT "Polymorphisms and deduced amino acid substitutions in the coding
RT sequence of the ryanodine receptor (RYR1) gene in individuals with
RT malignant hyperthermia.";
RL Genomics 13:1247-1254(1992).
RN [4]
RP VARIANT CCD HIS-2434.
RX MEDLINE=94035117; PubMed=8220422;
RA Zhang Y., Chen H.S., Khanna V.K., de Leon S., Phillips M.S.,
RA Schappert K., Britt B.A., Brownell A.K.W., MacLennan D.H.;
RT "A mutation in the human ryanodine receptor gene associated with
RT central core disease.";
RL Nat. Genet. 5:46-50(1993).
RN [5]
RP VARIANTS CCD CYS-163 AND MET-403.
RX MEDLINE=94035118; PubMed=8220423;
RA Quane K.A., Healy J.M.S., Keating K.E., Manning B.M., Couch F.J.,
RA Palmucci L.M., Doriguzzi C., Fagerlund T.H., Berg K., Ordling H.,
RA Bendixen D., Mortier W., Linz U., Muller C.R., McCarthy T.V.;
RT "Mutations in the ryanodine receptor gene in central core disease and
RT malignant hyperthermia.";
RL Nat. Genet. 5:51-55(1993).
RN [6]
RP VARIANT MH SER-522.
RX MEDLINE=95130087; PubMed=7829078;
RA Quane K.A., Keating K.E., Healy J.M.S., Manning B.M.,
RA Krivosic-Horber R., Krivosic I., Monnier N., Lunardi J.,
RA McCarthy T.V.;
RT "Mutation screening of the RYR1 gene in malignant hyperthermia:
RT detection of a novel Tyr to Ser mutation in a pedigree with
RT associated central cores.";
RL Genomics 23:236-239(1994).
RN [7]
RP VARIANT MH ARG-341.
RX MEDLINE=94282042; PubMed=8012359;
RA Quane K.A., Keating K.E., Manning B.M., Healy J.M.S., Monstieurs K.,
RA Heffron J.J.A., Lehane M., Heytons L., Krivosic-Horber R., Adnet P.,
RA Ellis F.R., Monnier N., Lunardi J., McCarthy T.V.;
RT "Detection of a novel common mutation in the ryanodine receptor gene
RT in malignant hyperthermia: implications for diagnosis and
RT heterogeneity studies.";
RL Hum. Mol. Genet. 3:471-476(1994).
RN [8]
RP VARIANT MH ARG-2433.
RX MEDLINE=95152512; PubMed=7849712;
RA Keating K.E., Quane K.A., Manning B.M., Lehane M., Hartung E.,
RA Censier K., Urwyler A., Klausnitzer M., Muller C.R., Heffron J.J.A.,
RA McCarthy T.V.;

RT "Detection of a novel RYR1 mutation in four malignant hyperthermia
RT pedigrees.";
RL Hum. Mol. Genet. 3:1855-1858(1994).
RN [9]
RP VARIANT MH ARG-2433.
RX MEDLINE=95187158; PubMed=7881417;
RA Phillips M.S., Khanna V.K., de Leon S., Prodis W., Britt B.A.,
RA McLennan D.H.;
RT "The substitution of Arg for Gly3433 in the human skeletal muscle
RT ryanodine receptor is associated with malignant hyperthermia.";
RL Hum. Mol. Genet. 3:2181-2186(1994).
RN [10]
RP VARIANT MH ARG-35.
RX MEDLINE=97219028; PubMed=9066328;
RA Lynch P.J., Krivosic-Horber R., Reyford H., Monnier N., Quane K.,
RA Adnet P., Haudecoeur G., Krivosic I., McCarthy T., Lunardi J.;
RT "Identification of heterozygous and homozygous individuals with the
RT novel RYR1 mutation Cys35Arg in a large kindred.";
RL Anesthesiology 86:620-626(1997).
RN [11]
RP VARIANT MH LEU-614.
RX MEDLINE=98051290; PubMed=9389851;
RA Quane K.A., Ordling H., Keating K.E., Manning B.M., Heine R.,
RA Bendixen D., Berg K., Krivosic-Horber R., Lehmann-Horn F.,
RA Fagerlund T., McCarthy T.V.;
RT "Detection of a novel mutation at amino acid position 614 in the
RT ryanodine receptor in malignant hyperthermia.";
RL Br. J. Anaesth. 79:332-337(1997).
RN [12]
RP VARIANT MH TRP-552.
RX MEDLINE=97284075; PubMed=9138151;
RA Keating K.E., Giblin L., Lynch P.J., Quane K.A., Lehane M.,
RA Heffron J.J.A., McCarthy T.V.;
RT "Detection of a novel mutation in the ryanodine receptor gene in an
RT Irish malignant hyperthermia pedigree: correlation of the IVCT
RT response with the affected and unaffected haplotypes.";
RL J. Med. Genet. 34:291-296(1997).
RN [13]
RP VARIANTS MH CYS-2162; HIS-2162; MET-2167 AND MET-2205.
RX MEDLINE=98163444; PubMed=9497245;
RA Manning B.M., Quane K.A., Ordling H., Urwyler A., Tegazzin V.,
RA Lehane M., O'Halloran J., Hartung E., Giblin L.M., Lynch P.J.,
RA Vaughan P., Censier K., Bendixen D., Comi G., Heytens L.,
RA Monstieurs K., Fagerlund T., Wolz W., Heffron J.J.A., Mueller C.R.,
RA McCarthy T.V.;
RT "Identification of novel mutations in the ryanodine-receptor gene
RT (RYR1) in malignant hyperthermia: genotype-phenotype correlation.";
RL Am. J. Hum. Genet. 62:599-609(1998).
RN [14]
RP VARIANTS MH CYS-2458 AND HIS-2458.
RX MEDLINE=98111378; PubMed=9450902;
RA Manning B.M., Quane K.A., Lynch P.J., Urwyler A., Tegazzin V.,
RA Krivosic-Horber R., Censier K., Comi G., Adnet P., Wolz W.,
RA Lunardi J., Muller C.R., McCarthy T.V.;
RT "Novel mutations at a CpG dinucleotide in the ryanodine receptor in
RT malignant hyperthermia.";
RL Hum. Mutat. 11:45-50(1998).
RN [15]
RP VARIANTS MH
RX MEDLINE=99415746; PubMed=10484775;
RA Brandt A., Schleithoff L., Jurkat-Rott K., Klingler W., Baur C.,
RA Lehmann-Horn F.;
RT "Screening of the ryanodine receptor gene in 105 malignant
RT hyperthermia families: novel mutations and concordance with the in
RT vitro contracture test.";
RL Hum. Mol. Genet. 8:2055-2062(1999).
RN [16]
RP VARIANTS MH LEU-2434 AND HIS-2453.
RX MEDLINE=99158296; PubMed=10051009;
RA Barone V., Massa O., Intravala E., Bracco A., Di Martino A.,
RA Tegazzin V., Cozzolino S., Sorrentino V.;
RT "Mutation screening of the RYR1 gene and identification of two novel
RT mutations in Italian malignant hyperthermia families.";

RL J. Med. Genet. 36:115-118(1999).
 RN [17]
 RP VARIANTS MH CYS-2453.
 RA MEDLINE-20081079; PubMed-10612851.
 RX Gencik M., Gencik A., Mortier W., Epplen J.T.;
 RT "Novel mutation in the RYR1 gene (R2454C) in a patient with malignant
 hyperthermia";
 RL Hum. Mutat. 15:122-124(2000).
 CC -1- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
 CC SARCOPASMIC RETICULUM. CONTRACTION OF SKELETAL MUSCLE IS
 CC TRIGGERED BY RELEASE OF CA⁺⁺ FROM SR FOLLOWING DEPOLARIZATION OF
 CC T-TUBULES.
 CC -1- SUBUNIT: HOMOTETRAMER (POTENTIAL).
 CC -1- DISEASE: A DEFICIENCY IN THE RYANODINE RECEPTOR MAY BE THE CAUSE
 CC OF MALIGNANT HYPERTHERMIA (MH) AND OF CENTRAL CORE DISEASE OF
 CC MUSCLE (CCD). MH IS AN AUTOSOMAL DOMINANT DISORDER OF SKELETAL
 CC MUSCLE AND IS ONE OF THE MAIN CAUSES OF DEATH DUE TO ANESTHESIA.
 CC IN SUSCEPTIBLE PEOPLE, AN MH EPISODE CAN BE TRIGGERED BY ALL
 CC COMMONLY USED INHALATIONAL ANESTHETICS SUCH AS HALOTHANE AND BY
 CC DEPOLARIZING MUSCLE RELAXANTS SUCH AS SUCCINYLCHOLINE. THE
 CC CLINICAL FEATURES OF THE MYOPATHY ARE HYPERTHERMIA, ACCELERATED
 CC MUSCLE METABOLISM, CONTRACTURES, METABOLIC ACIDOSIS, TACHYCARDIA
 CC AND DEATH, IF NOT TREATED WITH THE POSTSYNAPTIC MUSCLE RELAXANT,
 CC DANTROLENE. SUSCEPTIBILITY TO MH CAN BE DETERMINED WITH THE "IN
 CC VITRO" CONTRACTURE TEST (IVCT): OBSERVING THE MAGNITUDE OF
 CC CONTRACTURES INDUCED IN STRIPS OF MUSCLE TISSUE BY CAFFEINE ALONE
 CC AND HALOTHANE ALONE. PATIENTS WITH NORMAL RESPONSE ARE MH NORMAL
 CC (MNH), THOSE WITH ABNORMAL RESPONSE TO CAFFEINE ALONE OR HALOTHANE
 CC (ALONE) ARE MH EQUIVOCAL (MHE(C) AND MHE(H) RESPECTIVELY).
 CC -1- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL IS MODULATED BY CA⁺⁺,
 CC MG⁺⁺, ATP, AND CALMODULIN.
 CC -1- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE
 CC C-TERMINAL REGION WHILE THE REMAINING PART OF THE PROTEIN
 CC CONSTITUTES THE 'FOOT' STRUCTURE SPANNING THE JUNCTIONAL GAP
 CC BETWEEN THE SR AND THE T-TUBULE. IT IS POSSIBLE THAT THE FOOT
 CC STRUCTURE INTERACTS WITH THE CYTOPLASMIC REGION OF THE
 CC DIHYDROPYRIDINE RECEPTOR.
 CC -1- MISCELLANEOUS: RYANODINE IS AN ALKALOID THAT BINDS TO THE
 CC CA-RELEASE CHANNEL IN JUNCTIONAL SR AND MODULATES ITS ACTIVITY.
 CC -1- SIMILARITY: LOCAL & LOW WITH THE NICOTINIC ACETYLCHOLINE RECEPTOR
 CC (N-ACHR) SUBUNITS.
 CC -1- THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use.

Query Match 10.9%; Score 72; DB 1; Length 5032;
 Best Local Similarity 21.1%; Pred. No. 1;le+02;
 Matches 26; Conservative 26; Mismatches 43; Indels 28; Gaps 4;

OY 29 LKELIEELVNTQNASLCSGSMVSVN-----LTAGMYCALES--LINVSDCS 76
 DB 521 LYEELASLIRGNRSNCALFSTLMDLVSLDRLEASSGILEVLCVLSPEVLIQEN 580
 OY 77 AIO-----RQRMKALCSOKPAAGISSERSRDTKIE-----VIQVKNLLTV 120
 DB 581 HIKSIISLDKRGKRNKVLVLYSLCVCNGAVAVRSNODILENTLPGRELLQTLNINV 640
 OY 121 RGV 123
 DB 641 TSI 643

RESULT 11
 SPRE_HUMAN
 ID SPRE_HUMAN STANDARD: PRT; 261 AA.
 AC P35270;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
 GN SPR.
 OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
 OX NCBI_TaxId=9606;
 RX SEQUENCE FROM N.A.
 RP TISSUE=Liver;
 RC MEDLINE-91354248; PubMed-1883349;
 RA Ichinose H., Katoh S., Sueoka T., Titani K., Fujita K., Nagatsu T.;
 RT "Cloning and sequencing of cDNA encoding human sepiapterin
 RT reductase -- an enzyme involved in tetrahydrobiopterin biosynthesis";
 RL Biochem. Biophys. Res. Commun. 179:183-189(1991).
 CC -1- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
 CC HYDROBIOPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOPTERIN.
 CC -1- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOPTERIN + NADP(+) = SEPIAPTERIN +
 CC NADPH.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- DISEASE: DECREASED SYNTHESIS OF TETRAHYDROBIOPTERIN MAY PLAY A
 CC ROLE IN A VARIETY OF HUMAN DISEASES.

 CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 DR EMBL: M76231; AAA60314.1; -
 DR PIR: J01176; J01176.
 DR MIM: 182125; -
 DR InterPro: IPR002198; -
 DR Pfam: PF00106; adh_short; 1.
 DR KX Oxidoreductase; NADP; Acetylation.
 FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 FT NP_BIND 13 39 NADP (BY SIMILARITY).
 FT FT DOMAIN 28 32 PTERIN BINDING (POTENTIAL).
 FT SEQUENCE 261 AA; 28048 MW; 9C9BF76212826F47 CRC64;

Query Match 10.9%; Score 71.5; DB 1; Length 261;
 Best Local Similarity 24.7%; Pred. No. 4;
 Matches 24; Conservative 21; Mismatches 41; Indels 11; Gaps 4;

OY 36 LVNITQNASLCSGSMVSVN-----WSVNTAGMYCALES--LINVSDCSAIGRTQRMKALCSOK 92
 DB 104 LGSVSGFVLDSDSTQVNNWMLNITS-MCLTSSVYAKAPDPBGRNRYVNISSLCALQ 162
 OY 93 PAAG-----ISSERSRDTKIEVQVLR--NLTVYRG 122
 DB 163 PFKGMALYCAGKAARDMLFQVLALEBNVAVLVYAPG 199

RESULT 12
 YAB8_SCHPO
 ID YAB8_SCHPO STANDARD: PRT; 481 AA.
 AC Q09775;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE PUTATIVE ATP-DEPENDENT RNA HELICASE C22F3.08C.
 GN SPAC22F3.08C.
 OS Schizosaccharomyces pombe (Fission yeast).
 OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 OC Schizosaccharomycetes.
 OX NCBI_TaxId=4896;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=972;
 RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: PUTATIVE ATP-DEPENDENT RNA HELICASE.

```
CC -!- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; 254285; CAA91073.1; -
DR InterPro; IPR000629; -
DR InterPro; IPR001410; -
DR InterPro; IPR001650; -
DR Pfam; PF00270; DEAD; 1.
DR Pfam; PF00271; helicase_C; 1.
DR PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
KW Hypothetical protein; ATP-binding; RNA-binding; Helicase.
FT NP_BIND 90 97 ATP (POTENTIAL).
FT SITE 196 199 DEAD BOX.
SQ SEQUENCE 481 AA; 54026 MW; 872CAFC106E110A CRC64;

Query Match 10.9%; Score 71.5; DB 1; Length 481;
Best Local Similarity 24.3%; Pred. No. 8.1;
Matches 25; Conservative 25; Mismatches 48; Indels 5; Gaps 4;

QY 25 PSPTLKL-IEELVNITONQASLNGSVSV-NLTAGMYCAALESINSDCSAIQRTQ 82
DB 18 PQSIKEKEAKKLGITKGAQVGNPDIEEPGILCENLKKQ-NITECTIQ-- 74
QY 83 RMLKALCSQKPAAGISSERSRDTKIEVIQLVKNLLTYVRGVYR 125
DB 75 YAIPTIGSKRDLLACAPTGSCKTAYLFPILQKLQHPGGYR 117

RESULT 13
HIT_MACMU
ID HIT_MACMU STANDARD; PRT; 207 AA.
AC P40286;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE HISTONE H1T.
GN H1T OR H1T.
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94230585; PubMed=8175896;
RA Koppel D.A., Wolfe S.A., Fogelfield L., Grimes S.R.;
RT "Primate testicular histone H1 genes are highly conserved and the
RT human H1 gene is located on chromosome 6.";
RL J. Cell. Biochem. 54:219-230(1994).
CC -!- FUNCTION: HISTONES H1 ARE NECESSARY FOR THE CONDENSATION OF
CC NUCLEOSOME CHAINS INTO HIGHER ORDER STRUCTURES.
CC -!- SUBCELLULAR LOCATION: NUCLEAR.
CC -!- DEVELOPMENTAL STAGE: THIS HISTONE IS A TESTIS-SPECIFIC H1 VARIANT
CC THAT APPEARS DURING MEIOSIS IN SPERMATOGENESIS.
CC -!- SIMILARITY: BELONGS TO THE HISTONE H1/H5 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; M97756; AAA19937.1; -
```

```
DR HSP; P08287; IGHC.
DR InterPro; IPR001386; -
DR Pfam; PF00538; linker_histone; 1.
KW Chromosomal protein; Nuclear protein; DNA-binding; Multigene family;
KW Acetylation; Spermatogenesis; Testis.
FT INIT_MET 0 0 BY SIMILARITY.
FT MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
FT DOMAIN 39 112 GLOBULAR.
SQ SEQUENCE 207 AA; 21962 MW; 8812112C83727705 CRC64;

Query Match 10.7%; Score 70.5; DB 1; Length 207;
Best Local Similarity 25.6%; Pred. No. 3.8;
Matches 30; Conservative 17; Mismatches 31; Indels 39; Gaps 5;

QY 16 GLSPSPVTPSPTLKELIEELVNITONQASLNGSVSVNLTAGMYCAALESINSDC 75
DB 30 GLTSASRKAPNLVSKLITAEALSVQER-----VGMSLAALK----- 66
QY 76 SAIQRTQRLKALCSQKPAAGISSERSRD-TKIEVIQLV-KNLLTYVRGVYRHGNER 130
DB 67 -----KALA---AAGYDVEKNNSRIKLSKSLVKNKGLVQTRGTGASGESEK 109

RESULT 14
VR2A_BPT4
ID VR2A_BPT4 STANDARD; PRT; 725 AA.
AC P03690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RIIA PROTEIN.
GN RIIA.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
OC T4-like phages.
OX NCBI_TaxID=10665;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90337270; PubMed=2379817;
RA Daegelen P., Brody E.;
RT "The RIIA gene of bacteriophage T4. I. Its DNA sequence and discovery
RT of a new open reading frame between genes 60 and RIIA.";
RL Genetics 125:237-248(1990).
RN [2]
RP SEQUENCE OF 476-725 FROM N.A.
RX MEDLINE=84267841; PubMed=6748077;
RA Sugino A., Drake J.W.;
RT "Modulation of mutation rates in bacteriophage T4 by a base-pair
RT change a dozen nucleotides removed.";
RL J. Mol. Biol. 176:239-249(1984).
RN [3]
RP SEQUENCE OF 587-725 FROM N.A.
RX MEDLINE=82078066; PubMed=6273585;
RA Pribnow D., Sigurdson D.C., Gold L., Singer B.S., Napoli C.,
RA Brosius J., Dull T.J., Noller H.F.;
RT "rII cistrons of bacteriophage T4. DNA sequence around the
RT intercalon divide and positions of genetic landmarks.";
RL J. Mol. Biol. 149:337-376(1981).
CC -!- FUNCTION: TRANSCRIBED PRIOR TO REPLICATION. THIS PROTEIN FORM
CC PARTS OF THE REPLICATION COMPLEX AND HAS DNA-BINDING PROPERTIES.
CC -!- SUBCELLULAR LOCATION: ON THE INNER MEMBRANE OF THE HOST SHORTLY
CC AFTER INFECTION.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X52686; CAA36911.1; -
```


Result No.	Score	Query		Length	DB	ID	Description
		Match	%				
1	647.5	98.4	131	6	Q9N0W9	Q9n0w9	canis famill
2	383	58.2	114	6	Q9TV84	Q9tv84	bos taurus
3	157.5	23.9	49	4	Q9UDC7	Q9udc7	homo sapien
4	82.5	12.5	275	6	Q28609	Q28609	oryctolagus
	79	12.0	1183	4	Q94918	Q94918	homo sapien
5	79	12.0	1230	4	Q9P0H7	Q9p0h7	homo sapien
6	79	12.0	1230	11	P97536	p97536	rattus norv
7	79	12.0	1230	11	P97536	p97536	rattus norv
8	78.5	11.9	1448	5	Q9N949	Q9n949	trypanosoma
9	76.5	11.6	1448	5	Q9N946	Q9n946	trypanosoma
10	74	11.2	336	10	Q9SM4	Q9sm4	lycopersico
11	73.5	11.2	415	8	Q9MUM4	Q9mum4	mesostigma
12	73.5	11.2	607	10	Q9S143	Q9si143	arabidopsis
13	73.5	11.2	649	14	O10619	O10619	helicoverpa
14	73.5	11.2	1806	5	O45657	O45657	caenorhabdi
15	72.5	11.0	150	14	Q98779	Q98779	vesicular s
16	72.5	11.0	438	10	Q9MJH8	Q9mjh8	cicer ariet
17	72.5	11.0	1763	11	Q9JKX5	Q9jkk5	mus musculu
18	72	10.9	5038	4	Q9NPX1	Q9npk1	homo sapien
19	71.5	10.9	150	14	Q98791	Q98791	vesicular s

AC 09TV84:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (FRAGMENT).
GN IL-13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.T., Hirano A., Brown W.:
RT "Biological activities of interleukin-13 (IL-13) on bovine
RT lymphocytes: Implications for signaling through IL-13R α 1.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF072807; AAD22748.1; -
DR HSSP: P35225; 31TR.
DR INTERPRO: IPR001325; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; UNKNOWN_1.
FT NON_TER 114
SQ SEQUENCE 114 AA; 12355 MW; D8C56E5627D030A CRC64;

Query Match 58.2%; Score 383; DB 6; Length 114;
Best Local Similarity 70.8%; Pred. No. 1.4e-32;
Matches 80; Conservative 10; Mismatches 21; Indels 2; Gaps 2;

OY 1 MALMTVIALTCLGLASPPVPTSPPTKLEIEELVNITQNO-ASLCSNWSVNLTA 59
Db 1 MALMTVIALTCLGLASPPVPTSPPTKLEIEELVNITQNO-KVPLCGSNWSVNLTS 60
OY 60 GWYCAALBSLNVSDCSAIOQTQRMKALCSQPA-A-GISSESRDPTKEIVQ 111
Db 61 SMYCAALBSLISNCSVIOQTQRMKALCPKPKSAKVSSSEYVROTKLEVAQ 113

RESULT 3
Q9UDC7 PRELIMINARY; PRT; 49 AA.
AC 09UDC7:
DT 01-MAY-2000 (TRENBLREL. 13, Created)
DT 01-MAY-2000 (TRENBLREL. 13, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE P600 HOMOLOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93027259; Pubmed=1408833;
RT Morgan J.G., Dolgoy G.M., Robbins S.E., Hinton L.M., Lovett M.:
RT "The selective isolation of novel cDNAs encoded by the regions
RT surrounding the human interleukin 4 and 5 genes.";
RL Nucleic Acids Res. 20:5173-5179(1992).
DR HSSP: P35225; 31TR.
SQ SEQUENCE 49 AA; 5109 MW; 679CD23A190C778E CRC64;

Query Match 23.9%; Score 157.5; DB 4; Length 49;
Best Local Similarity 71.4%; Pred. No. 1.9e-09;
Matches 35; Conservative 1; Mismatches 12; Indels 1; Gaps 1;

OY 1 MALMTVIALTCLGLASPPVPTSPPTKLEIEELVNITQNO-ASLCLN 48
Db 1 MALMTVIALTCLGLASPPVPTSPPTKLEIEELVNITQNO-KAPLCN 49

RESULT 4
Q28609 PRELIMINARY; PRT; 275 AA.
ID Q28609

AC 028609:
DT 01-NOV-1996 (TRENBLREL. 01, Created)
DT 01-NOV-1996 (TRENBLREL. 01, Last sequence update)
DT 01-OCT-2000 (TRENBLREL. 15, Last annotation update)
DE PUTATIVE PREPROSPERMINGEN PRECURSOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NEW ZEALAND WHITE; TISSUE=TESTIS;
RX MEDLINE=94368861; Pubmed=8086468;
RA Richardson R.T., O'Rand M.G.:
RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
RT preproacrosin-related cDNA.";
RL Biochim. Biophys. Acta 1219:215-218(1994).
DR EMBL: U05203; AAA61629.1; -
DR HSSP: P00734; 2HNT.
DR INTERPRO: IPR001254; -
DR PFAM: PF00089; trypsin_1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW SIGNAL.
FT CHAIN 17 16 POTENTIAL.
FT SIGNAL 17 275 PROSPERMINGEN.
SQ SEQUENCE 275 AA; 29965 MW; 8FC2467414069C61 CRC64;

Query Match 12.5%; Score 82.5; DB 6; Length 275;
Best Local Similarity 30.0%; Pred. No. 0.88;
Matches 24; Conservative 12; Mismatches 35; Indels 9; Gaps 3;

OY 10 ALTCL---GGLASPPVPTSPPTKLEIEELVNITQNOASLCSNWSVNLTA 66
Db 172 AGCYVYAGMGVYENAPRSPPTLMEARVDLNL-----ELCSNWSVNLTA 226
OY 67 ESLNVSDCSAIOQTQRMK 86
Db 227 PS-GKIDTCQRLQOOLVEVLK 245

RESULT 5
O94918 PRELIMINARY; PRT; 1183 AA.
AC 094918:
DT 01-MAY-1999 (TRENBLREL. 10, Created)
DT 01-MAY-1999 (TRENBLREL. 10, Last sequence update)
DT 01-MAY-2000 (TRENBLREL. 13, Last annotation update)
DE KIA0829 PROTEIN (FRAGMENT).
GN KIA0829.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE=BRIN;
RX MEDLINE=99156230; Pubmed=10048485;
RA Nagase T., Ishikawa K., Suyama M., Kikuno R., Hirosewa M.,
RA Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.:
RT "Prediction of the coding sequences of unidentified human genes. XII.
RT The complete sequences of 100 new cDNA clones from brain which code
RT for large proteins in vitro.";
RL DNA Res. 5:355-364(1998).
DR EMBL: AB020636; BAA74852.1; -
DR NON_TER 1
SQ SEQUENCE 1183 AA; 130962 MW; 1FE0E56C0DFEE3A CRC64;

Query Match 12.0%; Score 79; DB 4; Length 1183;
Best Local Similarity 31.2%; Pred. No. 11;
Matches 39; Conservative 19; Mismatches 51; Indels 16; Gaps 5;


```

OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TRU927;
RA Hall N., Bowman S., Quail M., Ivens A.C., Ray M.P., Bray-Allen S.,
RA Lennard N.J., Clark L.N., Harris B.R., Melville S., Lawson D.,
RA Gerrard C., Rajadream M.A., Barrell B.G.;
RL Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL359782; CAB95333.1; -
SQ SEQUENCE 1448 AA; 160479 MW; 688B26228AD2046B CRC64;

Query Match 11.6%; Score 76.5; DB 5; Length 1448;
Best Local Similarity 29.3%; Pred. No. 24;
Matches 36; Conservative 18; Mismatches 34; Indels 35; Gaps 7;

QY 13 CLGLASPSPTPLKELIELNITQNONA--SLCNGSMWVSVL-----TAGMYCA 64
DB 557 CLGNN-----POLKMLDISGNT-DNESLRSLCSQTVASLNLSHCKMKNVSHIS 606
QY 65 ALESL-INVSPD-----SAIORTQMLKALCSQKPAAGISSERSRPTKIEVIQLVKN 115
DB 607 SLEANEELNSCIRINMGWEAIEKLOLVNAI-----LSNHTITRDISHSKCKN 658
QY 116 LVT 118
DB 659 LVT 661

RESULT 10
Q9SMD4 PRELIMINARY; PRT; 336 AA.
AC Q9SMD4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBLrel. 14, Last annotation update)
DE CYCD3.3 PROTEIN.
GN CYCD3.3.
OS Lycopersicon esculentum (Tomato).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I;
OC Solanales; Solanaceae; Solanum.
OX NCBI_TaxID=4081;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_U082B;
RA Kvarnheden A., Yao J.L., O'Brien I., Morris B.;
RT "Differential expression of three D3 cyclin genes during tomato fruit
RT set and development."
RL Submitted (NOV-1997) to the EMBL/Genbank/DBJ databases.
DR EMBL; AJ002590; CAB60838.1; -
DR INTERPRO: IPR000553; -
DR PRAM: PF00134; cyclin; 1.
SQ SEQUENCE 336 AA; 38687 MW; 58B8B6DD0852031 CRC64;

Query Match 11.2%; Score 74; DB 10; Length 336;
Best Local Similarity 23.9%; Pred. No. 8.5;
Matches 37; Conservative 24; Mismatches 54; Indels 40; Gaps 9;

QY 4 WLTVIALTCLGLASPPVTPSPPLKEL-IEEL-----VNTTONQASLCNGSMWVSVN- 56
DB 125 WMNLVAATCL-SLAAKEEDTDPVPLLDLQVESESGFLPESKTIQNMEMILSTLKKKNMP 183
QY 57 -----TAGM--YCAALE-----SLINVS-----CSAIORTQMLKALCS 90
DB 184 VTPESLDFITRRRLGLKHLCLSLFLRCEKVLTYTTDRFGILPSMAASATMHLVHDR 243
QY 91 QKPAAGISSERSRPTKIEVIQLVKNLLTYVGRVYR 125
DB 244 EKPCIG---EKYDOLLGILTIKVE--KVEGCYR 272

```

```

RESULT 11
Q9MUM4 PRELIMINARY; PRT; 415 AA.
AC Q9MUM4;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PUTATIVE PLASTID DIVISION PROTEIN.
GN FTSM.
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendrales; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Olis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
RT branch of green plant evolution."
RL Nature 403:649-652(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lemieux C., Olis C., Turmel M.;
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF166114; AAF43874.1; -
KW Chloroplast.
SQ SEQUENCE 415 AA; 46813 MW; E35116E9692EC782 CRC64;

Query Match 11.2%; Score 73.5; DB 8; Length 415;
Best Local Similarity 28.7%; Pred. No. 12;
Matches 27; Conservative 19; Mismatches 29; Indels 19; Gaps 4;

QY 36 LVNITONQSLCNGSMWVSVNLTAGMYCALESILNVSQSAI-----QRTQRMKAL 88
DB 188 LIOPNLSTASLC-GAIIWALTAGIHWFIINLSIGAVTALISLSOEYQRRIISFL 246
QY 89 CSQKPAAGISSERSRPTKIEVIQLVKNLLTYVGR 122
DB 247 ---NPMANPTSG-----YQLVOSLLAVGSG 269

RESULT 12
Q9S143 PRELIMINARY; PRT; 607 AA.
AC Q9S143;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PUTATIVE METHYLMALONATE SEMI-ALDEHYDE DEHYDROGENASE.
GN AT2G14170.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV_COLUMBIA;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
RA Buehl C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhagen G.P., Preuss D., Niernm W.C., White O., Elsen J.A.,
RA Salberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana."
RL Nature 402:761-768(1999).
DR EMBL; AC007197; AAD25855.1; -
DR HSP; P56533; TAAS.

```

```
DR INTERPRO: IPR001064; -
DR INTERPRO: IPR002086; -
DR PFAM: PF00171; aldedh.1.
DR PROSITE: PS00070; ALDHYDE_DHYPD_CYS; UNKNOWN1.
DR PROSITE: PS00225; CRYSTALLIN_BETAGAMMA; UNKNOWN1.
SQ SEQUENCE 607 AA; 65926 MW; 0257A3606B31165C CRC64;

Query Match 11.2%; Score 73.5; DB 10; Length 607;
Best Local Similarity 26.4%; Pred. No. 19;
Matches 23; Conservative 16; Mismatches 31; Indels 17; Gaps 4;

QY 59 AGMYCAALESINVSQCSA-----IQTQMLKALCSQKPAAGISSERSRDTKIEVLQV 113
DB 387 AGORCMALSTVVFVGDGAKSWEDKLVERA-KALKVTCGSEPDADLGPVTSQAKERICRLI 445
QY 114 KN-----LLTVRVGV-----YRHGNF 129
DB 446 QSGVDDGAKLLLDGRDIVVPGYEKGNF 472

RESULT 13
ID O10619 PRELIMINARY; PRT; 649 AA.
AC O10619; Q82480;
DT 01-JUL-1997 (TrEMBLrel. 04, Created)
DT 01-JUL-1997 (TrEMBLrel. 04, Last sequence update)
DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
DE IMMEDIATE EARLY PROTEIN 1.
GN IE1.
OS Helicoverpa zea nuclear polyhedrosis virus.
OC Viruses; GSDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OC NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ELKAR;
RX MEDLINE=95053907; PubMed=7964631;
RA Cowan P., Bulach D., Goode K., Robertson A., Tribe D.E.;
RT "Nucleotide sequence of the polyhedrin gene region of Helicoverpa zea
RT single nucleocapsid nuclear polyhedrosis virus: placement of the virus
RT in lepidopteran nuclear polyhedrosis virus group II."
RL J. Gen. Virol. 75:3211-3218(1994).
RN [2]
RP REVISIONS.
RC STRAIN=ELKAR (ELCAR);
RA Le T.H., Wu T., Robertson A., Bulach D., Cowan P., Goode K.,
RA Tribe D.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL; U67264; AAB54100.1; -
SQ SEQUENCE 649 AA; 75522 MW; B0D133AC9FEBD0E4 CRC64;

Query Match 11.2%; Score 73.5; DB 14; Length 649;
Best Local Similarity 25.5%; Pred. No. 20;
Matches 26; Conservative 18; Mismatches 35; Indels 23; Gaps 3;

QY 19 SPSPVTP-----SPTKELTEELVNITQNASLCSGSMVWSVNLTAGMYCAALESLIN-- 71
DB 102 SPQITPRSRSENVSLESPESLSLKQVTVSLRRGS-----GLYGNKIQNLKENY 152
QY 72 -----VSDCSAIQTQMLKALCSQKPAAGISSERSRDTK 106
DB 153 EKTMDPYESDSSSLELTPPKPKRSNTTEKKIAGVGEKRSKKEK 194

RESULT 14
ID O45657 PRELIMINARY; PRT; 1806 AA.
AC O45657;
DT 01-JUN-1998 (TrEMBLrel. 06, Created)
DT 01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
```

```
DE K04B12.1 PROTEIN.
GN K04B12.1.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RA Steward C.;
RL Submitted (DEC-1996) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=94150718; PubMed=7906398;
RA Wilson R., Alnsough R., Anderson K., Baynes C., Berks M.,
RA Bonfield J., Burton J., Connell M., Copsey T., Cooper J., Coulson A.,
RA Craxton M., Dear S., Du Z., Durbin R., Favello A., Fulton L.,
RA Gardner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,
RA Lighthouse J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smaildon N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Thierry-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterston R.,
RA Watson A., Weinstock L., Wilkison-Sproat J., Wohlman P.;
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans."
RL Nature 368:32-38(1994).
DR EMBL; Z83232; CAB05755.1; -
DR INTERPRO: IPR002165; -
DR INTERPRO: IPR002909; -
DR PFAM: PF01437; Plectin_repeat; 3.
DR PFAM: PF01833; TIG; 3.
SQ SEQUENCE 1806 AA; 200429 MW; DB2F3085B6BB28AD CRC64;

Query Match 11.2%; Score 73.5; DB 5; Length 1806;
Best Local Similarity 25.7%; Pred. No. 64;
Matches 35; Conservative 24; Mismatches 50; Indels 27; Gaps 7;

QY 2 ALMLTVIALTCGLGASPVPVTPSPPTLKELTEELVNITQNASL-----CNGSMVWS 54
DB 575 ANWTTT-----CVSCPSEIFTPNTEFEL-LTSTISNNPISRHNFVYDCSGYGTCS 625
QY 55 VNLTAGMYCAALESINVS-CAIQTQMLKALCSQKPAAGISSERSRDTKIEVLQV 113
DB 626 SCMSSEYNCAMCSGLHKCSNCGALEKSKACVKIQMRLPIA-IGSQ-----EIVLEA 678
QY 114 KNLITYVGVYRHGNF 129
DB 679 SNLDTLDR---RHEHF 691

RESULT 15
QY8779 PRELIMINARY; PRT; 150 AA.
AC QY8779;
DT 01-FEB-1997 (TrEMBLrel. 02, Created)
DT 01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
DT 01-MAY-2000 (TrEMBLrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0888CRB;
RX MEDLINE=97075113; PubMed=8917539;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the
RT evolution of vesicular stomatitis virus."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL; U39211; AAB50939.1; -
DR INTERPRO: IPR000224; -
```


GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:47:36 ; Search time 79.9 Seconds
(without alignments)
78.698 Million cell updates/sec

Title: US-09-451-527-105

Perfect score: 556

Sequence: 1 SPVTPSPTLKELIELVNIT.....QLVKNLLTYRGVYRHGNGFR 110

Scoring table:

BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 390729 seqs, 57163235 residues

Total number of hits satisfying chosen parameters: 390729

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

- A_Geneseq_0401.*
- 1: /cgnl_8/gcgdata/geneseq/geneseq/AA1980.DAT.*
 - 2: /cgnl_8/gcgdata/geneseq/geneseq/AA1981.DAT.*
 - 3: /cgnl_8/gcgdata/geneseq/geneseq/AA1982.DAT.*
 - 4: /cgnl_8/gcgdata/geneseq/geneseq/AA1983.DAT.*
 - 5: /cgnl_8/gcgdata/geneseq/geneseq/AA1984.DAT.*
 - 6: /cgnl_8/gcgdata/geneseq/geneseq/AA1985.DAT.*
 - 7: /cgnl_8/gcgdata/geneseq/geneseq/AA1986.DAT.*
 - 8: /cgnl_8/gcgdata/geneseq/geneseq/AA1987.DAT.*
 - 9: /cgnl_8/gcgdata/geneseq/geneseq/AA1988.DAT.*
 - 10: /cgnl_8/gcgdata/geneseq/geneseq/AA1989.DAT.*
 - 11: /cgnl_8/gcgdata/geneseq/geneseq/AA1990.DAT.*
 - 12: /cgnl_8/gcgdata/geneseq/geneseq/AA1991.DAT.*
 - 13: /cgnl_8/gcgdata/geneseq/geneseq/AA1992.DAT.*
 - 14: /cgnl_8/gcgdata/geneseq/geneseq/AA1993.DAT.*
 - 15: /cgnl_8/gcgdata/geneseq/geneseq/AA1994.DAT.*
 - 16: /cgnl_8/gcgdata/geneseq/geneseq/AA1995.DAT.*
 - 17: /cgnl_8/gcgdata/geneseq/geneseq/AA1996.DAT.*
 - 18: /cgnl_8/gcgdata/geneseq/geneseq/AA1997.DAT.*
 - 19: /cgnl_8/gcgdata/geneseq/geneseq/AA1998.DAT.*
 - 20: /cgnl_8/gcgdata/geneseq/geneseq/AA1999.DAT.*
 - 21: /cgnl_8/gcgdata/geneseq/geneseq/AA2000.DAT.*
 - 22: /cgnl_8/gcgdata/geneseq/geneseq/AA2001.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	556	100.0	110	Y58224	Canine mature inte
2	556	100.0	130	Y58223	Canine interleukin
3	545.5	98.1	111	Y58222	Canine mature inte
4	545.5	98.1	131	Y58221	Canine interleukin
5	377.5	67.9	111	R2794	Human interleukin-
6	367	66.0	112	R27347	protein with cytot
7	367	66.0	112	R92793	Human interleukin-
8	367	66.0	132	R48624	Sequence of human
9	360	64.7	112	R27346	Protein with cytot
10	360	64.7	146	R27348	Cytokine NC30. R
11	302	54.3	131	R48625	Sequence of mouse

12	299	53.8	111	17	R92795	Murine p600. Mus
13	75	13.5	634	20	R21548	Human heparin-bind
14	72	12.9	5072	12	R11510	Ryanodine receptor
15	70	12.6	330	21	G06262	Arabidopsis thalia
16	70	12.6	407	21	G06261	Arabidopsis thalia
17	69	12.4	286	21	Y58998	Wheat sulfite redu
18	69	12.4	4987	12	R10834	Rianodin receptor.
19	67	12.1	21	20	Y49702	Human interleukin
20	67	12.1	673	21	Y58996	Rice sulfite reduc
21	65	11.7	197	21	G31561	Arabidopsis thalia
22	65	11.7	213	21	G31560	Arabidopsis thalia
23	65	11.7	300	21	G31559	Arabidopsis thalia
24	65	11.7	514	21	G55503	Arabidopsis thalia
25	65	11.7	602	21	G55502	Arabidopsis thalia
26	65	11.7	620	21	G55501	Arabidopsis thalia
27	65	11.7	1015	21	G41796	Arabidopsis thalia
28	65	11.7	1074	21	G41795	Arabidopsis thalia
29	65	11.7	1100	21	G41794	Arabidopsis thalia
30	65	11.7	5035	13	R25450	MH mutant porcine
31	64	11.5	383	13	R28947	Alcohol dehydrogen
32	64	11.5	383	18	W07698	Zymomonas mobilis
33	64	11.5	383	19	W80730	Z. mobilis alcohol
34	64	11.5	504	20	W93429	A. thaliana EL3 pr
35	64	11.5	1461	19	W64468	Human secreted pro
36	63.5	11.4	168	21	B35513	Baculovirus RNA ba
37	63.5	11.4	168	21	B32216	RNA baculovirus ph
38	63.5	11.4	621	20	Y21549	Porcine heparin-bi
39	63.5	11.4	2548	20	Y05781	Human myosin IXa.
40	62.5	11.2	150	16	R85457	Flax rust resistan
41	62.5	11.2	220	21	G06263	Arabidopsis thalia
42	62.5	11.2	401	21	G51250	Arabidopsis thalia
43	62.5	11.2	404	21	G51249	Arabidopsis thalia
44	62.5	11.2	534	21	B42909	Human ORFX ORF2673
45	62.5	11.2	570	21	Y51174	Human brain PARP2

ALIGNMENTS

RESULT 1

Y58224 Y58224 standard; Protein; 110 AA.

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

XX AC Y58224;

```
XX Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 110 AA:

Query Match 100.0%; Score 556; DB 21; Length 110;
Best Local Similarity 100.0%; Pred. No. 1.2e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPVTPSPFLKELIEELVNTQNOASLNGSMWSVNLTAGMYCAALESILNVSDCSAIOR 60
Db 1 spvtpspflkelleelvtlqngaslcnsgsmwsvnltagmycaalesilnvdscaiaqr 60
OY 61 TQRMKALCSQKPAAGISSERSRDTKIEVTLQVKNLLTYRGVYRHGNER 110
Db 61 tqrmkalcsgkpaagissersrdtkievltqvknlltyrgvyryhgnfr 110

RESULT 2
ID Y58223 standard; Protein; 130 AA.
XX
AC Y58223;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine interleukin-13 (IL-13) clone 78.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PE 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
XX
DR N-PSDB: 255561, 255562, 255563, 255564.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 3; Page 237; 264pp; English.
XX
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
```

```
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, their associated
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.
XX
SQ Sequence 130 AA:

Query Match 100.0%; Score 556; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 1.5e-61;
Matches 110; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SPVTPSPFLKELIEELVNTQNOASLNGSMWSVNLTAGMYCAALESILNVSDCSAIOR 60
Db 21 spvtpspflkelleelvtlqngaslcnsgsmwsvnltagmycaalesilnvdscaiaqr 80
OY 61 TQRMKALCSQKPAAGISSERSRDTKIEVTLQVKNLLTYRGVYRHGNER 110
Db 81 tqrmkalcsgkpaagissersrdtkievltqvknlltyrgvyryhgnfr 130

RESULT 3
ID Y58222 standard; Protein; 111 AA.
XX
AC Y58222;
XX
DT 14-MAR-2000 (first entry)
XX
DE Canine mature interleukin-13 (IL-13) clone 80.
XX
KW Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.
XX
OS Canis familiaris.
XX
PN WO9961618-A2.
XX
PD 02-DEC-1999.
XX
PE 28-MAY-1999; 99WO-US11942.
XX
PR 29-MAY-1998; 98US-0087306.
XX
PA (HESK-) HESKA CORP.
XX
PI Sim G, Yang S, Drelitz MJ, Wonderling RS;
XX
DR WPI: 2000-072623/06.
XX
DR N-PSDB: 255559, 255560.
XX
PT Nucleic acids encoding immunoregulatory proteins from cats or dogs,
XX useful for treating or preventing e.g. tumors or autoimmune disease
XX
PS Claim 3; Page 234; 264pp; English.
XX
CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
```

CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage
CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, and inhibitors may be used as
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.

XX Sequence 111 AA;

Query Match 98.1%; Score 545.5; DB 21; Length 111;
Best Local Similarity 99.1%; Pred. No. 2.5e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SPVTPPTLKELIEELVNITONQASLCNGSMVSVNLTAGMYCAALESINVSDCSAIOR 60
DB 1 SPVTPPTLKELIEELVNITONQASLCNGSMVSVNLTAGMYCAALESINVSDCSAIOR 60
QY 61 TQMLKALCSOKPAAG-ISSERSRDTKIEVIQVKNLLTYVRGVYRHGNFR 110
DB 61 TQMLKALCSOKPAAG-ISSERSRDTKIEVIQVKNLLTYVRGVYRHGNFR 111

RESULT 4

ID Y58221 standard; Protein; 131 AA.

XX Y58221;

DT 14-MAR-2000 (first entry)

DE Canine interleukin-13 (IL-13) clone 80.

XX Interleukin-13; IL-13; antibody; canine; inhibitor; immune response;
KW immunoregulation; tumour; cancer; autoimmune disease; vaccine.

XX Canis familiaris.

PN WO9961618-A2.

PD 02-DEC-1999.

XX 28-MAY-1999; 99WO-US11942.

PR 29-MAY-1998; 98US-0087306.

XX (HESK-) HESKA CORP.

PI Sim G, Yang S, Dreitz MJ, Wonderling RS;

XX WPI: 2000-072623/06.

DR N-PSDB; Z55555, Z55556, Z55557, Z55558.

XX Nucleic acids encoding immunoregulatory proteins from cats or dogs,
PT useful for treating or preventing e.g. tumors or autoimmune disease

XX Claim 31; Page 231; 264pp; English.

CC Sequences Y58221-Y58222 and Y58223-Y58224 represent encoded and mature
CC canine interleukin-13 (IL-13) clones 80 and 78. The invention relates to
CC canine IL-4, canine or feline Flt-3 ligand, canine or feline CD40,
CC canine or feline CD154 (CD40 ligand), canine IL-5, canine IL-13, feline
CC interferon-alpha (IFN-alpha) and feline granulocyte macrophage

CC colony-stimulating factor (GM-CSF), and nucleotides which encode these
CC immunoregulatory proteins. The proteins, and inhibitors may be used as
CC nucleic acids, specific antibodies and inhibitors may be used as
CC vaccines for therapeutic or prophylactic regulation of an immune
CC response in animals (particularly cats, dogs, horses and humans).
CC They may be used to treat autoimmune or infectious diseases including
CC allergies, tumours, inflammation and graft rejection, and to increase
CC the response from a co-administered antigen. The nucleotide sequences
CC can also be used for the recombinant production of a protein, while
CC nucleotide fragments are useful as probes, as amplification primers and
CC as sources of inhibitory therapeutics (e.g., antisense oligonucleotides).
CC The proteins may be used to raise antibodies and to screen for
CC modulators of activity, while the antibodies may be used in detection,
CC and in drug targeting.

XX Sequence 131 AA;

Query Match 98.1%; Score 545.5; DB 21; Length 131;
Best Local Similarity 99.1%; Pred. No. 3.2e-60;
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 SPVTPPTLKELIEELVNITONQASLCNGSMVSVNLTAGMYCAALESINVSDCSAIOR 60
DB 21 SPVTPPTLKELIEELVNITONQASLCNGSMVSVNLTAGMYCAALESINVSDCSAIOR 60
QY 61 TQMLKALCSOKPAAG-ISSERSRDTKIEVIQVKNLLTYVRGVYRHGNFR 110
DB 81 TQMLKALCSOKPAAG-ISSERSRDTKIEVIQVKNLLTYVRGVYRHGNFR 131

RESULT 5

ID R92794 standard; Protein; 111 AA.

XX R92794;

DT 24-MAY-1996 (first entry)

DE Human interleukin-13 mutein 2.

XX Cytokine; mutein; interleukin-13; IL-13; agonist; antagonist;
KW diagnosis; therapy; cancer; inflammation; degenerative disease.

XX Synthetic.

XX Key Location/Qualifiers

FT Misc-difference 11 /note= "Glu at position 11 may be replaced by an
FT amidated amino acid, including Lys"

FT Misc-difference 64 /note= "Arg at position 64 may be replaced by an
FT acidic amino acid, including Asp"

XX WO9604306-A2.

XX 15-FEB-1996.

XX 31-JUL-1995; 95WO-US08950.

XX 01-AUG-1994; 94US-0284393.

XX (SCHE) SCHERING CORP.

XX Zurawski G, Zurawski SM;

XX WPI: 1996-129335/13.

XX Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
PT murine P600 contg. amino acid substitutions. - useful for the
PT diagnosis and treatment of cancer, inflammation, etc.

XX Claim 12; Page 46; 52pp; English.

Sequence 112 AA;

Sequence 112 AA;

Query Match 66.0%; Score 367; DB 17; Length 112;

RESULT	9	
R27346		
ID	R27346 standard; Protein; 112 AA.	
XX	AC	
XX	R27346;	
XX		
XX	24-FEB-1993 (first entry)	
XX		
DE	Protein with cytokine activity encoded by Nal.	
XX		
KW	Interleukin; chemotaxis; immunomodulation; inflammation.	
XX		
PN	EP506574-A.	
XX		
PD	30-SEP-1992.	
XX		
PF	27-MAR-1992; 92EP-0400858.	
XX		
PR	29-MAR-1991; 91FR-0003904.	
PR	08-JAN-1992; 92FR-0000137.	
XX		
XX	(SNFI) ELF SANOFI.	
XX		
PI	Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-le Bouteil	
PI	Leplatols P, Magazln M, Minty A;	
XX		
DR	WPI; 1992-325841/40.	
DR	N-PSDB; Q28943.	
XX		
PT	New cytokine having immunomodulatory activity - useful for	
PT	treating tumours and infectious or inflammatory conditions	
XX		
PS	Claim 1; Page 60; 78pp; French.	
XX		
CC	This protein is one of two possible forms of a new cytokine	
CC	produced by T lymphocytes induced by phorbol-2-myristate-3- and phytohaemagglutinin. The proteins differ only in the amino	
CC	at position 41 which is either Asp or Gly. The cytokine acts on	
CC	monocytes and B lymphocytes and is useful in treatment of	
CC	and some infections and inflammatory conditions.	
CC	See Q28941-Q28947.	
XX		
SQ	Sequence 112 AA;	
Query Match	64.7%; Score 360; DB 13; Length 112	
Best Local Similarity	68.2%; Pred. No. 3.6e-37;	
Matches 75; Conservative 11; Mismatches 22; Indels		
QY	2 PVPSPILKELIELVNITQKQ-ASLNGSMVSNVLNAGMYCAALESINVS	
	:	
Db	2 pvpstalrelielelvnitqkqplcngsmvsnvlnltadmycaaleslnvsg	
	:	
QY	61 TORMLKALCSQKPAAG-ISSERSRDTKTEVIQLVKNLITYVRGVYRHGNF 109	
	: :	
Db	62 tqrmisgfcphkvaagfsslhvrdtkievagfvkdlhlhkklfregf 111	
	: :	
RESULT	10	
R27348		
ID	R27348 standard; Protein; 146 AA.	
XX		
AC	R27348;	
XX		
DT	24-FEB-1993 (first entry)	
XX		
DE	Cytokine NC30.	
XX		
KW	Interleukin; chemotaxis; immunomodulation; inflammation.	
XX		
FH	Key	Location/Qualifiers

```

FT cleavage_site 20..21 /note= "putative signal peptide cleavage site"
FT cleavage_site 24..25 /note= "putative signal peptide cleavage site"
FT cleavage_site 32..33 /note= "putative signal peptide cleavage site"
FT cleavage_site 34..35 /note= "putative signal peptide cleavage site"
FT protein 35..146 /note= "putative signal peptide cleavage site"
FT /label= NC30
XX
XX EP506574-A.
XX
XX 30-SEP-1992.
XX
XX 27-MAR-1992; 92EP-0400858.
XX
XX 29-MAR-1991; 91FR-0003904.
XX 08-JAN-1992; 92FR-0000137.
XX
XX (SNFI ) ELF SANOFI.
XX
XX Caput D, Ferrara P, Guillemot J, Kaghad M, Labit-Je Bouteiller C;
XX Leglatois P, Magazin M, Minty A;
XX
XX WPI: 1992-325841/40.
XX
XX N-PSDB: Q28947.
XX
XX New cytokine having immunomodulatory activity - useful for
XX treating tumours and infectious or inflammatory conditions
XX
XX Claim 1; Page 52-53; 78pp; French.
XX
XX A novel cytokine produced by T lymphocytes induced by phorbol-2-
XX myristate-3-acetate and phytohaemagglutinin was coded for by the
XX sequence in clone pSE1-NC30. A second clone was also identified
XX (pSE1-NC30bis) which differed only in the identity of codon 41.
XX The corresponding proteins differ in the amino acid at position 41
XX which is either Asp (in NC30) or Gly (in NC30bis). The cytokine
XX acts on monocytes and B lymphocytes and is useful in treatment of
XX tumours and some infections and inflammatory conditions.
XX See Q28941-Q28947.
XX
XX Sequence 146 AA:
SQ
Query Match 64.7%; Score 360; DB 13; Length 146;
Best Local Similarity 68.2%; Pred. No. 5,1e-37;
Matches 75; Conservative 11; Mismatches 22; Indels 2; Gaps 2;
OY 2 PVTSPTEKELIEELVNTQNO-ASLCNGSMWVSVNLTAGMYCALESILNVSQSAIOR 60
DB 36 pvpptalrelleelvtltnqkqplcngsmwsvlnltadmycaalesllnvsqsaiek 95
OY 61 TORMLKALCSOKPAG-1SSERSRDTKIEVIQLVKNLLTYVGVYRHGNF 109
DB 96 tqrmisgfcphkvsagqsslhvrdtkievafvkdlllhkklifegrif 145
RESULT 11
R48625
ID R48625 standard; Protein: 131 AA.
XX
XX R48625;
XX
XX 14-SEP-1994 (first entry)
XX
XX Sequence of mouse P600.
XX
XX Interleukin-13; Lymphokine; P600; immunological disorder; therapy;
XX diagnostic.
XX
XX Mus musculus.
XX
XX

```

```

XX
XX PN MO9404680-A.
XX
XX PD 03-MAR-1994.
XX
XX PF 18-AUG-1993; 93MO-US07645.
XX
XX PR 21-AUG-1992; 92US-0933416.
XX 29-JAN-1993; 93US-0010977.
XX 01-FEB-1993; 93US-0012543.
XX
XX (SCHE ) SCHERING CORP.
XX
XX Aversa G, Banherreau J, Briere F, Coffman RL, Cooks BG;
XX Culpepper, Dang W, De Vries J, De Waal Malefyt R;
XX Doherty TM, Heath A, McKenzie A, Punnonen J, Zurawski G;
XX
XX WPI: 1994-083197/10.
XX
XX N-PSDB: Q56693.
XX
XX Purified interleukin-13 proteins and antibodies - obtd. using
XX mouse gene encoding related protein P600
XX
XX Disclosure; Page 128-129; 135pp; English.
XX
XX An approx. 400 bp DNA fragment derived from a Pst/PvuII restriction
XX digest of the mouse P600 cDNA clone was isolated. This fragment,
XX which encompasses most of the coding region of the mouse P600 cDNA,
XX was radioactively labelled and hybridised with filter lifts prep.
XX from a cDNA library made from a clone of an A10 T cell line. One
XX clone, designated PA.10.66, was subcloned into M13 and sequenced.
XX This sequence encodes human IL-13.
XX
XX Sequence 131 AA:
SQ
Query Match 54.3%; Score 302; DB 15; Length 131;
Best Local Similarity 58.8%; Pred. No. 7.6e-30;
Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;
OY 8 TLKELIEELVNTQNOASLCNGSMWVSVNLTAGMYCALESILNVSQSAIORMLKA 67
DB 32 tlkelleelsnltqdgplcngsmwsvldlaagfcvaldsiltnsncnalrtgrllhg 91
OY 68 LCSQKPAAGISERSRDTKIEVIQLVKNLLTYVGVYRHGNF 109
DB 92 lcnrkaptlvs--lpdtkievahflklislyckqlftrhpf 131
RESULT 12
R92795
ID R92795 standard; Protein: 111 AA.
XX
XX R92795;
XX
XX 24-MAY-1996 (first entry)
XX
XX Murine P600.
XX
XX Cytokine; mutein; P600; interleukin-13; IL-13; agonist; antagonist;
XX diagnosis; therapy; cancer; inflammation; degenerative disease.
XX
XX Mus musculus.
XX
XX Key Location/Qualifiers
XX MISC-difference 67 /note= "Arg at position 67 may be replaced by an
XX acid amino acid, including Asp"
XX
XX MO9604306-A2.
XX
XX 15-FEB-1996.
XX
XX

```

PF 31-JUL-1995; 95WO-US08950.
 XX
 PR 01-AUG-1994; 94US-0284393.
 XX
 PA (SCHE) SCHERING CORP.
 XX
 PI Zurawski G, Zurawski SM;
 XX
 DR WPI; 1996-129335/13.
 XX

PT Mutein(s) of human and murine cytokine(s), esp. interleukin(s) and
 PT murine p60 contg. amino acid substitutions. - useful for the
 PT diagnosis and treatment of cancer, inflammation, etc.
 XX
 PS Claim 12; Page 46; 52pp; English.
 XX

CC Mutelins of mouse p60 (R92795) contain amino acid substitutions at
 CC amino acid position 67 in helix C. They are obtd. by site-directed
 CC mutagenesis of natural p600 sequences. The muteins antagonise the
 CC activity of IL-13 or IL-4. They have partial cytokine agonist
 CC activity, exhibit less than 80% maximal agonist activity of natural
 CC IL-2, and/or antagonize cytokine activity by least about 50% when
 CC present at a 100-fold excess. They and other cytokine muteins
 CC (see also R92790-94, R92796-802) are useful in the screening of
 CC cytokine and cytokine receptor levels, and in the diagnosis or
 CC treatment of e.g. inflammation, cancer, and degenerative disorders.
 XX
 SQ Sequence 111 AA;

Query Match 53.8%; Score 299; DB 17; Length 111;
 Best Local Similarity 57.8%; Pred. No. 1.4e-29;
 Matches 59; Conservative 17; Mismatches 24; Indels 2; Gaps 1;

QY 8 TLKELIEELVNITQNOASLCNGSMVSVNLTAGMYCAALESINVSQSAIQTORMLKA 67
 DB 12 tlkelielsnitqdetplngsmvsvdlaagfcvaldslnisncnalyrcqrlhng 71
 QY 68 LCSQKPAAGISSRSRDRTKIEVIQLVKNLLTYRGVYRHGNF 109
 DB 72 lcnrkapttvss--lptdkievahfickllsyckqlfrhpgf 111

RESULT 13
 Y21548
 ID Y21548 standard; Protein; 634 AA.

XX Y21548;
 AC Y21548;
 XX
 DT 03-AUG-1999 (first entry)
 XX
 DE Human heparin-binding protein (HBP).

XX Heparin-binding protein; HBP; apoptosis; Islets of Langerhans; beta cell;
 KW endothelial cell; nerve cell; azurophil granule; chemoattractant; cancer;
 KW polymorphonuclear leukocyte; monocyte; neurodegenerative disorder; human;
 KW neuromuscular disorder; human immunodeficiency virus; ischemic stroke;
 KW proteoglycan; mitochondrial matrix targeting protein; viral infection;
 KW apoptosis inhibitor; immune-mediated glomerulonephritis.

XX Homo sapiens.
 OS
 PN WO926647-A1.
 XX
 PD 03-JUN-1999.
 XX
 PF 20-NOV-1998; 98WO-DK00510.
 XX
 XX 03-DEC-1997; 97DK-0001394.
 PR 20-NOV-1997; 97DK-0001324.
 XX
 PA (NOVO) NOVO-NORDISK AS.

XX

PI Flodgaard HJ;
 XX
 DR WPI; 1999-347615/29.
 DR N-PSDB; X60692.

PT Modulating or decreasing apoptosis in cells useful for treating
 PT neurodegenerative disorders and neuromuscular disorders
 XX

PS Claim 4; Page 10; 74pp; English.

XX The invention relates to a new method of modulating or decreasing
 CC apoptosis in mammalian beta cells of Islets of Langerhans, endothelial
 CC cells or nerve cells. The method comprises administering a mammalian
 CC heparin-binding protein (HBP) which in a glycosylated form has: (i) a
 CC molecular weight of 28 kDa; (ii) is produced in the azurophil granules
 CC of polymorphonuclear leukocytes; and (iii) is a chemoattractant for
 CC monocytes. The new protein is useful for preventing or treating a
 CC disorder (preferably in human patients) resulting from apoptosis of
 CC mammalian cells, including insufficient functioning of insulin production
 CC or insulin action, a neurodegenerative disorder, a neuromuscular
 CC disorder, human immunodeficiency virus and ischemic stroke. Compositions
 CC comprising HBP and a proteoglycan which binds the HBP; and (b)
 CC comprising the HBP and a protein which is a mammalian mitochondrial
 CC matrix targeting protein and which binds to the HBP are useful for
 CC modulating or decreasing apoptosis in mammalian beta cells of Islets of
 CC Langerhans, endothelial cells or nerve cells. Unlike prior inhibitors,
 CC the new apoptosis inhibitor does not cause disorders associated with the
 CC inhibition of apoptosis such as cancer, autoimmune disorders such as
 CC systemic lupus erythematosus, immune-mediated glomerulonephritis, and
 CC viral infections. The present sequence represents a mature human HBP.

XX Sequence 634 AA;

Query Match 13.5%; Score 75; DB 20; Length 634;
 Best Local Similarity 27.2%; Pred. No. 1.4;
 Matches 25; Conservative 16; Mismatches 23; Indels 28; Gaps 4;

QY 40 GMYCAALESINVSQSA-----IQTORMLKALCSQK---PAAGISSER----- 81
 DB 79 glyalaleilehisalaargphevalmethtralaalasercyspheginserglhasnp 138
 QY 82 -----SRDTKIEVIQLVKNLLTYRGVYR 105
 DB 139 rglyvalserthvalvallegl--yalatyr 168

RESULT 14
 R11510
 ID R11510 standard; Protein; 5072 AA.

XX R11510;
 XX
 DT 17-JUN-1991 (first entry)
 XX
 DE Ryanodine receptor deduced from cDNA clone.
 XX
 KW Malignant hyperthermia; hypermetabolic syndrome; inhalation;
 KW anaesthetics; probe; calcium release channel; sarcoplasmic;
 KW reticulum.

XX Homo sapiens.
 XX
 FH Key Location/Qualifiers
 FT Peptide 1629..1632
 FT Peptide 1742..1748
 FT Peptide 3119..3130
 FT Peptide 3196..3210
 FT Active-site 3981..3985
 FT /label= phosphorylation site
 FT 4315..4318
 FT /label= phosphorylation site
 XX

PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.
PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145276.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145918.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151068.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.

PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 28-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159329.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
PR 21-OCT-1999; 99US-0160767.
PR 21-OCT-1999; 99US-0160768.
PR 21-OCT-1999; 99US-0160770.
PR 21-OCT-1999; 99US-0160814.
PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 12.6%; Score 70; DB 21; Length 330;

Best Local Similarity 25.0%; Pred. NO. 2.4;

Matches 31; Conservative 21; Mismatches 38; Indels 34; Gaps 7;

Qy 12 LIEELVN---ITONQASLCNGSMWWSV-NLTAGMYCAALESLINVSDCSA-----IORTQ- 62
| | | | | : : : : : | | | | : : : : :
| | | | | : : : : : | | | | : : : : :

Db 107 lyeevmkfhvishkrqlqscgtssmhhlnmeqlaktitslyniydanrkpdyiyenea 166
| | | | | : : : : : | | | | : : : : :

Qy 63 --RMLKALCSQKPAAGISSE-----RSROTKIEVIOLVKLLTYVRGVYRH 106
| | | | | : : : : : | | | | : : : : :

Db 167 efrslyvllhinpsngvgmgeplslwfrkltfalkvske-----icfvnllr-----lyrm 217
| | | | | : : : : : | | | | : : : : :

Qy 107 GNFR 110
| | |

Db 218 gnyk 221

Search completed: May 13, 2001, 17:47:37

Job time: 12337 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: May 13, 2001, 17:48:33 ; Search time 42.06 Seconds
(without alignments)
50.242 Million cell updates/sec

Title: US-09-451-527-105
Perfect score: 556
Sequence: 1 SPVTPSPFLKELIELVNIT.....QLVKLLTYRGVYRGNFR 110

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 185757 seqs, 19210857 residues

Total number of hits satisfying chosen parameters: 185757

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA.*
1: /cgnl_7/ptodata/1/iaa/5A_COMB.pep.*
2: /cgnl_7/ptodata/1/iaa/5B_COMB.pep.*
3: /cgnl_7/ptodata/1/iaa/6A_COMB.pep.*
4: /cgnl_7/ptodata/1/iaa/6B_COMB.pep.*
5: /cgnl_7/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgnl_7/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	377.5	67.9	111	1	US-08-284-393B-5
2	377.5	67.9	111	5	PCT-US95-08950-5
3	367	66.0	112	1	US-08-284-393B-4
4	367	66.0	112	5	PCT-US95-08950-4
5	367	66.0	132	1	US-08-012-543-2
6	367	66.0	132	5	PCT-US93-07645A-2
7	367	66.0	132	5	PCT-US93-07645-2
8	366.5	65.9	111	1	US-08-284-393B-15
9	360	64.7	112	1	US-08-371-121-1
10	360	64.7	146	1	US-08-371-121-16
11	356	64.0	112	1	US-08-284-393B-14
12	352	54.3	131	1	US-08-012-543-4
13	352	54.3	131	1	US-08-371-121-25
14	352	54.3	131	5	PCT-US93-07645A-4
15	352	54.3	131	5	PCT-US93-07645-4
16	299	53.8	111	1	US-08-284-393B-6
17	299	53.8	111	5	PCT-US95-08950-6
18	292	52.5	111	1	US-08-284-393B-16
19	64	11.5	383	1	US-08-486-037B-2
20	64	11.5	1461	2	US-08-993-228-10
21	63.5	11.4	168	3	US-09-188-579-85
22	62.5	11.2	1209	5	PCT-US95-04589-107
23	62.5	11.2	1258	2	US-08-310-912A-107
24	62.5	11.2	1294	3	US-08-930-996A-10
25	62.5	11.2	1589	3	US-08-755-587-189
26	60.5	10.9	731	1	US-08-731-716-2
27	60.5	10.9	2004	1	US-08-375-709-15

28	60.5	10.9	2004	1	US-08-752-929-15	Sequence 15, Appl
29	60.5	10.9	2004	4	US-09-090-793-9	Sequence 9, Appl
30	60	10.8	735	3	US-09-191-647-9	Sequence 9, Appl
31	59	10.6	119	2	US-08-318-157B-57	Sequence 57, Appl
32	59	10.6	305	1	US-08-420-235B-25	Sequence 25, Appl
33	59	10.6	305	4	US-08-793-624-25	Sequence 25, Appl
34	59	10.6	305	5	PCT-US95-10194-25	Sequence 25, Appl
35	59	10.6	832	3	US-08-630-820-7	Sequence 7, Appl
36	58.5	10.5	232	1	US-07-990-301A-4	Sequence 4, Appl
37	58	10.4	477	2	US-08-770-544-16	Sequence 16, Appl
38	58	10.4	915	2	US-08-818-070-2	Sequence 2, Appl
39	58	10.4	915	2	US-08-723-585-2	Sequence 2, Appl
40	57.5	10.3	260	2	US-08-675-921B-9	Sequence 9, Appl
41	57.5	10.3	353	3	US-08-803-603-3	Sequence 3, Appl
42	57.5	10.3	503	3	US-08-803-603-1	Sequence 1, Appl
43	57.5	10.3	503	3	US-08-369-822C-8	Sequence 8, Appl
44	57.5	10.3	503	3	US-08-779-764A-26	Sequence 26, Appl
45	57.5	10.3	503	3	US-08-779-764A-27	Sequence 27, Appl

ALIGNMENTS

RESULT 1
US-08-284-393B-5
; Sequence 5, Application US/08284393B
; Patent No. 5696234
; GENERAL INFORMATION:
; APPLICANT: Zurawski, Sandra M.
; APPLICANT: Zurawski, Gerard
; TITLE OF INVENTION: MUTEINS OF MAMMALIAN CYTOKINES
; NUMBER OF SEQUENCES: 16
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DNAX Research Institute
; STREET: 901 California Avenue
; CITY: Palo Alto
; STATE: California
; COUNTRY: USA
; ZIP: 94304-1104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/284,393B
; FILING DATE: 01-AUG-1994
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Ching, Edwin P.
; REGISTRATION NUMBER: 34,090
; REFERENCE/DOCKET NUMBER: DX0389
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-852-9196
; TELEFAX: 415-496-1200
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 111 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-284-393B-5

Query Match 67.9%; Score 377.5; DB 1; Length 111;
Best Local Similarity 69.7%; Pred. No. 2.9e-41;
Matches 76; Conservative 11; Mismatches 21; Indels 1; Gaps 1;
QY 2 PVTSPFTKLKELIELVNITQNC-ASLNCNGSMVSNLTAGMYCAALESINVSQSAIOR 60
DB 2 PVPSTALRELIELVNITQNKAPLCNGSMVSNLTAGMYCAALESINVSQSAIEK 61

REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 112 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US95-08950-4

Query Match 66.0%; Score 367; DB 5; Length 112;
Best Local Similarity 69.1%; Pred. No. 6.5e-40;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PVTPTLKLIEELVNITQNG-ASLCNGSMVSVNLTAGMYCAALESLINVSDCSAIOR 60
DB 2 PVPSTALRELIEELVNITQNGKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEK 61
QY 61 TQRLMKALCSQKPAAG-ISSERSRDTKIEVIQVLYKLLTYVGVYRHGNF 109
DB 62 TQRLMSGFCPHKVSAGQFSSLHVHRTKIEVAQFVKDLLLHLKFLFREGRF 111

RESULT 5

US-08-012-543-2
Sequence 2, Application US/08012543
Patent No. 5596072
GENERAL INFORMATION:
APPLICANT: Culpepper, Janice
APPLICANT: McKenzie, Andrew
APPLICANT: Dang, Warren
APPLICANT: de Waal Malefyt, Rene
APPLICANT: Heath, Andrew
APPLICANT: Aversa, Gregorio
APPLICANT: Briere, Francine
APPLICANT: Banchereau, Jacques
APPLICANT: de Vries, Jan
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: Human Interleukin-13
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,543
FILING DATE: 01-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933,416
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0302K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:

LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-012-543-2

Query Match 66.0%; Score 367; DB 1; Length 132;
Best Local Similarity 69.1%; Pred. No. 8.3e-40;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PVTPTLKLIEELVNITQNG-ASLCNGSMVSVNLTAGMYCAALESLINVSDCSAIOR 60
DB 22 PVPSTALRELIEELVNITQNGKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEK 81
QY 61 TQRLMKALCSQKPAAG-ISSERSRDTKIEVIQVLYKLLTYVGVYRHGNF 109
DB 82 TQRLMSGFCPHKVSAGQFSSLHVHRTKIEVAQFVKDLLLHLKFLFREGRF 131

RESULT 6

PCT-US93-07645A-2
Sequence 2, Application PC/TUS9307645A
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Human Interleukin-13
NUMBER OF SEQUENCES: 6
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07645A
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012543
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010977
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933416
FILING DATE: 21-AUG-1992
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-07645A-2

Query Match 66.0%; Score 367; DB 5; Length 132;
Best Local Similarity 69.1%; Pred. No. 8.3e-40;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PVTPTLKLIEELVNITQNG-ASLCNGSMVSVNLTAGMYCAALESLINVSDCSAIOR 60
DB 22 PVPSTALRELIEELVNITQNGKAPLCNGSMVWSINLTAGMYCAALESLINVSGCSAIEK 81
QY 61 TQRLMKALCSQKPAAG-ISSERSRDTKIEVIQVLYKLLTYVGVYRHGNF 109
DB 82 TQRLMSGFCPHKVSAGQFSSLHVHRTKIEVAQFVKDLLLHLKFLFREGRF 131

RESULT 7

PCT-US93-07645-2
Sequence 2, Application PC/TUS9307645
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Human Interleukin-13
NUMBER OF SEQUENCES: 6

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macintosh 6.0.5
SOFTWARE: Microsoft Word 5.1a
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US93/07645
FILING DATE: 19930818
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/012543
FILING DATE: 01-FEB-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/010977
FILING DATE: 29-JAN-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933416
FILING DATE: 21-AUG-1992
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 132 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US93-07645-2

Query Match 66.0%; Score 367; DB 5; Length 132;
Best Local Similarity 69.1%; Pred. No. 8.3e-40;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PYTPSPFLKLEIELVNTQNO-ASLCNGSNWVNLTAGWYCAALSLINWSDCSAQR 60
DB 22 PVPSTALRKLEIELVNTQNO-KAPLCNGSNWVNLTAGWYCAALSLINWSDCSAIEK 81
QY 61 TORMLKALCSOKPAGG-SSERSRDTKIEVIQLVKNLTYVGVYRHGNE 109
DB 82 TORMLSGCFPHKVSAGFSSSLHVROTKIEVQFVADLLHLKKLFREGRE 131

RESULT 8
US-08-284-393B-15
Sequence 15, Application US/08284393B
Patent No. 5696234
GENERAL INFORMATION:
APPLICANT: Zurawski, Sandra M.
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: MUTAINS OF MAMMALIAN CYTOKINES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284, 393B
FILING DATE: 01-AUG-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0389
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:

LENGTH: 111 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-284-393B-15

Query Match 65.9%; Score 366.5; DB 1; Length 111;
Best Local Similarity 67.9%; Pred. No. 7.5e-40;
Matches 74; Conservative 12; Mismatches 22; Indels 1; Gaps 1;

QY 2 PYTPSPFLKLEIELVNTQNO-ASLCNGSNWVNLTAGWYCAALSLINWSDCSAQR 60
DB 2 PVPSTALRKLEIELVNTQNO-KAPLCNGSNWVNLTAGWYCAALSLINWSDCSAIEK 61
QY 61 TORMLKALCSOKPAGG-SSERSRDTKIEVIQLVKNLTYVGVYRHGNE 109
DB 62 TORMLSGCFPHKVSAGFSSSLHVROTKIEVQFVADLLHLKKLFREGRE 110

RESULT 9
US-08-371-121-1
Sequence 1, Application US/08371121
Patent No. 5652123
GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascal
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrien
APPLICANT: KAGHAD, Mourad
APPLICANT: MAGAZIN, Marilynn
TITLE OF INVENTION: Protein having a cytokine type
TITLE OF INVENTION: activity, recombinant DNA coding for this protein,
transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136

OY 2 PVTSPITLKEIEELVNTQNO-ASLNGSMWVSNLTAGMCALESILNVSQSAIOR 60
DB 2 PVPSTALRKLEIEELVNTQNOKAPLNGSMWVSNLTAGMCALESILNVSQSAIOR 61
OY 61 TORMLKALCSQKPAAG-SSERSRDTKIEVITQVKNLLTYVGVYRHGNF 109
DB 62 TQDMLSGCPKHKVSGQSFSSLIHVRDTKIEVAFVADLLHLKLRREGNF 111

RESULT 12
US-08-012-543-4
Sequence 4, Application US/08012543
Patent No. 5596072
GENERAL INFORMATION:
APPLICANT: Culpepper, Janice
APPLICANT: McKenzie, Andrew
APPLICANT: Dang, Mairen
APPLICANT: de Maal Malefyt, Rene
APPLICANT: Heath, Andrew
APPLICANT: Aversa, Gregorio
APPLICANT: Briere, Francine
APPLICANT: Bancheureau, Jacques
APPLICANT: de Vries, Jan
APPLICANT: Zurawski, Gerard
TITLE OF INVENTION: Human Interleukin-13
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/012,543
FILING DATE: 01-FEB-1993
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/933,416
FILING DATE: 21-AUG-1992
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0302K1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-012-543-4

Query Match 54.3%; Score 302; DB 1; Length 131;
Best Local Similarity 58.8%; Pred. No. 2e-31;
Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

OY 8 TLKELIEELVNTQNOASLNGSMWVSNLTAGMCALESILNVSQSAIOR 67
DB 32 TLKELIEELVNTQNOQPLNGSMWVSDLAAGFCVALDSLNTMISNCNAIYRTORILHG 91
OY 68 LCSQKPAAGISSERSRDTKIEVITQVKNLLTYVGVYRHGNF 109
DB 92 LCNRAKPTVSS-LPDKIEVAHFITKLLSTYKOLFRRHGF 131

RESULT 13
US-08-371-121-25
Sequence 25, Application US/08371121
Patent No. 5652123

GENERAL INFORMATION:
APPLICANT: CAPUT, Daniel
APPLICANT: FERRARA, Pascual
APPLICANT: GUILLEMOT, Jean-Claude
APPLICANT: LEPLATOIS, Pascal
APPLICANT: MINTY, Adrian
APPLICANT: KAGHAD, Mourad
APPLICANT: LABIT-LE BOUTELLIER, Christine
APPLICANT: MAGAZIN, Marilyn
TITLE OF INVENTION: Protein having a cytokine type
activity, recombinant DNA coding for this protein,
TITLE OF INVENTION: transformed cells and microorganisms.
NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: FOLEY & LARDNER
STREET: 3000 K Street, N.W., Suite 500
CITY: Washington, D.C.
COUNTRY: USA
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/371,121
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/938,161
FILING DATE: 30-NOV-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/FR92/00280
FILING DATE: 27-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 00137
FILING DATE: 08-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FR 91 03904
FILING DATE: 29-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Saxe, Bernhard D.
REGISTRATION NUMBER: 28,665
REFERENCE/DOCKET NUMBER: 16781/383
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 672-5300
TELEFAX: (202) 672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 25:
SEQUENCE CHARACTERISTICS:
LENGTH: 131 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-371-121-25

Query Match 54.3%; Score 302; DB 1; Length 131;
Best Local Similarity 58.8%; Pred. No. 2e-31;
Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

OY 8 TLKELIEELVNTQNOASLNGSMWVSNLTAGMCALESILNVSQSAIOR 67
DB 32 TLKELIEELVNTQNOQPLNGSMWVSDLAAGFCVALDSLNTMISNCNAIYRTORILHG 91
OY 68 LCSQKPAAGISSERSRDTKIEVITQVKNLLTYVGVYRHGNF 109
DB 92 LCNRAKPTVSS-LPDKIEVAHFITKLLSTYKOLFRRHGF 131

Db 92 LCNRKAPTIVSS--LPDTKIEVAHFITKLLSYTKQLFRHGPF 131

RESULT 14

PCT-US93-07645A-4

; Sequence 4, Application PC/TUS9307645A

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Human Interleukin-13

; NUMBER OF SEQUENCES: 6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 6.0.5

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/07645A

; FILING DATE:

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/012543

; FILING DATE: 01-FEB-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/010977

; FILING DATE: 29-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/933416

; FILING DATE: 21-AUG-1992

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 131 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US93-07645A-4

Query Match 54.3%; Score 302; DB 5; Length 131;

Best Local Similarity 58.8%; Pred. No. 2e-31;

Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

Qy 8 TLKELIEELVNITQNASLCSNGSMWVSNLTAGMYCAALESILNVSDCSATQRTQRMKA 67

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 32 TLKELIEELSNITQDOTPLCSNGSMWVSDLAAGGFCVALDSLNTISNCNAIYRTQRIHG 91

Qy 68 LCSQKPAAGISSRSRDTKIEVIQLVKNLLTYVRGVYRHGNF 109

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 92 LCNRKAPTIVSS--LPDTKIEVAHFITKLLSYTKQLFRHGPF 131

RESULT 15

PCT-US93-07645-4

; Sequence 4, Application PC/TUS9307645

; GENERAL INFORMATION:

; APPLICANT:

; TITLE OF INVENTION: Human Interleukin-13

; NUMBER OF SEQUENCES: 6

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: Apple Macintosh

; OPERATING SYSTEM: Macintosh 6.0.5

; SOFTWARE: Microsoft Word 5.1a

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: PCT/US93/07645

; FILING DATE: 19930818

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/012543

; FILING DATE: 01-FEB-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 08/010977

; FILING DATE: 29-JAN-1993

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: US 07/933416

; FILING DATE: 21-AUG-1992

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 131 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

PCT-US93-07645-4

Query Match 54.3%; Score 302; DB 5; Length 131;

Best Local Similarity 58.8%; Pred. No. 2e-31;

Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

Qy 8 TLKELIEELVNITQNASLCSNGSMWVSNLTAGMYCAALESILNVSDCSATQRTQRMKA 67

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 32 TLKELIEELSNITQDOTPLCSNGSMWVSDLAAGGFCVALDSLNTISNCNAIYRTQRIHG 91

Qy 68 LCSQKPAAGISSRSRDTKIEVIQLVKNLLTYVRGVYRHGNF 109

||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

Db 92 LCNRKAPTIVSS--LPDTKIEVAHFITKLLSYTKQLFRHGPF 131

Search completed: May 13, 2001, 17:48:34

Job time: 12137 sec

Db 36 PVPSTALRELELVNTQNGKAPLCSGSMWSVNLTAGMCALESILINVSQSAIEK 95
 QY 61 TQRMKALCSQKPAAG-ISSERSRDTKIEVQLVKNLITVRYRGVRRGNF 109
 Db 96 TQRMKSGFCPRKVSAGQFSSLHVRDKIEVAQFVKDLLHLKLFREGRF 145

RESULT 2

E30552
 T-cell activation protein P60 precursor - mouse
 C:Species: Mus musculus (house mouse)
 C:Date: 28-Aug-1989 #sequence_revision 28-Aug-1989 #text_change 16-Jul-1999
 C:Accession: E30552
 R:Brown, K.D.; Zurawski, S.M.; Mosmann, T.R.; Zurawski, G.
 J. Immunol. 142, 679-687, 1989
 A:Title: A family of small inducible proteins secreted by leukocytes are members of a new class of various activation processes.
 A:Reference number: A30552; MUID:89093958
 A:Accession: E30552
 A:Molecule type: mRNA
 A:Residues: 1-131 <BRO>
 A:Cross-references: GB:M23504; NID:9533246; PIDN:AAA0149.1; PID:9533247
 C:Superfamily: Interleukin-13

Query Match 54.3%; Score 302; DB 2; Length 131;
 Best Local Similarity 58.8%; Pred. No. 8, 4e-25;
 Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;

QY 8 TLKELIEELVNTQNGASGSMWSVNLTAGMCALESILINVSQSAIORTQRLKA 67
 Db 32 TLKELIEELVNTQDPTPLCSGSMWSVDLAAGFCVALDSLINISNCALIVRTQRLHC 91
 QY 68 LCSQKPAAGISSERSRDTKIEVQLVKNLITVRYRGVRRGNF 109
 Db 92 LCNRAKPTTVSS-LPDTKIEVAHFITKLSTYKQLFRHOPF 131

RESULT 3

Interleukin-13 - rat
 I52290
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 16-Jul-1999
 C:Accession: I52290
 R:Lakkis, F.G.; Gruet, E.N.
 Biochem. Biophys. Res. Commun. 197, 612-618, 1993
 A:Title: Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expression.
 A:Reference number: I52290; MUID:94092138
 A:Accession: I52290
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-131 <RES>
 A:Cross-references: GB:L26913; NID:9438875; PIDN:AAAI6478.1; PID:9438876
 C:Genetics:
 A:Gene: IL-13
 C:Superfamily: Interleukin-13

Query Match 53.0%; Score 294.5; DB 2; Length 131;
 Best Local Similarity 58.5%; Pred. No. 5, 2e-24;
 Matches 62; Conservative 18; Mismatches 23; Indels 3; Gaps 3;

QY 4 TSPSTLKELELVNTQNGASLCSGSMWSVNLTAGMCALESILINVSQSAIORTQ 62
 Db 28 SPVALREIEELVNTQDPTPLCSGSMWSVDLAAGFCVALDSLINISNCALIVRTQRLHC 91
 QY 63 RMLKALCSQKPAAGISSERSRDTKIEVQLVKNLITVRYRGVRRGNF 108
 Db 88 RLNLGLCNOK-ASDVASS-PPDTKIEVAQFISKLNLNYSKQLFRYGH 131

RESULT 4

A35041

ryanodine receptor type 1, skeletal muscle - human
 N:Alternate names: calcium release channel protein
 C:Species: Homo sapiens (man)
 C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jan-2000
 C:Accession: A35041; I84622; S66630
 R:Zoratto, F.; Fujita, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Weisner, G.
 J. Biol. Chem. 265, 2244-2256, 1990
 A:Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) release channel.
 A:Reference number: A35041; MUID:90130482
 A:Accession: A35041
 A:Status: preliminary; not compared with conceptual translation
 A:Molecule type: mRNA
 A:Residues: 1-5032 <COR>
 A:Cross-references: GB:M05200; NID:9337721; PIDN:AAA60294.1; PID:9337722
 R:Otsu, K.; Phillips, M.S.; Khanna, V.K.; de Leon, S.; MacLennan, D.H.
 Genomics 13, 835-837, 1992
 A:Title: Refinement of diagnostic assays for a probable causal mutation for porcine aortic aneurysm.
 A:Reference number: I46644; MUID:92347867
 A:Accession: I84622
 A:Status: translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 598-722 <RES>
 A:Cross-references: GB:M91455; NID:9337723; PIDN:AAA60295.1; PID:9553643
 R:Lynn, S.; Morgan, J.M.; Lamb, H.K.; Weisner, G.; Gillespie, J.I.
 FEBS Lett. 372, 6-12, 1995
 A:Title: Isolation and partial cloning of ryanodine-sensitive Ca(2+) release channel cDNA.
 A:Reference number: S66630; MUID:96032536
 A:Accession: S66630
 A:Molecule type: mRNA
 A:Residues: 4690-4968 <LYN>
 A:Experimental source: myometrial smooth muscle
 C:Genetics:
 A:Gene: GDB:RYR1
 A:Cross-references: GDB:120359; OMIM:180901
 A:Map position: 19q13.1-19q13.1
 A:Insertions: 642/2
 C:Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 hom C:Keywords: calcium channel; homotrimer; phosphoprotein; skeletal muscle; transmembrane protein; transcription initiation factor sigma region 1 homology <SRI>
 F:1788-1984/Domain: transcription initiation factor sigma region 1 homology <SRI>

Query Match 12.9%; Score 72; DB 1; Length 5032;
 Best Local Similarity 21.1%; Pred. No. 1, 1e+02;
 Matches 26; Conservative 26; Mismatches 43; Indels 28; Gaps 4;

QY 9 LKELIEELVNTQNGASLCSGSMWSVNLTAGMCALESILINVSQSAIORTQRLKA 67
 Db 521 LKELIEELVNTQNGASLCSGSMWSVNLTAGMCALESILINVSQSAIORTQRLKA 67
 QY 57 AIDQ-----RYQMLKALCSQKPAAGISSERSRDTKIE-----VIQVKNLITVY 100
 Db 581 HIKSIISLDKGRNHVLDVLCISGCVAVRNSQDLITENLPGRELLQNLINIVY 640
 QY 101 RGV 103
 Db 641 TSI 643

RESULT 5

QJ1176
 sepiapterin reductase (EC 1.1.1.153) - human
 C:Species: Homo sapiens (man)
 C:Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 21-Jul-2000
 C:Accession: J01176; P11579; I51849
 R:Richinose, H.; Katoh, S.; Sueoka, T.; Titani, K.; Fujita, K.; Nagatsu, T.
 Biochem. Biophys. Res. Commun. 179, 183-189, 1991
 A:Title: Cloning and sequencing of cDNA encoding human sepiapterin reductase-an enzyme.
 A:Reference number: J01176; MUID:91354248
 A:Accession: J01176
 A:Molecule type: mRNA
 A:Residues: 1-261 <ICH>
 A:Cross-references: GB:M76231; NID:9338020; PIDN:AAA60314.1; PID:9338021
 A:Experimental source: liver

R;Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Exp. Cell Res. 204, 217-222, 1993
A:Title: Detection of a novel septaplerin reductase mRNA: Assay of mRNA in various cells
A:Reference number: A49174; MUID:93178546
A:Accession: PH1579
A:Molecule type: mRNA
A:Residues: 208-254 <RES>
R;Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Adv. Exp. Med. Biol. 338, 195-198, 1993
A:Title: Northern blot analysis of septaplerin reductase mRNA in mammalian cell lines and
A:Reference number: I51849; MUID:94136218
A:Accession: I51849
A:Status: translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 208-254 <RES>
A:Cross-references: GB:S71376; NID:9557903; PIDN:AAD14079.1; PID:94261779
A:Comment: This enzyme catalyzes the NADPH-dependent reduction of septaplerin to produce
C:Genetics:
A:Gene: GDB:SPR
A:Cross-references: GDB:128778
A:Map position: 2p14-2p12
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: NADP; oxidoreductase
F:8-199/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:28-32/Region: pterin binding #status predicted

Query Match 12.9%; Score 71.5; DB 2; Length 261;
Best Local Similarity 24.7%; Pred. No. 4.2;
Matches 24; Conservative 21; Mismatches 41; Indels 11; Gaps 4;

Qy 16 LVNITQNASLNGSMV---WSVNLTAGMYCAALESINVSDCSAIQTQRMKALCSQK 72
Db 104 LGDVSXGFDLSDTQNNYWNALNLTSLCLTSSVLPGLNRTVNVNLSLCAQ 162

Qy 73 PAAG---ISSRSRDTKIEVLQV---NLLTVYVRG 102
Db 163 PPKGNALYCAGRAARDMLQVLAEEPNVRLNYPAG 199

RESULT 6
S62423
ATP-dependent RNA helicase - fission yeast (Schizosaccharomyces pombe)
C:Species: Schizosaccharomyces pombe
C:Date: 16-May-1996 #sequence_revision 13-Mar-1997 #text_change 17-Nov-2000
C:Accession: T38183; S62423
R:Lye, G.; Churcher, C.M.; Barrell, B.G.; Rajandream, M.A.; Walsh, S.V.
submitted to the EMBL Data Library, October 1995
A:Reference number: Z21776
A:Accession: T38183
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: DNA
A:Residues: 1-481 <LV2>
A:Cross-references: EMBL:Z54285; PIDN:CAA91073.1; PID:g1008436; GSPDB:GN000066; SPDB:SPAC
A:Experimental source: strain 972h; cosmid c22F3
C:Genetics:
A:Gene: SPAC22F3.08c
A:Map position: 1L
C:Keywords: ATP; P-loop
F:90-97/Region: nucleotide-binding motif A (P-loop)
F:192-197/Region: nucleotide-binding motif B
F:196-199/Region: DEAD motif

Query Match 12.9%; Score 71.5; DB 2; Length 481;
Best Local Similarity 24.3%; Pred. No. 8.5;
Matches 25; Conservative 25; Mismatches 48; Indels 5; Gaps 4;

Qy 5 PSPTELKLEIEELVNITQNASLNGSMVSV-NLTAGMYCAALESINVSDCSAIQTQ 62
Db 18 POPSKEAKKLGKTKGKAVTGNPDPIEEFEGILCENLKKO-NITECTIQR-- 74

Qy 63 RMLKALCSQKPAAGISSRSRDTKIEVLQVKNLLTVYVRGVR 105

Db 75 YAIFPTGSKRDLACAPTGSCKTIAYLPFILOKLOLHVPGGYR 117

RESULT 7
A36024
septaplerin reductase (EC 1.1.1.153) - rat
C:Species: Rattus norvegicus (Norway rat)
C:Date: 11-Jan-1991 #sequence_revision 07-Jul-1995 #text_change 01-Dec-2000
C:Accession: A36024; A36400; PH1577; I64799; A49174
R:Citron, B.A.; Milstien, S.; Gutierrez, J.C.; Levine, R.A.; Yanak, B.L.; Kaufman, S.
Proc. Natl. Acad. Sci. U.S.A. 87, 6436-6440, 1990
A:Title: Isolation and expression of rat liver septaplerin reductase cDNA.
A:Reference number: A36024; MUID:90349631
A:Accession: A36024
A:Molecule type: mRNA
A:Residues: 4-262 <CIT>
A:Cross-references: GB:M36410; NID:g206895; PIDN:AAA42130.1; PID:g206896
R:Oyama, R.; Katoh, S.; Sueoka, T.; Suzuki, M.; Ichinose, H.; Nagatsu, T.; Titani, K.
Biochem. Biophys. Res. Commun. 173, 627-631, 1990
A:Title: The complete amino acid sequence of the mature form of rat septaplerin reductase
A:Reference number: A36400; MUID:91083647
A:Accession: A36400
A:Molecule type: protein
A:Residues: 1-32;34;41-92,1'-96-124;126-262 <OVA>
R;Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Exp. Cell Res. 204, 217-222, 1993
A:Title: Detection of a novel septaplerin reductase mRNA: Assay of mRNA in various ce
A:Reference number: A49174; MUID:93178546
A:Accession: PH1577
A:Molecule type: mRNA
A:Residues: 209-255 <MAI>
A:Cross-references: GB:S55545; NID:g266077; PIDN:AAB25506.1; PID:g266078
R;Maier, J.; Schott, K.; Werner, T.; Bacher, A.; Ziegler, I.
Adv. Exp. Med. Biol. 338, 195-198, 1993
A:Title: Northern blot analysis of septaplerin reductase mRNA in mammalian cell lines
A:Reference number: I51849; MUID:94136218
A:Accession: I64799
A:Status: preliminary; translated from GB/EMBL/DDBJ
A:Molecule type: mRNA
A:Residues: 209-255 <RES>
A:Cross-references: GB:S71374; NID:g557901
C:Function:
A:Description: catalyzes the NADPH-dependent reduction of septaplerin to produce 7,8-
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: acetylated amino end; homodimer; oxidoreductase
F:9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>
F:1/Modified site: acetylated amino end (Met) #status experimental

Query Match 12.8%; Score 71; DB 2; Length 262;
Best Local Similarity 23.5%; Pred. No. 4.8;
Matches 24; Conservative 25; Mismatches 41; Indels 12; Gaps 4;

Qy 8 TLKELIELVNITQNASLNGSMVSVNLTAGMYCAALESINVSDCSAIQTQRMKLA 67
Db 104 TLGDVSKGFLNIN---DLAEVNNYWNALNLTSLCLTGTGLNAPNSPGLSKTVVNISS 158

Qy 68 LCSQKPAAG----ISSRSRDTKIEVLQV---NLLTVYVRG 102
Db 159 LCALQPPKGGWGLYCAGKAARDMLQVLAEEPSVRVLSYAPG 200

RESULT 8
T00035
nonstructural polyprotein - Plautia stali intestine virus
C:Species: Plautia stali intestine virus
C:Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 21-Jul-2000
C:Accession: T00035
R:Sasaki, J.; Nakashima, N.; Saito, H.; Noda, H.
Virology 244, 50-58, 1998
A:Title: An insect picorna-like virus, Plautia stali intestine virus, has genes of ca
A:Reference number: Z14072; MUID:98240933

A:Accession: T00035
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: genomic RNA
A:Residues: 1-1811 <SAS>
A:Cross-references: EMBL:AB006531; NID:g2344756; PIDN:BA21898.1; PID:g2344757
C:Keywords: polyprotein

Query Match 12.7%; Score 70.5; DB 2; Length 1811;
Best Local Similarity 23.3%; Pred. No. 50;
Matches 21; Conservative 23; Mismatches 41; Indels 5; Gaps 3;

OY 13 IEELV-NITONQASL-NGSMWMSVNLTAGMCALESLINSDCSAIGRTORMLKALCS 70
Db 983 IRQSVNRATSDSVNMQNGNV---ENLALQNYKSVNEMLTVEGCSDDQNAEILSKVCR 1039
OY 71 OKPACISSESRSDPTKIEVTLQVKNLLTVV 100
Db 1040 NYVALFVCRRPDGRESRLGHILFLKDKIGYM 1069

RESULT 9
22BPA4
rapid lysis protein IIA - phage T4
N:Alternate names: gp rIIA; rIIA protein
C:Species: phage T4
A:Note: host Escherichia coli
C:Date: 19-Feb-1984 #sequence_revision 03-Oct-1995 #text_change 16-Jun-2000
A:Accession: J00400; A92909; A92868; S52613; A04304; PS0469
R:Daegelen, P.; Brody, E.
Genetics 125, 237-248, 1990
A:Title: The rIIA gene of bacteriophage T4. I. Its DNA sequence and discovery of a new c
A:Reference number: PS0194; MUID:90337270
A:Accession: J00400
A:Molecule type: DNA
A:Residues: 1-725 <DAE>
A:Cross-references: GB:X52686; GB:X00905; NID:g15177; PIDN:CMA36911.1; PID:g15179
R:Sungno, A.; Drake, J.W.
J. Mol. Biol. 176, 239-249, 1984
A:Title: Modulation of mutation rates in bacteriophage T4 by a base-pair change a dozen
A:Reference number: A92909; MUID:84267841
A:Accession: A92909
A:Molecule type: DNA
A:Residues: 476-725 <HER>
A:Note: the authors translated the codon ACA for residue 517 as Lys
R:Pitnow, D.; Sigurdson, D.C.; Gold, L.; Slinger, B.S.; Napoli, C.; Brosius, J.; Dull, T
J. Mol. Biol. 149, 337-376, 1981
A:Title: rII clusters of bacteriophage T4. DNA sequence around the interstronic divide
A:Reference number: A92868; MUID:82078066
A:Accession: A92868
A:Molecule type: DNA
A:Residues: 587-615, 'D', 617-725 <PRL>
A:Note: the authors translated the codon GCT for residue 595 as Ser
R:Kumagai, M.; Yamashita, T.; Honda, M.; Ikeda, H.
Genetics 135, 255-264, 1993
A:Title: Effects of uvxX, uvvY and DNA topoisomerase on the formation of tandem duplicat
A:Reference number: S52613; MUID:94063467
A:Accession: S52613
A:Status: preliminary; translation not shown
A:Molecule type: DNA
A:Residues: 244-725 <KUM>
A:Cross-references: EMBL:DI6359; NID:g303761; PIDN:BA23634.1; PID:g2648161
C:Comment: This protein is found on the inner membrane of the host shortly after infecti
C:Comment: The rIIA gene is one of two rII genes, loss of which gives rise to large, shat
C:Genetics:
A:Gene: rIIA
A:Map position: 0.014-2.189
C:Superfamily: phage T4 rIIA protein
C:Keywords: DNA binding; membrane protein

Query Match 12.6%; Score 70; DB 1; Length 725;
Best Local Similarity 27.0%; Pred. No. 20;

```

Oy      8 TLKEL-IEELVNTTONQASLCNGSMWVSVLTAGYCALESILNVSDCSAIOFTORMLK 66
       | | | : : : : : | | | : : : | | | : : : | | | : : : |
Db     342 TTKNKKYSKMOSMEFPDCKLACAGVYEVDND-----PRLKRIKOSHETSAVVSSRYLF- 395

Oy      67 ALCSGKPAAGISSERSRDTKE-VIQLYNKLITLYRGYYR 105
       . | | : : : | | | | | | | | | | | | | | | | | |
Db     396 -----GIWT-----TKINIVIDNIKRNVINIRGLAR 421

RESULT 10
S47538
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 26-Dec-1994 #sequence_revision 10-Nov-1995 #text_change 22-Jun-1999
C:Accession: S47538
R:Richardson, R.T.; O'Rand, M.G.
Biochim. Biophys. Acta 1219, 215-218, 1994
A>Title: Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel preproaa
A:Reference number: S47538; MUID:94368861
A:Accession: S47538
A:Molecule type: mRNA
A:Residues: 1-431 <RTIC>
A:Cross-references: EMBL:U05204; NID:g451841; PIDN:AA61630.1; PID:g451842
C:Superfamily: acrosin; trypsin homology
C:Keywords: glycoprotein; hydrolase; serine proteinase
F:40-283/Domain: trypsin homology <TRY>

Query Match          12.5% Score 69.5; DB 2; Length 431;
Best Local Similarity 36.4%; Pred. No. 12;
Matches 16; Conservative 7; Mismatches 16; Indels 5; Gaps 1;

Oy      5 PSPTLKELELVNTTONQASLCNGSMWSVNLTAAGYCALES 48
       ||||| | : | | : | | | : | | | | | |
Db     190 PPSPLMEARVDLINL-----ELCNSTQMYNGRRITASNLCAGYPS 228

RESULT 11
S52110
sepiapterin reductase (EC 1.1.1.153) - mouse
C:Species: Mus musculus (house mouse)
C:Date: 14-Jul-1995 #sequence_revision 21-Jul-1995 #text_change 18-Feb-2000
C:Accession: S52110; PH1578
R:Ota, A.; Ichinose, H.; Nagatsu, T.
Biochim. Biophys. Acta 1260, 320-322, 1995
A>Title: Mouse sepiapterin reductase: an enzyme involved in the final step of tetrahy
A:Reference number: S52110; MUID:95176553
A:Accession: S52110
A>Status: Preliminary
A:Molecule type: mRNA
A:Residues: 1-261 <OTYA>
A:Cross-references: GB:S77493; NID:g957229; PIDN:AAB3611.1; PID:g957230
Exp. Cell Res. 204, 217-222, 1993
A>Title: Detection of a novel sepiapterin reductase mRNA: Assay of mRNA in various ce
A:Reference number: A49174; MUID:93178546
A:Accession: PH1578
A:Molecule type: mRNA
A:Residues: 209-255 <MAI>
C:Comment: This enzyme catalyzes the reduction of both C1' and C2' oxo group.
C:Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C:Keywords: oxidoreductase
F:9-200/Domain: short-chain alcohol dehydrogenase homology <SADH>

Query Match          12.4% Score 69; DB 2; Length 261;
Best Local Similarity 21.5%; Pred. No. 7;
Matches 23; Conservative 26; Mismatches 46; Indels 12; Gaps 4;

Oy      3 VTPSPTLKELELVNTTONQASLCNGSMWSVNLTAAGYCALESILNVSDCSAIOFTO 62
       : | | : : : : | | : : : | | | : | | | | | | | | | | | |

```

Db 99 INNAATLGDSKGFNVN----DLAEVNNYWALNLTs-MLCLTSGTLNFAQDSPGLSKTV 153
QY 63 RMLXALCSOKPAAG-----ISSRSRDTKTEVTLQVVK---NLLTYVRG 102
Db 154 VNISLALQPKYKGNGLYCAGKAARDMLYQVLAEEPSRVRLSYAPG 200
RESULT 12
I46646
ryanodine receptor, skeletal muscle - pig
N:Alternate names: calcium release channel protein
C:Species: Sus scrofa domestica (domestic pig)
C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 10-Sep-1999
C:Accession: I46646; I46645; S31395; I47133; S26624; A37105; I47212; S18135
R:Fujii, J.; Otsu, K.; Zorzato, F.; De Leon, S.; Khanna, V.K.; Weiler, J.E.; O'Brien, P.
Science 253, 448-451, 1991
A:Title: Identification of a mutation in porcine ryanodine receptor associated with malignant hyperthermia
A:Reference number: I46645; MUID:91320118
A:Accession: I46646
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-5035 <FUJ>
A:Cross-references: GB:M91452; NID:g164647; PIDN:AAA31119.1; PID:g164648
A:Accession: I46645
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-614; C', 616-5035 <FU2>
A:Cross-references: GB:M91451; NID:g164645; PIDN:AAA31118.1; PID:g164646
R:Leeb, T.; Brem, G.; Brenig, B.
submitted to the EMBL Data Library, November 1992
A:Description: Genomic organization of porcine skeletal muscle ryanodine receptor gene
A:Reference number: S31395
A:Accession: S31395
A:Molecule type: DNA
A:Residues: 1542-2643 <LBE>
A:Cross-references: EMBL:X69465
R:Leeb, T.; Schmoelzl, S.; Brem, G.; Brenig, B.
Genomics 18, 349-354, 1993
A:Title: Genomic organization of the porcine skeletal muscle ryanodine receptor (RYR1) gene
A:Reference number: A48915; MUID:94117003
A:Contents: annotation
R:Harbitz, I.; Kristensen, T.; Bosnes, M.; Kran, S.; Davies, W.
Anim. Genet. 23, 395-402, 1992
A:Title: DNA sequence of the skeletal muscle calcium release channel cDNA and verification
A:Reference number: I47133; MUID:93036581
A:Accession: I47133
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 2-2091; A', 2093-3494; L', 3496-4163; S', 4165-4182; R', 4184-4411; W', 4413-4971
A:Cross-references: EMBL:X62880; NID:g1936; PIDN:CAA44674.1; PID:g1937
R:Harbitz, I.; Kristensen, T.; Kran, T.; Davies, W.
submitted to the EMBL Data Library, August 1992
A:Reference number: S26624
A:Accession: S26624
A:Molecule type: DNA
A:Residues: 482-706 <HAW>
A:Cross-references: EMBL:X68247
R:Harbitz, I.; Chowdhary, B.; Thomsen, P.D.; Davies, W.; Kaufmann, U.; Kran, S.; Gustavs
Genomics 8, 243-248, 1990
A:Title: Assignment of the porcine calcium release channel gene, a candidate for the malignant hyperthermia gene
A:Reference number: A37105; MUID:91065640
A:Accession: A37105
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 4785-4971, R', 4973-5035 <HA2>
A:Cross-references: GB:M32501; NID:g164428; PIDN:AAA31022.1; PID:g164429
R:Leibetter, M.W.; Preiner, J.K.; Louis, C.F.; Mickelson, J.R.
J. Biol. Chem. 269, 31544-31551, 1994
A:Title: Tissue distribution of ryanodine receptor isoforms and alleles determined by reverse transcription-polymerase chain reaction
A:Reference number: A55660; MUID:95081095
A:Accession: I47212
A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA
A:Residues: 516-676 <LED>
A:Cross-references: EMBL:U15965; NID:g562095; PIDN:AAA60467.1; PID:g562096
C:Genetics: RYR1
A:Gene: RYR1
A:Introns: 527/1; 559/1; 598/3; 643/2; 1570/3; 1646/2; 1850/3; 1939/3; 2006/3; 2044/1
A:Note: the list of introns may be incomplete
C:Superfamily: ryanodine receptor; transcription initiation factor sigma region 1 homology
C:Keywords: calcium channel
Query Match 12.4%; Score 69; DB 1; Length 5035;
Best Local Similarity 20.3%; Pred. No. 2.4e+02;
Matches 25; Conservative 26; Mismatches 44; Indels 28; Gaps 4;
QY 9 LKELIEELVNTQASICNGSMVSVN-----LTAGMYCAALES--LINVSDCS 56
Db 522 LYEILASLRGNRANCAIFSNLDWLVSKLDRLSEASSILEVLCVLESFEVLNIEN 581
QY 57 AIQ-----RTQRLKALCSQKPAAGISSRSRDTKIE-----VIQLVKNLLTYV 100
Db 582 HIKSIISLLDKHGRNHKVLVDVLCSLVCVGVAVRSNQDLITENLLPGRELLQTNLINVY 641
QY 101 RGV 103
Db 642 TSI 644
RESULT 13
B35041
ryanodine receptor, skeletal muscle - rabbit
N:Alternate names: calcium-release channel protein; junctional channel complex
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 27-Jul-1990 #sequence_revision 10-Mar-1994 #text_change 20-Aug-1999
C:Accession: S04654; B35041; A36181; S53794; S32504
R:Takeshima, H.; Nishimura, S.; Matsumoto, T.; Ishida, H.; Kangawa, K.; Minamino, N.; Nature 339, 439-445, 1989
A:Title: Primary structure and expression from complementary DNA of skeletal muscle ryanodine receptor
A:Reference number: S04654; MUID:89262082
A:Accession: S04654
A:Molecule type: mRNA
A:Residues: 1-5037 <TAK>
A:Cross-references: EMBL:X15750; NID:g1709; PIDN:CAA33762.1; PID:g1710
A:Note: part of this sequence was confirmed by protein sequencing
R:Zorzato, F.; Fujii, J.; Otsu, K.; Phillips, M.; Green, N.M.; Lai, F.A.; Meissner, G.
J. Biol. Chem. 265, 2244-2256, 1990
A:Title: Molecular cloning of cDNA encoding human and rabbit forms of the Ca(2+) rele
A:Reference number: A35041; MUID:90130482
A:Accession: B35041
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 1-66; Y', 68-2014; D', 2016-3246; E', 3248-3480; 3486-4497; LE', 4498-4521; Q'
R:Marks, A.R.; Tempst, P.; Hwang, K.S.; Taubman, M.B.; Inui, M.; Chadwick, C.; Fleisc
Proc. Natl. Acad. Sci. U.S.A. 86, 8683-8687, 1989
A:Title: Molecular cloning and characterization of the ryanodine receptor/junctional
A:Reference number: A36181; MUID:90046857
A:Accession: A36181
A:Status: nucleic acid sequence not shown; not compared with conceptual translation
A:Molecule type: mRNA; protein
A:Residues: X', 1223-1235; XX', 1238-1251; 1334-1348; 1566-1569; X', 1571, X', 1573; 1597-1
-4679; X', 4681-4689; X', 4691-4693; X', 4695; X', 4697-4700 <MAR>
A:Note: the proteolytic fragments sequenced here from the junctional channel complex
R:Varsanyi, M.; Meyer, H.E.
Biol. Chem. Hoppe-Seyler 376, 45-49, 1995
A:Title: Sarcoplasmic reticular Ca(2+) release channel is phosphorylated at serine 28
A:Reference number: S53794; MUID:95336639
A:Accession: S53794
A:Molecule type: protein
A:Residues: 2841-2852 <VAR>
R:Takeshima, H.; Nishimura, S.; Nishi, M.; Ikeda, M.; Sugimoto, T.
FEBS Lett. 322, 105-110, 1993
A:Title: A brain-specific transcript from the 3'-terminal region of the skeletal musc

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2001, 06:02:08 ; Search time 44.64 Seconds
(without alignments)
84.411 Million cell updates/sec

Title: US-09-451-527-105

Perfect score: 556

Sequence: 1 SPVTPSPTLKELIELVNIT.....QLVKNLLTYRGVYRHGNFR 110

Scoring table:
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	367	66.0	132	1 IL13_HUMAN	P35225 homo sapien
2	345	62.1	132	1 IL13_BOVIN	Q9XSV9 bos taurus
3	302	54.3	131	1 IL13_MOUSE	P20109 mus musculus
4	294.5	53.0	131	1 IL13_RAT	P42203 rattus norv
5	72	12.9	5032	1 RYNR_HUMAN	P21817 homo sapien
6	71.5	12.9	261	1 SPRE_HUMAN	P35270 homo sapien
7	71.5	12.9	481	1 YAB8_SCHPO	Q09775 schizosacch
8	71	12.8	262	1 SPRE_RAT	P18297 rattus norv
9	70	12.6	725	1 VR2A_BPT4	P03690 bacterioph
10	69.5	12.5	192	1 FLHC_SALTY	O52222 salmone
11	69.5	12.5	431	1 ACRO_RABIT	P48038 oryctolagus
12	69	12.4	261	1 SPRE_MOUSE	O64105 mus musculus
13	69	12.4	5035	1 RYNR_PIG	P16980 sus scrofa
14	69	12.4	5037	1 RYNR_RABIT	P11716 oryctolagus
15	68	12.2	805	1 UBP5_YEAST	P39944 saccharomyc
16	68	12.2	936	1 FHL1_YEAST	P39521 saccharomyc
17	67.5	12.1	1164	1 KEL1_YEAST	P38853 saccharomyc
18	67	12.1	1231	1 TOP2_TRYBB	P12531 trypanosoma
19	65.5	12.0	323	1 GC_RABIT	P01870 oryctolagus
20	65.5	11.8	510	1 MUTL_THEMA	P74925 thermotoga
21	65.5	11.8	638	1 DNAK_RHILE	O33528 rhizobium
22	65	11.7	1477	1 A113_RAT	P14046 rattus norv
23	64.5	11.6	211	1 H1T_PIG	P06348 sus scrofa
24	64.5	11.6	701	1 UBP2_XENLA	P25980 xenopus lae
25	64	11.5	382	1 ADH2_ZYMO	P06758 zymomonas m
26	64	11.5	503	1 ZNT1_MOUSE	O60738 mus musculus
27	63.5	11.4	168	1 PTP_NPVAC	P24656 autographa
28	63.5	11.4	1004	1 YG21_YEAST	P53067 saccharomyc
29	63.5	11.4	1234	1 MED_MYCTU	P96380 mycobacteri
30	63	11.3	507	1 ZNT1_RAT	O62720 rattus norv
31	63	11.3	758	1 SC18_YEAST	P18759 saccharomyc
32	62.5	11.2	491	1 G6PD_RHIME	O92382 rhizobium m
33	62.5	11.2	952	1 YK15_CAEEL	P46012 caenorhabdi

34	62	11.2	171	1 TOXS_VIBPA	Q05939 vibrio para
35	62	11.2	192	1 FLHC_ECOLI	P11165 escherichia
36	62	11.2	774	1 LON1_BACSU	P37945 bacillus su
37	62	11.2	830	1 VP41_CAEEL	Q19954 caenorhabdi
38	62	11.2	1037	1 ACRD_ECOLI	P24177 escherichia
39	62	11.2	3329	1 BRC2_MOUSE	P97929 mus musculus
40	61.5	11.1	522	1 IMA2_XENLA	P52171 xenopus lae
41	61.5	11.1	677	1 UBFL_XENLA	P25979 xenopus lae
42	61.5	11.1	724	1 PAL2_PEA	Q04593 pisum sativ
43	61.5	11.1	901	1 MSH5_YEAST	Q12175 saccharomyc
44	61.5	11.1	1189	1 SC11_CHICK	O90988 gallus gall
45	61.5	11.1	1351	1 RPOM_YEAST	P13433 saccharomyc

ALIGNMENTS

RESULT 1
IL13_HUMAN
ID IL13_HUMAN STANDARD; PRT; 132 AA.
AC P35225; O43644;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13).
GN IL13 OR NC30.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=93211479; PubMed=8096327;
RA Minty A.J., Chalton P., Derocq J.M., Dumont X., Guillemot J.C.,
RA Kaghad M., Labit C., Lepatois P., Liauzun P., Miloux B.,
RA Minty C., Casellas P., Loison G., Lupker J., Shire D., Ferrara P.,
RA Caput D.;
RT "Interleukin-13 is a new human lymphokine regulating inflammatory and
RT immune responses.";
RL Nature 362:248-250(1993).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=93234572; PubMed=8097324;
RA McKenzie A.N., Cuipepper J.A., Waal Malefyt R., Briere F.,
RA Punnonen J., Aversa G., Sato A., Dang W., Cocks B.G., Menon S.,
RA de Vries J.E., Banchereau J., Zurawski G.R.;
RT "Interleukin 13, a T-cell-derived cytokine that regulates human
RT monocyte and B-cell function.";
RL Proc. Natl. Acad. Sci. U.S.A. 90:3735-3739(1993).
RN [3]
RP SEQUENCE FROM N.A.
RX Dolganov G., Lewis D.B., Lovett M., Burr J., Bort S., Short D.,
RA McGurn M., Gibson C.;
RL Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX TISSUE=Blood;
RL MEDLINE=95237624; PubMed=7721105;
RA Smirnov D.V., Smirnova M.G., Korobko V.G., Frolova E.I.;
RT "Tandem arrangement of human genes for interleukin-4 and
RT interleukin-13: resemblance in their organization.";
RL Gene 155:277-281(1995).
RN [5]
RP SEQUENCE FROM N.A.
RA Jang J.S., Kim B.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [6]
RP 3D-STRUCTURE MODELING.
RX MEDLINE=95132583; PubMed=7530359;
RA Bamorough P., Duncan D., Richards W.G.;
RT "Predictive modelling of the 3-D structure of interleukin-13.";
RL Protein Eng. 7:1077-1082(1994).
RN [7]

RP VARIANT GLN-130.
RX MEDLINE=20164293; PubMed=10699178;
RA Heinemann A., Mao X.-Q., Akaiwa M., Kreomer R.T., Gao P.-S.,
RA Ohshima K., Umeshita R., Aoe Y., Braun S., Yamashita T., Roberts M.H.,
RA Sugimoto R., Arima K., Arinobu Y., Yu B., Kruse S., Enomoto T.,
RA Date Y., Kawel M., Shimazu S., Sasaki S., Adra C.N., Kitachi M.,
RA Inoue H., Yamuchi K., Tomachi N., Kurimoto F., Hamasaki N.,
RA Hopkin J.M., Izuhara K., Shirakawa T., Delchmann K.A.;
"Genetic variants of IL-13 signalling and human asthma and atopy";
RL Hum. Mol. Genet. 9:549-559(2000).
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES.
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- POLYMORPHISM: GLN AT POSITION 130 IS A SIGNIFICANT RISK FACTOR FOR
CC ASTHMA DEVELOPMENT.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL: L06801; AAA36107.1; -
DR EMBL: X69079; CAA48824.1; -
DR EMBL: X69079; CAA48823.1; ALT_INIT.
DR EMBL: U31120; AAB01681.1; -
DR EMBL: U10307; AAB83738.1; -
DR EMBL: AF043334; AAC03535.1; -
DR PIR: A47481; A47481.
DR PDB: 3ITR; 15-JAN-95.
DR PDB: 3ITS; 26-JAN-95.
DR MIM: 147683; -
DR InterPro: IPR001325; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal; 3D-structure; Polymorphism.
FT SIGNAL 1 20
FT CHAIN 21 132 INTERLEUKIN-13.
FT DISULFID 48 76
FT DISULFID 64 90
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 72 72 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT VARIANT 130 130 R -> Q.
FT /FTID=VAR_010037.
FT CONFLICT 45 45 A -> R (IN REF. 4).
FT CONFLICT 87 87 S -> G (IN REF. 5).
FT CONFLICT 98 98 MISSING (IN REF. 4).
SQ SEQUENCE 132 AA; 14319 MW; 123FIDCAB87FD78B CRC64;

Query Match 66.0%; Score 367; DB 1; Length 132;
Best Local Similarity 69.1%; Pred. No. 4.3e-33;
Matches 76; Conservative 11; Mismatches 21; Indels 2; Gaps 2;

QY 2 PVTPSPFTLKELELVNTQNO-ASLCNGSMWSVNLTAAGCALESILNVSQSAIQ 60
ID IL13_MOUSE STANDARD: PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;

DT 30-MAY-2000 (Rel. 39, Last sequence update)
DE 30-MAY-2000 (Rel. 39, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13).
GN IL13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovine; Bos.
NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Bultkamp J., Jann O., Fries R.;
RT "The bovine interleukin-13 gene: genomic organization, chromosomal
RT location and evolution of the promoter";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS. MAY
CC BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY
CC SIMILARITY).
CC -1- SUBCELLULAR LOCATION: SECRETED.
CC -1- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@sib-sib.ch).

DR EMBL: A1132441; CAB46636.1; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; 1.
KW Cytokine; Glycoprotein; Signal.
FT SIGNAL 1 20
FT CHAIN 21 132 BY SIMILARITY.
FT DISULFID 48 76 INTERLEUKIN-13.
FT DISULFID 64 90 BY SIMILARITY.
FT CARBOHYD 38 38 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 57 57 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
SQ SEQUENCE 132 AA; 14623 MW; 723BD42375C161F3 CRC64;

Query Match 62.1%; Score 345; DB 1; Length 132;
Best Local Similarity 64.9%; Pred. No. 1.1e-30;
Matches 72; Conservative 16; Mismatches 21; Indels 2; Gaps 2;

QY 1 SPVTPSPFTLKELELVNTQNO-ASLCNGSMWSVNLTAAGCALESILNVSQSAIQ 59
ID IL13_MOUSE STANDARD: PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;

QY 60 PQRMKALCQKPAAG-GISSESRDPTKIEVLQVKNLLTYGVGRHGNF 109
ID IL13_MOUSE STANDARD: PRT; 131 AA.
AC P20109;
DT 01-FEB-1991 (Rel. 17, Created)
DT 01-FEB-1991 (Rel. 17, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
GN IL13 OR IL-13.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathu; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89093958; PubMed=2521353;

Brown K.D., Zurawski S.M., Mosmann T.R., Zurawski G.;
 "A family of small inducible proteins secreted by leukocytes are members of a new superfamily that includes leukocyte and fibroblast-derived inflammatory agents, growth factors, and indicators of various activation processes.";
 J. Immunol. 142:679-687(1989).
 CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.
 CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
 CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; M23504; AAA40149.1; -
 CC PIR; E30552; E30552.
 CC HSP; P35225; 31TR.
 CC MGD; MGI:96541; I113.
 CC InterPro; IPR001325; -
 CC PROSITE; PS00838; INTERLEUKIN_4_13; 1.
 CC Cytokine; Glycoprotein; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC CHAIN 22 131 INTERLEUKIN-13.
 CC DISULFID 51 79 BY SIMILARITY.
 CC DISULFID 67 93 BY SIMILARITY.
 CC CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 52 52 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 75 75 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 131 AA; 14107 MW; 954F93FF105713FED CRC64;
 SQ
 Query Match 54.3%; Score 302; DB 1; Length 131;
 Best Local Similarity 58.8%; Pred. No. 5e-26;
 Matches 60; Conservative 16; Mismatches 24; Indels 2; Gaps 1;
 QY 8 TLKELIEELVNITQNCASLCNGSMVSVNLTAGMYCAALESILNVSDCSATQRTQMLKA 67
 DB 32 TLKELIEELSNITQDQTPCLNGSMVSVNLAAGGFCVALDSLTNISCNAILYRTQRLHG 91
 QY 68 LCSOKPAAGTSSRSRDTKIEVLQVKNLLTYVRGVYRHGNF 109
 DB 92 LCNRKAPTIVSS--LPDTKIEVAHFITKLLSYTKQLFRHGF 131
 RESULT 4
 ID IL13_RAT STANDARD; PRT; 131 AA.
 AC P42203;
 DT 01-NOV-1995 (Rel. 32, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE INTERLEUKIN-13 PRECURSOR (IL-13) (T-CELL ACTIVATION PROTEIN P600).
 GN IL13 OR IL-13.
 OS Rattus norvegicus (Rat).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Rattus.
 CC NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-SPRAGUE-DAWLEY; TISSUE=Kidney cortex;
 RX MEDLINE=94092138; PubMed=7916615;
 RA Lakkis F.G., Cruet E.N.;
 RT "Cloning of rat interleukin-13 (IL-13) cDNA and analysis of IL-13 gene expression in experimental glomerulonephritis.";
 RL Biochem. Biophys. Res. Commun. 197:612-618(1993).
 CC -!- FUNCTION: CYTOKINE. INHIBITS INFLAMMATORY CYTOKINE PRODUCTION.

CC SYNERGIZES WITH IL2 IN REGULATING INTERFERON-GAMMA SYNTHESIS.
 CC MAY BE CRITICAL IN REGULATING INFLAMMATORY AND IMMUNE RESPONSES (BY SIMILARITY).
 CC -!- SUBCELLULAR LOCATION: SECRETED.
 CC -!- SIMILARITY: BELONGS TO THE IL-4 / IL-13 FAMILY.
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See <http://www.isb-sib.ch/announce/> or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL; L26913; AAA16478.1; -
 CC HSP; P35225; 31TR.
 CC InterPro; IPR001325; -
 CC PROSITE; PS00838; INTERLEUKIN_4_13; 1.
 CC Cytokine; Glycoprotein; Signal.
 CC SIGNAL 1 21 BY SIMILARITY.
 CC CHAIN 22 131 INTERLEUKIN-13.
 CC DISULFID 52 80 BY SIMILARITY.
 CC DISULFID 68 94 BY SIMILARITY.
 CC CARBOHYD 42 42 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 53 53 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC CARBOHYD 76 76 N-LINKED (GLCNAC. . .) (POTENTIAL).
 CC SEQUENCE 131 AA; 14093 MW; E5008CAB8DE8C201 CRC64;
 SQ
 Query Match 53.0%; Score 294.5; DB 1; Length 131;
 Best Local Similarity 58.5%; Pred. No. 3.3e-25;
 Matches 62; Conservative 18; Mismatches 23; Indels 3; Gaps 3;
 QY 4 TSPITLKELIEELVNITQNCASLCNGSMVSVNLTAGMYCAALESILNVSDCSATQRTQ 62
 DB 28 SPVALRELIEELSNITQDQTKSLCNSMVSVDLTAGGCALESILNISCNAIHRQT 87
 QY 63 RMLKALCSOKPAAGTSSRSRDTKIEVLQVKNLLTYVRGVYRHGN 108
 DB 88 RLNLGLCNQK-ASDVASS-PPDTKIEVAQFISKLLNSKQLFRYGH 131
 RESULT 5
 ID RYNR_HUMAN STANDARD; PRT; 5032 AA.
 AC P21817;
 DT 01-MAY-1991 (Rel. 18, Created)
 DT 01-MAY-1991 (Rel. 18, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE CHANNEL).
 DE GN RYR1 OR RYDR.
 OS Homo sapiens (Human).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Skeletal muscle;
 RX MEDLINE=90130482; PubMed=2298749;
 RA Zorzato F., Fujii J., Otsu K., Phillips M., Green N.M., Lai F.A., Weissner G., MacLennan D.H.;
 RT "Molecular cloning of cDNA encoding human and rabbit forms of the Ca2+ release channel (ryanodine receptor) of skeletal muscle sarcoplasmic reticulum.";
 RT J. Biol. Chem. 265:2244-2256(1990).
 RN [2]
 RP VARIANT MH CYS-614.
 RX MEDLINE=92128959; PubMed=1774074;
 RA Gillard E.F., Otsu K., Fujii J., Khanna V.K., de Leon S., Derdemezi J., Britt B.A., Duff C.L., Worton R.G., McLennan D.H.;
 RT "A substitution of cysteine for arginine 614 in the ryanodine

RT receptor is potentially causative of human malignant hyperthermia.";
RL Genomics 11:751-755(1991).
RN [3]
RP VARIANT MH ARG-248, AND VARIANTS CYS-471, LEU-1786 AND CYS-2059.
RX MEDLINE-92372020; PubMed-1354642;
RA Gillard E.F., Otsu K., Fujii J., Duff C., de Leon S., Khanna V.K.,
RT Britl B.A., Morton R.G., Mcleenan D.H.;
RT "Polymorphisms and deduced amino acid substitutions in the coding
sequence of the ryanodine receptor (RyR1) gene in individuals with
malignant hyperthermia.";
RL Genomics 13:1247-1254(1992).
RN [4]
RP VARIANT CCD HIS-2434.
RX MEDLINE-94035117; PubMed-8220422;
RA Zhang Y., Chen H.S., Khanna V.K., de Leon S., Phillips M.S.,
RT Schappert K., Britl B.A., Brownell A.K.W., Macleenan D.H.;
RT "A mutation in the human ryanodine receptor gene associated with
central core disease.";
RL Nat. Genet. 5:46-50(1993).
RN [5]
RP VARIANTS CCD CYS-163 AND MET-403.
RX MEDLINE-94035118; PubMed-8220423;
RA Quane K.A., Healy J.M.S., Keating K.E., Manning B.M., Couch F.J.,
RT Palmucci L.M., Doriguzzi C., Fagerlund T.H., Berg K., Ordling H.,
RA Bendixen D., Mortier W., Linz U., Muller C.R., McCarthy T.V.;
RT "Mutations in the ryanodine receptor gene in central core disease and
malignant hyperthermia.";
RL Nat. Genet. 5:51-55(1993).
RN [6]
RP VARIANT MH SER-522.
RX MEDLINE-95130087; PubMed-7829078;
RA Quane K.A., Keating K.E., Healy J.M.S., Manning B.M.,
RT Krivosic-Horber R., Krivosic I., Monnier N., Lunardi J.,
RA McCarthy T.V.;
RT "Mutation screening of the RyR1 gene in malignant hyperthermia:
detection of a novel Tyr to Ser mutation in a pedigree with
associated central cores.";
RL Genomics 23:236-239(1994).
RN [7]
RP VARIANT MH ARG-341.
RX MEDLINE-9428042; PubMed-8012359;
RA Quane K.A., Keating K.E., Manning B.M., Healy J.M.S., Monsieus K.,
RT Heffron J.J.A., Lehane M., Heytens L., Krivosic-Horber R., Adnet P.,
RA Ellis F.R., Monnier N., Lunardi J., McCarthy T.V.;
RT "Detection of a novel common mutation in the ryanodine receptor gene
in malignant hyperthermia: implications for diagnosis and
heterogeneity studies.";
RL Hum. Mol. Genet. 3:471-476(1994).
RN [8]
RP VARIANT MH ARG-2433.
RX MEDLINE-95152512; PubMed-7849712;
RA Keating K.E., Quane K.A., Manning B.M., Lehane M., Hartung E.,
RT Censier K., Urwyler A., Klausltzer M., Muller C.R., Heffron J.J.A.,
RA McCarthy T.V.;
RT "Detection of a novel RyR1 mutation in four malignant hyperthermia
pedigrees.";
RL Hum. Mol. Genet. 3:1855-1858(1994).
RN [9]
RP VARIANT MH ARG-2433.
RX MEDLINE-95187158; PubMed-7881417;
RA Phillips M.S., Khanna V.K., de Leon S., Frodis W., Britl B.A.,
RT Mcleenan D.H.;
RT "The substitution of Arg for Gly2433 in the human skeletal muscle
ryanodine receptor is associated with malignant hyperthermia.";
RL Hum. Mol. Genet. 3:2181-2186(1994).
RN [10]
RP VARIANT MH ARG-35.
RX MEDLINE-97219028; PubMed-9066328;
RA Lynch P.J., Krivosic-Horber R., Reyford H., Monnier N., Quane K.,
RT Adnet P., Haudecoeur G., Krivosic I., McCarthy T., Lunardi J.;
RT "Identification of heterozygous and homozygous individuals with the
novel RyR1 mutation Cys35Arg in a large kindred.";
RL Anesthesiology 86:620-626(1997).

RN [11]
RP VARIANT MH LEU-614.
RX MEDLINE-98051280; PubMed-9389851;
RA Quane K.A., Ordling H., Keating K.E., Manning B.M., Heine R.,
RT Bendixen D., Berg K., Krivosic-Horber R., Lehmann-Horn F.,
RA Fagerlund T., McCarthy T.V.;
RT "Detection of a novel mutation at amino acid position 614 in the
ryanodine receptor in malignant hyperthermia.";
RL Br. J. Anaesth. 79:332-337(1997).
RN [12]
RP VARIANT MH TRP-552.
RX MEDLINE-97284075; PubMed-9138151;
RA Keating K.E., Giblin L., Lynch P.J., Quane K.A., Lehane M.,
RT Heffron J.J.A., McCarthy T.V.;
RT "Detection of a novel mutation in the ryanodine receptor gene in an
Irish malignant hyperthermia pedigree: correlation of the IVCT
response with the affected and unaffected haplotypes.";
RL J. Med. Genet. 34:291-296(1997).
RN [13]
RP VARIANTS MH CYS-2162, HIS-2162, MET-2167 AND MET-2205.
RX MEDLINE-98163444; PubMed-9497245;
RA Manning B.M., Quane K.A., Ordling H., Urwyler A., Tegazzin V.,
RT Lehane M., O'Halloran J., Hartung E., Giblin L.M., Lynch P.J.,
RA Vaughan P., Censier K., Bendixen D., Comi G., Heytens L.,
RA Monsieus K., Fagerlund T., Wolz W., Heffron J.J.A., Mueller C.R.,
RT McCarthy T.V.;
RT "Identification of novel mutations in the ryanodine-receptor gene
(RyR1) in malignant hyperthermia: genotype-phenotype correlation.";
RL Am. J. Hum. Genet. 62:599-609(1998).
RN [14]
RP VARIANTS MH CYS-2458 AND HIS-2458.
RX MEDLINE-98111378; PubMed-9450902;
RA Manning B.M., Quane K.A., Lynch P.J., Urwyler A., Tegazzin V.,
RT Krivosic-Horber R., Censier K., Comi G., Adnet P., Wolz W.,
RA Lunardi J., Muller C.R., McCarthy T.V.;
RT "Novel mutations at a Cpg dinucleotide in the ryanodine receptor in
malignant hyperthermia.";
RL Hum. Mutat. 11:45-50(1998).
RN [15]
RP VARIANT MH.
RX MEDLINE-99415746; PubMed-10484775;
RA Brandt A., Schleithoff L., Jurkat-Rott K., Klingler W., Baur C.,
RT Lehmann-Horn F.;
RT "Screening of the ryanodine receptor gene in 105 malignant
hyperthermia families: novel mutations and concordance with the in
vitro contracture test.";
RL Hum. Mol. Genet. 8:2055-2062(1999).
RN [16]
RP VARIANTS MH LEU-2434 AND HIS-2453.
RX MEDLINE-99158296; PubMed-10051009;
RA Barone V., Massa O., Intravala E., Bracco A., Di Martino A.,
RT Tegazzin V., Cozzolino S., Sorrentino V.;
RT "Mutation screening of the RyR1 gene and identification of two novel
mutations in Italian malignant hyperthermia families.";
RL J. Med. Genet. 36:115-118(1999).
RN [17]
RP VARIANTS MH CYS-2453.
RX MEDLINE-20081079; PubMed-10612851;
RA Gencik M., Gencik A., Mortier W., Epplen J.T.;
RT "Novel mutation in the RyR1 gene (R2453C) in a patient with malignant
hyperthermia.";
RL Hum. Mutat. 15:122-122(2000).
RN [18]
RP FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
SARCOPLASMIC RETICULUM. CONTRACTION OF SKELETAL MUSCLE IS
TRIGGERED BY RELEASE OF CA++ FROM SR FOLLOWING DEPOLARIZATION OF
T-TUBULES.
CC -I- SUBUNIT: HOMOTETRAMER (POTENTIAL).
CC -I- DISEASE: A DEFICIENCY IN THE RYANODINE RECEPTOR MAY BE THE CAUSE
OF MALIGNANT HYPERTHERMIA (MH) AND OF CENTRAL CORE DISEASE OF
MUSCLE (CCD). MH IS AN AUTOSOMAL DOMINANT DISORDER OF SKELETAL
MUSCLE AND IS ONE OF THE MAIN CAUSES OF DEATH DUE TO ANESTHESIA.
CC IN SUSCEPTIBLE PEOPLE, AN MH EPISODE CAN BE TRIGGERED BY ALL
COMMONLY USED INHALATIONAL ANESTHETICS SUCH AS HALOTHANE AND BY

CC DEPOLARIZING MUSCLE RELAXANTS SUCH AS SUCCINYLCHOLINE. THE
 CC CLINICAL FEATURES OF THE MYOPATHY ARE HYPERTHERMIA, ACCELERATED
 CC MUSCLE METABOLISM, CONTRACTURES, METABOLIC ACIDOSIS, TACHYCARDIA
 CC AND DEATH, IF NOT TREATED WITH THE POSTSYNAPTIC MUSCLE RELAXANT,
 CC DANTRONE. SUSCEPTIBILITY TO MH CAN BE DETERMINED WITH THE "IN
 CC VITRO" CONTRACTURE TEST (IVCT): OBSERVING THE MAGNITUDE OF
 CC CONTRACTURES INDUCED IN STRIPS OF MUSCLE TISSUE BY CAFFEINE ALONE
 CC AND HALOTHANE ALONE. PATIENTS WITH NORMAL RESPONSE ARE MH NORMAL
 CC (MHN), THOSE WITH ABNORMAL RESPONSE TO CAFFEINE ALONE OR HALOTHANE
 CC ALONE ARE MH EQUIVOCAL (MHE(C) AND MHE(H) RESPECTIVELY).
 CC -!- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL IS MODULATED BY CA++,
 CC MG++, ATP, AND CALMODULIN.
 CC -!- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE
 CC C-TERMINAL REGION WHILE THE REMAINING PART OF THE PROTEIN
 CC CONSTITUTES THE "FOOT" STRUCTURE SPANNING THE JUNCTIONAL GAP
 CC BETWEEN THE SR AND THE T-TUBULE. IT IS POSSIBLE THAT THE FOOT
 CC STRUCTURE INTERACTS WITH THE CYTOPLASMIC REGION OF THE
 CC DIHYDROPYRIDINE RECEPTOR.
 CC -!- MISCELLANEOUS: RYANODINE IS AN ALKALOID THAT BINDS TO THE
 CC CA-RELEASE CHANNEL IN JUNCTIONAL SR AND MODULATES ITS ACTIVITY.
 CC -!- SIMILARITY: LOCAL & LOW WITH THE NICOTINIC ACETYLCHOLINE RECEPTOR
 CC (N-ACHR) SUBUNIT.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M76231; AAA60314.1; -
 CC PIR; JQ1176; JQ1176.
 CC MI; 182125; -
 CC InterPro; IPR002198; -
 CC Pfam; PF00106; adh_short; 1.
 CC Oxidoreductase; NADP; Acetylation.
 CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 CC NP_BIND 13 39 NADP (BY SIMILARITY).
 CC DOMAIN 28 32 PTERIN BINDING (POTENTIAL).
 CC SEQUENCE 261 AA; 28048 MW; 9C9BF76212826F47 CRC64;
 CC
 CC Query Match 12.9%; Score 72; DB 1; Length 5032;
 CC Best Local Similarity 21.1%; Pred. No. 43;
 CC Matches 26; Conservative 26; Mismatches 43; Indels 28; Gaps 4;
 CC
 CC QY 9 LKELIELVNITQNASLNGSMVSVN-----LFGMYCALES--LINVSDCS 56
 CC DB 521 LVELLASLIRGNRCALFSTNLDVLVSKLDREASSGILEVLYCVLSEPEVLNIQEN 580
 CC
 CC QY 57 ATO-----RTORMLKALCSQKPAAGISSERSRDTKIE-----VTQLVKNLITYV 100
 CC DB 581 HKSIISLLDKGRNHKVLVDVLCVCGNGVAVRSNODLITENLLPGLRELLQTNLNYV 640
 CC
 CC QY 101 RGV 103
 CC DB 641 TSI 643
 CC
 CC RESULT 6
 CC SPRE_HUMAN
 CC ID SPRE_HUMAN STANDARD; PRT; 261 AA.
 CC AC P35270;
 CC DT 01-FEB-1994 (Rel. 28, Created)
 CC DT 01-FEB-1994 (Rel. 28, Last sequence update)
 CC DT 01-OCT-2000 (Rel. 40, Last annotation update)
 CC DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
 CC GN SPR.
 CC OS Homo sapiens (Human).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC TISSUE=Liver;
 CC RX MEDLINE=91354248; PubMed=1883349;
 CC RA Ichinose H., Katoh S., Sueoka T., Titani K., Fujita K., Nagatsu T.;
 CC RT "Cloning and sequencing of cDNA encoding human sepiapterin
 CC RT reductase -- an enzyme involved in tetrahydrobiopterin biosynthesis.";
 CC RL Biochem. Biophys. Res. Commun. 179:183-189 (1991).
 CC -!- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
 CC HYDROBIPTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIPTERIN.
 CC -!- CATALYTIC ACTIVITY: 7,8-DIHYDROBIPTERIN + NADP(+) = SEPIAPTERIN +
 CC NADPH.
 CC -!- SUBUNIT: HOMODIMER.
 CC -!- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -!- DISEASE: DEPRESSED SYNTHESIS OF TETRAHYDROBIPTERIN MAY PLAY A
 CC ROLE IN A VARIETY OF HUMAN DISEASES.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; M76231; AAA60314.1; -
 CC PIR; JQ1176; JQ1176.
 CC MI; 182125; -
 CC InterPro; IPR002198; -
 CC Pfam; PF00106; adh_short; 1.
 CC Oxidoreductase; NADP; Acetylation.
 CC MOD_RES 1 1 ACETYLATION (BY SIMILARITY).
 CC NP_BIND 13 39 NADP (BY SIMILARITY).
 CC DOMAIN 28 32 PTERIN BINDING (POTENTIAL).
 CC SEQUENCE 261 AA; 28048 MW; 9C9BF76212826F47 CRC64;
 CC
 CC Query Match 12.9%; Score 71.5; DB 1; Length 261;
 CC Best Local Similarity 24.7%; Pred. No. 1.4;
 CC Matches 24; Conservative 21; Mismatches 41; Indels 11; Gaps 4;
 CC
 CC QY 16 LVNTITQNASLNGSMV---WSVNLTAGMYCALES--LINVSDCSAIQRTQRMKALCSQK 72
 CC DB 104 LGDVSKGFVLDSDSTQVNNYVALNLTSLMCLUTSSVLKAFDPSPGLNRTVVNISSICALQ 162
 CC
 CC QY 73 PAAG-----ISSERSRDTKIEVIQVVK---NLLTYVRG 102
 CC DB 163 PFKGWALYCAGKAARDMLFQVLALEENPVRLNYPG 199
 CC
 CC RESULT 7
 CC YA88_SCHPO
 CC ID YA88_SCHPO STANDARD; PRT; 481 AA.
 CC AC Q09775;
 CC DT 01-NOV-1995 (Rel. 32, Created)
 CC DT 01-NOV-1995 (Rel. 32, Last sequence update)
 CC DT 01-NOV-1995 (Rel. 32, Last annotation update)
 CC DE PUTATIVE ATP-DEPENDENT RNA HELICASE C22F3.08C.
 CC GN SPAC22F3.08C.
 CC OS Schizosaccharomyces pombe (Fission yeast).
 CC OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC OC Schizosaccharomycetales; Schizosaccharomycetaceae;
 CC OC Schizosaccharomycetes.
 CC OX NCBI_TaxID=4896;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC STRAIN=972;
 CC RA Lye G., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
 CC RL Submitted (SEP-1995) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: PUTATIVE ATP-DEPENDENT RNA HELICASE.
 CC -!- SIMILARITY: BELONGS TO THE "DEAD" BOX FAMILY HELICASE.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
 CC or send an email to license@isb-sib.ch).
 CC
 CC EMBL; Z54285; CAA91073.1; -
 CC InterPro; IPR000629; -
 CC InterPro; IPR001410; -
 CC InterPro; IPR001650; -
 CC Pfam; PF00270; DEAD; 1.
 CC Pfam; PF00271; helicase_C; 1.
 CC PROSITE; PS00039; DEAD_ATP_HELICASE; 1.
 CC KW Hypothetical protein; ATP-binding; RNA-binding; Helicase.
 CC FT NP_BIND 90 97 ATP (POTENTIAL).

FT SITE 196 199 DEAD BOX.
SQ SEQUENCE 481 AA: 54026 MW: 872ECAF0106E110A CRC64;

Query Match 12.9%; Score 71.5; DB 1; Length 481;
Best Local Similarity 24.3%; Pred. No. 2.9;
Matches 25; Conservative 25; Mismatches 48; Indels 5; Gaps 4;

OY 5 PSPITKEL-TELUNTONQASLNGSMWVS-NLTAGYCALESINVSQSAIORPQ 62
Db 18 POPSITKEKAKKLOGITGKAKVTGNPDPIEPEEGILCENLKKO-NITECTIOR-- 74

OY 63 RLKALGSKPAAGISSERSRDTKIEVLIQVKNLITYGVYR 105
Db 75 YAIPTIGSRDLACAPGSGKTIATVPIPIQKLOLHVPGTR 117

RESULT 8
ID SPRE_RAT STANDARD; PRT; 262 AA.

AC P18297;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
GN SPR.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;

RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
RC TISSUE=Liver;
RX MEDLINE=90349631; PubMed=2201030;
RA Clifton B.A., Mjstlien S., Gutierrez J.C., Levine R.A., Yanak B.L.,
KAufman S.;
RT Isolation and expression of rat liver sepiapterin reductase cDNA.";
RL Proc. Natl. Acad. Sci. U.S.A. 87:6436-6440(1990).
RN [2]

RP MEDLINE=91083647; PubMed=2260974;
RA Oyama R., Kato S., Sueoka T., Suzuki M., Ichinose H., Nagatsu T.,
RA Tlcani K.;
RT "The complete amino acid sequence of the mature form of rat
RT sepiapterin reductase.";
RL Biochem. Biophys. Res. Commun. 173:627-631(1990).

CC -1- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
CC HYDROBIOTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOTERIN.
CC -1- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOTERIN + NADP(+) = SEPIAPTERIN +
CC NADPH.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL: M36410; AAA42130.1; -
CC PIR: A36400; A36400.
CC InterPro: IPR002198; -
CC DR Pfam: PF00106; adh_short; 1.
CC Oxidoreductase; NADP; Acetylation.
KW MOD_RES 1 ACETYLATION.
FT NP_BIND 14 40 NADP (BY SIMILARITY).
FT DOMAIN 29 33 PTERIN BINDING (POTENTIAL).
SQ SEQUENCE 262 AA: 28128 MW: EC992564A033C61 CRC64;

Query Match 12.8%; Score 71; DB 1; Length 262;

Best Local Similarity 23.5%; Pred. No. 1.6;
Matches 24; Conservative 25; Mismatches 41; Indels 12; Gaps 4;

OY 8 TLKELIELVNITONQASLNGSMWVS-NLTAGYCALESINVSQSAIORPMLKA 67
Db 104 TLGVSGKPLININ---DLAEVNNYVALNLITS-MLCITGTLNMFNSPGLSKIVNMISS 158

OY 68 LCSOKPAAG-----ISSERSRDTKIEVLIQVKNLITYVNG 102
Db 159 LCALOPFGKGLYCAGKARDMLQVLAPEPSVYVLSYAFG 200

RESULT 9
ID VR2A_BP74 STANDARD; PRT; 725 AA.

AC P03690;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-MAY-1992 (Rel. 22, Last sequence update)
DT 01-OCT-2000 (Rel. 40, Last annotation update)
DE RIIA PROTEIN.
GN RIIA.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Tailed phages; Myoviridae;
OX T4-like phages.
OX NCBI_TaxID=10665;

RP SEQUENCE FROM N.A.
RX MEDLINE=90337270; PubMed=2379817;
RA Daegelen P., Brody E.;
RT "The rIIA gene of bacteriophage T4. I. Its DNA sequence and discovery
RT of a new open reading frame between genes 60 and rIIA.";
RL Genetics 125:237-248(1990).
RN [2]

RP SEQUENCE OF 476-725 FROM N.A.
RX MEDLINE=84267841; PubMed=6748077;
RA Sugino A., Drake J.W.;
RT Modulation of mutation rates in bacteriophage T4 by a base-pair
RT change a dozen nucleotides removed.";
RL J. Mol. Biol. 176:239-249(1984).
RN [3]

RP SEQUENCE OF 587-725 FROM N.A.
RX MEDLINE=82078066; PubMed=6273585;
RA Probow D., Sigurdson D.C., Gold L., Singer B.S., Nappoli C.,
RA Brosius J., Dull T.J., Noller H.F.;
RT "rII cistrons of bacteriophage T4. DNA sequence around the
RT intergenic divide and positions of genetic landmarks.";
RL J. Mol. Biol. 149:337-376(1981).

CC -1- FUNCTION: TRANSCRIBED PRIOR TO REPLICATION. THIS PROTEIN FORM
CC PARTS OF THE REPLICATION COMPLEX AND HAS DNA-BINDING PROPERTIES.
CC -1- SUBCELLULAR LOCATION: ON THE INNER MEMBRANE OF THE HOST SHORTLY
CC AFTER INFECTION.

CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).

CC -----
CC EMBL: X52686; CAA36911.1; -
CC PIR: A04304; Z2BP44.
CC DR PIR: J00400; J00400.
CC Early protein; DNA-binding; DNA replication; Inner membrane; Repeat.
KW REPEAT 101 179 APPROXIMATE.
FT REPEAT 481 559 APPROXIMATE.
FT DNA_BIND 544 570 H-T-H MOTIF (BY SIMILARITY).
FT CONFLICT 616 616 D -> H (TN REF. 2).
SQ SEQUENCE 725 AA: 82893 MW: 2290FE341BB45416 CRC64;

Query Match 12.6%; Score 70; DB 1; Length 725;
Best Local Similarity 27.0%; Pred. No. 6.9;

```

DE ACROSIN PRECURSOR (EC 3.4.21.10).
GN ACR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxId=9986;
[1]
RN SEQUENCE FROM N.A.
RP STRAIN=NEW ZEALAND WHITE; TISSUE=Testis;
RX MEDLINE=94368861; PubMed=8086468;
RA Richardson R.T., O'Rand M.G.;
RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
RT preproacrosin-related cDNA.";
RL Biochim. Biophys. Acta 1219:215-218(1994).
CC -1- FUNCTION: ACROSIN IS THE MAJOR PROTEASE OF MAMMALIAN SPERMATOZOA.
CC IT IS A SERINE PROTEASE OF TRYPSIN-LIKE CLEAVAGE SPECIFICITY. IT
CC IS SYNTHESIZED IN A ZYMOGEN FORM, ACROCRIN AND STORED IN THE
CC ACROSOME.
CC -1- CATALYTIC ACTIVITY: HYDROLYSIS OF ARG- AND LYS-BONDS; PREFERENTIAL
CC CLEAVAGE ARG-XAA >> LYS-LYS >> LYS-XAA.
CC -1- SUBUNIT: HEAVY CHAIN (CATALYTIC) AND A LIGHT CHAIN LINKED BY TWO
CC DISULFIDE BONDS.
CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY S1; ALSO KNOWN AS THE
CC TRYPSIN FAMILY.
-----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL: U05204; AAA61630.1; -
DR MEROPS: S01.223; -
DR InterPro: IPR001254; -
DR InterPro: IPR001314; -
DR Pfam: PF00089; trypsin; 1.
DR PRINTS: P000722; CHYMOTRYPSIN.
DR PROSITE: PS00134; TRYPSIN_HIS; 1.
DR PROSITE: PS00135; TRYPSIN_SER; 1.
DR Hydrolase; Serine protease; Glycoprotein; Zymogen; Sperm; Signal.
KW SIGNAL
FT SIGNAL 1 16
FT CHAIN 17 431 ACROSIN.
FT CHAIN 17 39 ACROSIN LIGHT CHAIN (BY SIMILARITY).
FT CHAIN 40 ? ACROSIN HEAVY CHAIN (BY SIMILARITY).
FT PROPEP ? 431 PRO-RICH.
FT FT DISULFID 22 152 INTERCHAIN (BY SIMILARITY).
FT FT DISULFID 26 160 INTERCHAIN (BY SIMILARITY).
FT FT DISULFID 71 87 BY SIMILARITY.
FT FT DISULFID 175 244 BY SIMILARITY.
FT FT DISULFID 207 223 BY SIMILARITY.
FT FT DISULFID 234 264 BY SIMILARITY.
FT FT CARBOHYD 19 19 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT CARBOHYD 208 208 N-LINKED (GLCNAC. . .) (POTENTIAL).
FT FT ACT_SITE 86 86 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT FT ACT_SITE 140 140 CHARGE RELAY SYSTEM (BY SIMILARITY).
FT FT ACT_SITE 238 238 CHARGE RELAY SYSTEM (BY SIMILARITY).
SQ SEQUENCE 431 AA; 45422 MW; 1C0154AE0BC0C668 CRC64;
Query Match 12.5%; Score 69.5; DB 1; Length 431;
Best Local Similarity 36.4%; Pred. No. 4.1;
Matches 16; Conservative 7; Mismatches 16; Indels 5; Gaps 1;
Qy 5 PSPTKLIELVNIQTQASLCNGSMVSWNLTAGMYCAALES 48
||||| :||: ||| : :||| :|
Db 190 PSPTLMEARVDLNL-----ELCNSQTQWNGRITASNLCAGYPS 228
RESULT 12
SPRE_MOUSE
ID SPRE_MOUSE STANDARD; PRT; 261 AA.

```

AC Q64105: Q63996;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-OCT-2000 (Rel. 40, Last annotation update)
 DE SEPIAPTERIN REDUCTASE (EC 1.1.1.153) (SPR).
 GN SPR.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95178553; PubMed=7873607;
 RA Ota A., Ichinose H., Nagatsu T.;
 RT "Mouse sepiapterin reductase: an enzyme involved in the final step of
 tetrahydrobiopterin biosynthesis. Primary structure deduced from the
 RT cDNA sequence."
 RL Biochim. Biophys. Acta 1260:320-322(1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX STRAIN=129;
 RX MEDLINE=99227131; PubMed=10209270;
 RA Lee S.W., Park I.Y., Hahn Y., Lee J.E., Seong C.S., Chung J.H.,
 RA Park Y.S.;
 RT "Cloning of mouse sepiapterin reductase gene and characterization of
 RT its promoter region."
 RL Biochim. Biophys. Acta 1445:165-171(1999).
 RN [3]
 RP SEQUENCE OF 209-261 FROM N.A.
 RX MEDLINE=94136218; PubMed=8304109;
 RA Meier J., Schott K., Werner T., Bacher A., Ziegler I.;
 RT "Northern blot analysis of sepiapterin reductase mRNA in mammalian
 RT cell lines and tissues."
 RL Adv. Exp. Med. Biol. 338:195-198(1993).
 RN [4]
 RP X-RAY CRYSTALLOGRAPHY (1.25 ANGSTROMS).
 RX MEDLINE=98070299; PubMed=9405351;
 RA Auerbach G., Herrmann A., Gutlich M., Fischer M., Jacob U., Bacher A.,
 RA Huber R.;
 RT "The 1.25-A crystal structure of sepiapterin reductase reveals its
 RT binding mode to pterins and brain neurotransmitters."
 RL EMBO J. 16:7219-7230(1997).
 CC -1- FUNCTION: CATALYZES THE FINAL ONE OR TWO REDUCTIONS IN TETRA-
 CC HYDROBIOTERIN BIOSYNTHESIS TO FORM 5,6,7,8-TETRAHYDROBIOTERIN.
 CC -1- CATALYTIC ACTIVITY: 7,8-DIHYDROBIOTERIN + NADPH(+) = SEPIAPTERIN +
 CC NADPH.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement (see <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: S77493; AAB33611.1; -;
 DR EMBL: U78077; AAC69364.1; -;
 DR EMBL: U78076; AAC69364.1; JOINED.
 DR EMBL: S71375; -; NOT_ANNOTATED_CDS.
 DR PDB: 1SEP; 13-JAN-99.
 DR PDB: 1OAA; 16-FEB-99.
 DR PDB: 1NAB; 30-MAR-99.
 DR MGI: 103078; Spr.
 DR InterPro: IPR002198; -;
 DR Pfam: PF00106; adh_short; 1.
 KW Oxidoreductase; NADP; 3D-structure.
 FT NE_BIND 14 40 NADP (BY SIMILARITY).
 FT DOMAIN 29 33 PTERIN BINDING (POTENTIAL).
 FT CONFLICT 4 4 D -> G (IN REF. 2).
 SO SEQUENCE 261 AA; 27883 MW; 102294E439C8BAEC CMC64;

Query Match 12.4%; Score 69; DB 1; Length 261;
 Best Local Similarity 21.5%; Pred. No. 2.6;
 Matches 23; Conservative 26; Mismatches 46; Indels 12; Gaps 4;
 Oy 3 VTSPFLKEIEELVNTNQASICNGSWVSNLTGMYCALDESILNVDSAGIQRTO 62
 Db 99 INNAATLGDVSKRFLVNN----DLAEVNNWALNTLS-MCLTSGITANQDSFGLSKTV 153
 Oy 63 RMLKALCSORPAAG---ISSERSRDTKIEVIOLVK--MLTYVRG 102
 Db 154 VNISICALQPYKGWGLYCAGKAARDMLYQVLAAEBSVRLSVAPG 200
 RESULT 13
 ID RYNR_PIG STANDARD; PRT; 5035 AA.
 AC P16960;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-NOV-1995 (Rel. 32, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE RYANODINE RECEPTOR, SKELETAL MUSCLE (SKELETAL MUSCLE CALCIUM RELEASE
 DE CHANNEL).
 GN RYR1 OR CRC.
 OS Sus scrofa (Pig).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
 NX NCBI_TaxID=9823;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=NORWEGIAN LANDRACE; TISSUE=skeletal muscle;
 RX MEDLINE=93036581; PubMed=1329581;
 RA Harritz I., Kristensen T., Bosnes M., Kran S., Davies W.;
 RT "DNA sequence of the skeletal muscle calcium release channel cDNA and
 RT verification of the Arg615->Cys615 mutation, associated with porcine
 RT malignant hyperthermia, in Norwegian landrace pigs."
 RL Ann. Genet. 23:395-402(1992).
 RN [2]
 RP SEQUENCE OF 1129-2801 FROM N.A.
 RA Brenig B.;
 RL Submitted (APR-1996) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 1129-2643 FROM N.A.
 RC STRAIN=GERMAN LANDRACE; TISSUE=Liver;
 RX MEDLINE=94117003; PubMed=8288238;
 RA Leeb T., Schmolzi S., Brem G., Brenig B.;
 RT "Genomic organization of the porcine skeletal muscle ryanodine
 RT receptor (RYR1) gene coding region 4624 to 7929."
 RL Genomics 18:349-354(1993).
 RN [4]
 RP SEQUENCE OF 4785-5035 FROM N.A.
 RX MEDLINE=91065640; PubMed=2174405;
 RA Harritz I., Chowdhary B., Thomsen P.D., Davies W., Kautman U.,
 RA Kran S., Gustavsson I., Christensen K., Haug J.G.;
 RT "Assignment of the porcine calcium release channel gene, a candidate
 RT for the malignant hyperthermia locus, to the 6p11-->q21 segment of
 RT chromosome 6."
 RL Genomics 8:243-248(1990).
 CC -1- FUNCTION: COMMUNICATION BETWEEN TRANSVERSE-TUBULES AND
 CC SARCOPLASMIC RETICULUM. CONTRACTION OF SKELETAL MUSCLE IS
 CC TRIGGERED BY RELEASE OF CA++ FROM SR FOLLOWING DEPOLARIZATION OF
 CC T-TUBULES.
 CC -1- SUBUNIT: HOMOTETRAMER (POTENTIAL).
 CC -1- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL IS MODULATED BY CA++,
 CC MG++, ATP, AND CALMODULIN.
 CC -1- MISCELLANEOUS: THE CALCIUM RELEASE CHANNEL ACTIVITY RESIDES IN THE
 CC C-TERMINAL REGION WHILE THE REMAINING PART OF THE PROTEIN
 CC CONSTITUTES THE 'FOOT' STRUCTURE SPANNING THE JUNCTIONAL GAP
 CC BETWEEN THE SR AND THE T-TUBULE. IT IS POSSIBLE THAT THE FOOT
 CC STRUCTURE INTERACTS WITH THE CYTOPLASMIC REGION OF THE
 CC DIHYDROPYRIDINE RECEPTOR.
 CC -1- MISCELLANEOUS: RYANODINE IS AN ALKALOID THAT BINDS TO THE
 CC CA-RELEASE CHANNEL IN JUNCTIONAL SR AND MODULATES ITS ACTIVITY.

FT REPEAT 956 1069 2.
 FT REPEAT 1345 1360 3 (INCOMPLETE).
 FT REPEAT 1373 1388 4 (INCOMPLETE).
 FT REPEAT 2726 2845 5.
 FT REPEAT 2846 2959 6.
 FT MOD_RRS 2843 2843 PHOSPHORYLATION (BY CAPK AND CGPK).
 FT MOD_RRS 3952 3952 PHOSPHORYLATION (POTENTIAL).
 FT MOD_RRS 4323 4323 PHOSPHORYLATION (POTENTIAL).
 FT SIMILAR 4628 4861 WITH ACHR-SUBUNIT TRANSMEMBRANE SEGMENTS
 M2 AND M3.
 FT CARBOHYD 3466 3466 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 3909 3909 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 3950 3950 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 4149 4149 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 4864 4864 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CONFLICT 2015 2015 E -> D (IN REF. 2).
 FT CONFLICT 3481 3485 MISSING (IN REF. 2).
 SQ SEQUENCE 5037 AA; 565238 MW; 4ABD87AA26697070 CRC64;

Query Match 12.4%; Score 69; DB 1; Length 5037;
 Best Local Similarity 21.1%; Pred. No. 92;
 Matches 26; Conservative 25; Mismatches 44; Indels 28; Gaps 4;

OY 9 LKELIEELVNTITONQASICNGSMWVSVN-----LTAGMYCALES--LINVSDS 56
 DB 522 LVELLASLRGNRANCAFLSTNLDVNSKLDRLASSGLELVYCVLIESPEVNLITQEN 581
 OY 57 AIQ-----RTQMLKALCSOKPAAGISERSRDTKRI-----VIOVKMLITVY 100
 DB 582 HIKETISLIDKHGRHKHKLVDVLCISLCVNGVAVRSNODLITNLLPGRLLIQTNLINIV 641
 OY 101 RGV 103
 DB 642 TSI 644

RESULT 15
 UBPS_YEAST STANDARD; PRT; 805 AA.
 AC P39944;
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-FEB-1995 (Rel. 32, Last annotation update)
 DE UBIQUITIN CARBOXYL-TERMINAL HYDROLASE 5 (EC 3.1.2.15) (UBIQUITIN
 DE THIOLESTERASE 5) (UBIQUITIN-SPECIFIC PROCESSING PROTEASE 5)
 DE (DEUBIQUITINATING ENZYME 5).
 GN UBPS OR YER144C.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
 OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
 OX NCBI_TaxID=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC MEDLINE=95176708; PubMed=7871889;
 RA Xiao M., Fontaine T., Yang M.;
 RT "UBP5 encodes a putative yeast ubiquitin-specific protease that is
 RL related to the human Tre-2 oncogene product.";
 RL Yeast 10:1497-1502(1994).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=S288C / AB972;
 RA Dietrich F.S., Mulligan J.T., Hennessey K.M., Allen E., Araujo R.,
 RA Aviles E., Berno A., Brennan T., Carpenter J., Chen E., Cherry J.M.,
 RA Chung E., Duncan M., Guzman E., Hartzell G., Hunnicke-Smith S.,
 RA Hyman R., Kayser A., Komp C., Lashkari D., Lew H., Lin D.,
 RA Moseedale D., Nakahara K., Namath A., Norgren R., Oelner P., Oh C.,
 RA Petel F.X., Roberts D., Schl P., Schramm S., Shogren T., Smith V.,
 RA Taylor P., Wei Y., Yellon M., Botstein D., Davis R.W.;
 RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: UBIQUITIN C-TERMINAL THIOLESTER + H(2)O =,
 CC -1- UBIQUITIN + A THIOI.
 CC -1- SIMILARITY: BELONGS TO PEPTIDASE FAMILY C19; ALSO KNOWN AS

CC FAMILY 2 OF UBIQUITIN CARBOXYL-TERMINAL HYDROLASES.
 CC -----
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
 CC the European Bioinformatics Institute. There are no restrictions on its
 CC use by non-profit institutions as long as its content is in no way
 CC modified and this statement is not removed. Usage by and for commercial
 CC entities requires a license agreement. (See <http://www.isb.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC -----
 CC EMBL: U10082; AAC48928.1; -;
 CC EMBL: U18917; AAB64671.1; -;
 CC MEROPS: C19.006; -;
 CC SGD: S0000946; UBPS.
 CC InterPro: IPR001394; -;
 CC InterPro: IPR001763; -;
 CC Pfam: PF00581; Rhodanese; 1.
 CC Pfam: PF00442; UCH-1; 1.
 CC Pfam: PF00443; UCH-2; 1.
 CC PROSITE: PS00972; UCH-2_1; 1.
 CC PROSITE: PS00973; UCH-2_2; 1.
 CC PROSITE: PS0235; UCH-2_3; 1.
 CC Ubiqutin conjugation: Hydrolase: Thiol protease; Multigene family.
 FT ACT_SITE 455 455 BY SIMILARITY.
 FT ACT_SITE 753 753 BY SIMILARITY.
 FT ACT_SITE 761 761 BY SIMILARITY.
 SQ SEQUENCE 805 AA; 92260 MW; 884054A66370DEF7 CRC64;

Query Match 12.2%; Score 68; DB 1; Length 805;
 Best Local Similarity 22.5%; Pred. No. 13;
 Matches 25; Conservative 22; Mismatches 44; Indels 20; Gaps 4;
 OY 6 SPTLKEIEELVNTITONQASICNGSMWVSNTLAGMYCALESILINVSDC-----SAI 58
 DB 415 SPRIRPLPQD--NLSSRQIILNLSQVLDLDLIV-----LENGNCCYMANCIQCL 464
 OY 59 QRTQMLKALCSOKPAAGISERSRDTKRIEVLQVKNLITVYRGVYRGNF 109
 DB 465 VGTNLDVRFMLDVTYLNFINFSSRGSK---GLAKNFALLVNMHRHGA 512

Search completed: May 14, 2001, 06:02:12
 Job time: 43369 sec

GenCore version 4.5
Copyright (c) 1993 - 2000 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: May 14, 2001, 06:01:15 ; Search time 133.94 Seconds
(without alignments)
96.259 Million cell updates/sec

Title: US-09-451-527-105
Perfect score: 556
Sequence: 1 SPVTPSPFLKELIELVNIT.....QLVKNLLTYVRGVYRHGNFR 110

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

SPTREMBL15:*
1: sp_archaea:*
2: sp_bacteria:*
3: sp_fungi:*
4: sp_human:*
5: sp_invertebrate:*
6: sp_mammal:*
7: sp_mnc:*
8: sp_organelle:*
9: sp_phase:*
10: sp_plant:*
11: sp_protist:*
12: sp_unclassified:*
13: sp_vertebrate:*
14: sp_virus:*

pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	ID	Description
1	545.5	98.1	131	6 Q9N0W9	Q9N0W9 canis famil
2	316	56.8	114	6 Q9TV84	Q9TV84 bos taurus
3	87.5	15.7	49	4 Q9UDC7	Q9UDC7 homo sapien
4	80	14.4	275	6 Q28609	Q28609 oryctolagus
5	73.5	13.2	415	8 Q9MUM4	Q9MUM4 mesostigma
6	73.5	13.2	607	10 Q9SI43	Q9SI43 arabidopsis
7	72.5	13.0	150	14 Q98779	Q98779 vesicular s
8	72.5	13.0	438	10 Q9M3H8	Q9M3H8 cicer ariet
9	72.5	13.0	1763	11 Q9JKX5	Q9JKX5 mus musculus
10	72	12.9	5038	4 Q9NPK1	Q9NPK1 homo sapien
11	71.5	12.9	150	14 Q98791	Q98791 vesicular s
12	71	12.8	155	11 Q9RIG1	Q9RIG1 rattus norv
13	71	12.8	589	5 Q96661	Q96661 trypanosoma
14	71	12.8	649	4 O10619	O10619 helicoverpa
15	70.5	12.7	150	14 Q98780	Q98780 vesicular s
16	70.5	12.7	150	14 Q98787	Q98787 vesicular s
17	70.5	12.7	150	14 Q98789	Q98789 vesicular s
18	70.5	12.7	1811	14 Q36184	Q36184 plautia sta
19	70	12.6	482	9 Q36165	Q36165 bacterioph

20	70	12.6	1448	5 Q9N949	Q9N949 trypanosoma
21	70	12.6	1510	5 Q9VX92	Q9VX92 drosophila
22	69.5	12.5	274	14 Q89048	Q89048 vesicular s
23	69.5	12.5	1520	4 Q15087	Q15087 homo sapien
24	69.5	12.5	1781	4 Q9UKX0	Q9UKX0 homo sapien
25	69.5	12.5	1890	4 Q9UKW3	Q9UKW3 homo sapien
26	69.5	12.5	2073	4 Q9UKW2	Q9UKW2 homo sapien
27	69	12.4	1128	6 P79271	P79271 sus scrofa
28	69	12.4	5035	6 Q29105	Q29105 sus scrofa
29	68	12.2	198	4 Q9UBH1	Q9UBH1 homo sapien
30	68	12.2	1448	5 Q9N946	Q9N946 trypanosoma
31	67.5	12.1	150	14 Q98778	Q98778 vesicular s
32	67.5	12.1	2626	11 Q9Z1N3	Q9Z1N3 rattus norv
33	67	12.1	815	5 Q9W3N6	Q9W3N6 drosophila
34	67	12.1	837	5 Q9NFR8	Q9NFR8 drosophila
35	67	12.1	1102	11 Q9JHG7	Q9JHG7 mus musculus
36	66.5	12.0	350	14 Q9Q8P4	Q9Q8P4 myxoma viru
37	66.5	12.0	471	14 Q70156	Q70156 human immun
38	66.5	12.0	1112	10 Q9SSP2	Q9SSP2 arabidopsis
39	66	11.9	398	5 Q45966	Q45966 caenorhabdi
40	65.5	11.8	150	14 Q98790	Q98790 vesicular s
41	65.5	11.8	478	2 Q9KXF0	Q9KXF0 escherichia
42	65.5	11.8	478	9 Q9MCT4	Q9MCT4 bacterioph
43	65.5	11.8	483	9 Q9T1M4	Q9T1M4 bacterioph
44	65	11.7	284	2 Q9XBM2	Q9XBM2 acidaminoco
45	65	11.7	300	10 Q9SLJ6	Q9SLJ6 arabidopsis

ALIGNMENTS

RESULT 1

Q9N0W9
ID Q9N0W9 PRELIMINARY; PRT; 131 AA.
AC Q9N0W9;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE INTERLEUKIN-13.
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RA Yang S., Boroghs K.L., McDermott M.J.;
RT "Canine Interleukin-13: Molecular Cloning of Full-length cDNA and
Expression of Biologically Active Recombinant Protein.";
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF244915; AAF63204.1; -
SQ SEQUENCE 131 AA; 14268 MW; 9A142BAD0F80370F CRC64;

Query Match 98.1%; Score 545.5; DB 6; Length 131;
Best Local Similarity 99.1%; Pred. No. 3.8e-53;
Matches 110; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 SPVTPSPFLKELIELVNITQOASLCNSGWSVNLTAGMYCAALESINSDCSAIQR 60
|||||

Db 21 SPVTPSPFLKELIELVNITQOASLCNSGWSVNLTAGMYCAALESINSDCSAIQR 80
|||||

Qy 61 TQMLKALCSQKPAAG-ISSRSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 110
|||||

Db 81 TQMLKALCSQKPAAG-ISSRSRDTKIEVIQLVKNLLTYVRGVYRHGNFR 131
|||||

RESULT 2

Q9TV84 PRELIMINARY; PRT; 114 AA.

ID Q9TV84

AC Q9TV84;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE INTERLEUKIN-13 PRECURSOR (FRAGMENT).
IL-13.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Trigona W.T., Hlirano A., Brown W.;
RT "Biological activities of interleukin-13 (IL-13) on bovine
T lymphocytes: implications for signaling through IL-13R1.";
RL Submitted (JUN-1998) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF072807; AAD22748.1; -
DR HSSP: P35225; 31TR.
DR INTERPRO: IPR001325; -
DR PROSITE: PS00838; INTERLEUKIN_4_13; UNKNOWN_1.
FT NON_TER 114 114
SQ SEQUENCE 114 AA; 12355 MW; D8CC565627D030A CRC64;

Query Match 56.8%; Score 316; DB 6; Length 114;
Best Local Similarity 71.0%; Pred. No. 1.1e-27;
Matches 66; Conservative 10; Mismatches 15; Indels 2; Gaps 2;

OY 1 SPVTSPTLKELELVNTQNO-ASLCGNSWWSVNLTAGWCALESILNVDCAIO 59
DB 21 SEVPATLKELELVNTQNOKVPLCGNSWWSVNLTSWYCALDLSISNCSVIO 80
OY 60 RTORMKALCSQKPA-A-GISSESRPTKIEVIO 91
DB 81 RTKRMNLALCPHKPSAKOVSEVYRDTKIEVAD 113

RESULT 3
O9UDC7 PRELIMINARY; PRT; 49 AA.

ID O9UDC7;
AC O9UDC7;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE P600 HOMOLOG.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=93027259; PubMed=1408833;
RT Morgan J.G., Doljanov G.M., Robbins S.E., Hinton L.M., Lovett M.;
RT "The selective isolation of novel cDNAs encoded by the regions
surrounding the human Interleukin 4 and 5 genes.";
RL Nucleic Acids Res. 20:5173-5179(1992).
DR HSSP: P35225; 31TR.
SQ SEQUENCE 49 AA; 5109 MW; 679CD23A190C778E CRC64;

Query Match 15.7%; Score 87.5; DB 4; Length 49;
Best Local Similarity 71.4%; Pred. No. 0.011;
Matches 20; Conservative 1; Mismatches 6; Indels 1; Gaps 1;

OY 2 PVPSPTELELELVNTQNO-ASLGN 28
DB 22 PVPSTALRELELSNITQTKAPLGN 49

RESULT 4
O28609 PRELIMINARY; PRT; 275 AA.
AC O28609;
DT 01-NOV-1996 (TREMBLrel. 01, Created)
DT 01-NOV-1996 (TREMBLrel. 01, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)

DE PUTATIVE PREPROSPERMINGEN PRECURSOR.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=NEW ZEALAND WHITE; TISSUE=TESTIS;
RX MEDLINE=94368861; PubMed=8086468;
RA Richardson R.T., O'Rand M.G.;
RT "Cloning and sequencing of cDNAs for rabbit preproacrosin and a novel
preproacrosin-related cDNA.";
RL Biochim. Biophys. Acta 1219:215-218(1994).
DR EMBL: U05203; AAA61629.1; -
DR HSSP: P00734; 2HNT.
DR INTERPRO: IPR001254; -
DR PFAM: PF00089; trypsin_1.
DR PROSITE: PS00134; TRYPSIN_HIS; UNKNOWN_1.
KW signal.
FT SIGNAL 1 16 POTENTIAL.
FT CHAIN 17 275 PROSPERMINGEN.
SQ SEQUENCE 275 AA; 29965 MW; 8FC2467414069C61 CRC64;

Query Match 14.4%; Score 80; DB 6; Length 275;
Best Local Similarity 32.3%; Pred. No. 0.53;
Matches 20; Conservative 11; Mismatches 25; Indels 6; Gaps 2;

OY 5 PSPTELELELVNTQNOASLCGNSWWSVNLTAGWCALESILNVDCAIORGM 64
DB 190 PSPPLMARVDLNL-----ELCNSWYNGRITASNLCAGTSP-GKIDTQRIQOLVEV 243
OY 65 LK 66
DB 244 LK 245

RESULT 5
O9UM04 PRELIMINARY; PRT; 415 AA.

ID O9UM04;
AC O9UM04;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE PUTATIVE PLASTID DIVISION PROTEIN.
GN FTSW...
OS Mesostigma viride.
OC Chloroplast.
OC Eukaryota; Viridiplantae; Chlorophyta; Prasinophyceae;
OC Chlorodendraceae; Mesostigmataceae; Mesostigma.
OX NCBI_TaxID=41882;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=20150907; PubMed=10688199;
RA Lemieux C., Oltis C., Turmel M.;
RT "Ancestral chloroplast genome in Mesostigma viride reveals an early
branch of green plant evolution.";
RL Nature 403:649-652(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Lemieux C., Oltis C., Turmel M.;
RL Submitted (JUL-1999) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF166114; AAF43874.1; -
KW Chloroplast.
SQ SEQUENCE 415 AA; 46813 MW; E35116E992EC782 CRC64;

Query Match 13.2%; Score 73.5; DB 8; Length 415;
Best Local Similarity 28.7%; Pred. No. 4.5;
Matches 27; Conservative 19; Mismatches 29; Indels 19; Gaps 4;
OY 16 LVNTQNOASLCGNSWWSVNLTAGWCALESILNVDCAIO-----ORTORMKAL 68
DB 16 LVNTQNOASLCGNSWWSVNLTAGWCALESILNVDCAIO-----ORTORMKAL 68

Db 188 LIQPNLSTASLC-GAILIWLVALTAGIHWFYLSILSIGAVTALISLGSQEQYQORRIISFL 246
QY 69 CSQKPAAGTSSRSRDTKTEVIOVLVKNLLTYVRG 102
Db 247 ---NPWANPTSIG-----YOLVQSLLAVGSG 269
RESULT 6
Q9SI143 ID Q9SI143 PRELIMINARY; PRT; 607 AA.
AC Q9SI143;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE PUTATIVE METHYLMALONATE SEMI-ALDEHYDE DEHYDROGENASE.
GN AT2G14170.
OS Arabidopsis thaliana (Mouse-ear cross).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;
OC Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblum T.V.,
RA Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Moffat K.S.,
RA Cronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,
RA Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,
RA Copenhaver G.P., Preuss D., Nierman W.C., White O., Eisen J.A.,
RA Salzberg S.L., Fraser C.M., Venter J.C.;
RT "Sequence and analysis of chromosome II of Arabidopsis thaliana";
RL Nature 402:761-768 (1999).
DR EMBL: AC007197; AAD25855.1; -
DR HSSP: P56533; 1A4S.
DR INTERPRO: IPR001064; -
DR INTERPRO: IPR002086; -
DR PFAM: PF00171; aldedh; 1.
DR PROSITE: PS00070; ALDEHYDE DEHYDR. CYS; UNKNOWN.1.
DR PROSITE: PS00225; CRYSTALLIN. BETAGAMMA; UNKNOWN.1.
SQ SEQUENCE 607 AA; 65926 MW; 0257A3606B31165C CRC64;
Query Match 13.2%; Score 73.5; DB 10; Length 607;
Best Local Similarity 26.4%; Pred. No. 7;
Matches 23; Conservative 16; Mismatches 31; Indels 17; Gaps 4;
QY 39 AGMYCALESINVSDCSA-----IORTQMLKALCSQKPAAGTSSRSRDTKTEVIOVLV 93
Db 387 AGORCMALSTVVFVGDASKWEDKLVERA-KALKVTCGSEPDADLGPVISOAKERICRLI 445
QY 94 KN-----LLTVVRGV---YRHGNF 109
Db 446 QSGVDGCAKLLLDGRDIVVPGYKGNF 472
RESULT 7
Q98779 ID Q98779 PRELIMINARY; PRT; 150 AA.
AC Q98779;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DE 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0888CRB;
RX MEDLINE=97075113; PubMed=8917539;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;

RT "Ecological factors rather than temporal factors dominate the
RL evolution of vesicular stomatitis virus.";
DR Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL: U39211; AAB50939.1; -
DR INTERPRO: IPR000224; -
DR PFAM: PF00922; Phosphoprotein; 1.
FT NON_TER 1 150
FT NON_TER 150 150
SQ SEQUENCE 150 AA; 16711 MW; 16D11C4E8E8A65E7 CRC64;
Query Match 13.0%; Score 72.5; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 1.8;
Matches 29; Conservative 20; Mismatches 40; Indels 31; Gaps 6;
QY 2 PVTSPSTLKEIEEL-----VNITQQA-----SLCNGSMVWSYN-----LTAGMY 42
Db 14 PSWTQPVKENGERSLSLFFPVGLTQVTEQWKKTETVCSSKYWNLSQEQIVTSG-N 72
QY 43 CAALESINVSDCSAIQTQMLKALCSQKPAAGTSSRSR-----DTKIEVIOVLV 93
Db 73 CLILRGQVMTSDCSSAKSQNSRQS--SESPSPNSPEHASRASASPNLWDFKTEVQLI 130
RESULT 8
Q9M3H8 ID Q9M3H8 PRELIMINARY; PRT; 438 AA.
AC Q9M3H8;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE PUTATIVE UDP-GLYCOSE (FRAGMENT).
OS Cicer arietinum (Chickpea) (Garbanzo).
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
OC Fabales; Fabaceae; Papilionoideae; Cicer.
OX NCBI_TaxID=3827;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. CASTELLANA; TISSUE=ETIOLATED EPICOTYLS;
RA Dopico B., Munoz F.J., Labrador E.;
RT "A putative UDP-Glycose: Flavonoid glycosyltransferase is expressed in
RT chickpea epicotyls.";
RL Submitted (APR-2000) to the EMBL/GenBank/DDBJ databases.
DR EMBL: AJ400861; CAB88666.1; -
FT NON_TER 1 1
SQ SEQUENCE 438 AA; 48662 MW; 0BB7B805BD66E27C CRC64;
Query Match 13.0%; Score 72.5; DB 10; Length 438;
Best Local Similarity 26.1%; Pred. No. 6.2;
Matches 35; Conservative 20; Mismatches 48; Indels 31; Gaps 6;
QY 2 PVTSPSTLKEIEELVN-----ITONQASL-----CNGSMVWSYNLTAGMYC 43
Db 136 PIKSPGFEARLEPLVEAEKSGHGVIVNSFAELDEGYEYENLTGRKVVHVPSTSLMK 195
QY 44 AALESINVSDCSAIQTQMLKALCSQKPA-----GISSESRDTKIEV---IQLVK 94
Db 196 TTLEKTDNISNGSSTK--HKCLTLDLTREPSVVVYISFGSLCSLNDQLLELAKGEASK 253
QY 95 NLLTVVRGVYRHGN 108
Db 254 HQFLWV--VHRKGD 265
RESULT 9
Q9JXX5 ID Q9JXX5 PRELIMINARY; PRT; 1763 AA.
AC Q9JXX5;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

```
DE HISTONE ACETYLTRANSFERASE QUERKOPF.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=BRAIN;
RA Thomas T., Voss A.K., Chowdhury K., Gruss P.;
RT "Querkerpfl, a Myrist family histone acetyltransferase, is required for
RT normal cerebral cortex development."
RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
DR EMBL: AF222800; AAF26744.1; -
KW Transferase
SQ SEQUENCE 1763 AA; 196879 MW; 3A570C624B8094B0 CRC64;

Query Match 13.0%; Score 72.5; DB 11; Length 1763;
Best Local Similarity 31.5%; Pred. No. 31;
Matches 23; Conservative 11; Mismatches 34; Indels 5; Gaps 3;

QY 20 TONQASLNGSMWVSNTAGYCALESJLWVS-DCSAIORTQMLKALCSQKPAAGIS 78
DB 1390 SONS--CSYSLRTSSNLTQNS-CAVTQGMNSISGSCMLQOTSISSPPTCSVKSPQGCV 1445
QY 79 SERSDRTKIEVIQ 91
DB 1446 VERPPSSQOLAQ 1458

RESULT 10
Q9NPK1 PRELIMINARY; PRT; 5038 AA.
AC Q9NPK1;
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)
DE SKELETAL MUSCLE RYANODINE RECEPTOR.
GN RYR1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=96299657; PubMed=8661021;
RA Phillips M.S., Fujii J., Khanna V.K., Deleon S., Yokobata K.,
RA de Jong P.J., MacLennan D.H.;
RT "The structural organization of the human skeletal muscle ryanodine
RT receptor (RYR1) gene."
RL Genomics 34:24-41(1996).
DR EMBL: U48508; AAC51191.1; -
DR EMBL: U48449; AAC51191.1; JOINED.
DR EMBL: U48450; AAC51191.1; JOINED.
KW Receptor.
SQ SEQUENCE 5038 AA; 565171 MW; 1CEFC2C30B17879F9 CRC64;

Query Match 12.9%; Score 72; DB 4; Length 5038;
Best Local Similarity 21.1%; Pred. No. 1.2e+02;
Matches 26; Conservative 26; Mismatches 43; Indels 28; Gaps 4;

QY 9 LKELIELVNTONQASLNGSMWVSNTAGYCALES-LLWSDCS 56
DB 521 LKELIASLNGSRNCAFLSTNDMLVSKDRLEASSGILEVLYVLESPEVLIITQEN 580
QY 57 AIQ-----RTQRMKALCSQKPAAGISSERSDPTKIE-----VIOLVKNLLTV 100
DB 581 HIKSIISLDKHNHKKVLDVLCISLCVGNVAVRSNODLITENLLPGRELLLIQTNLIN 640
QY 101 RGV 103
DB 641 TSI 643
```

```
RESULT 11
Q98791 PRELIMINARY; PRT; 150 AA.
AC Q98791;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1286CRB3;
RA MEDLINE=97075113; PubMed=8917539;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the
RT evolution of vesicular stomatitis virus."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL: U93223; AAB50951.1; -
DR INTERPRO: IPR000224; -
DR PFAM: PF00922; Phosphoprotein; 1.
FT NON_TER 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16577 MW; E3D1095B842ACFFD CRC64;

Query Match 12.9%; Score 71.5; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 2.3;
Matches 29; Conservative 18; Mismatches 42; Indels 31; Gaps 6;

QY 2 PYTPSTLIKELIEEL-----VNITQNA-----SICNSMWSVN-----LTGM 42
DB 14 PSWTQPVIKENGESRLSPPPGLTVQTEQMKKTIEIVCESSKYWNISECOIVISG-N 72
QY 43 CAALLESILWSDCSAIORTQMLKALCSQKPAAGISSERS 93
DB 73 CILIRQVWMTSDCSSAKSGN--SGSSSESPSPNSPEHARSASPNLMDLKFTEVQLI 130

RESULT 12
Q9RIG1 PRELIMINARY; PRT; 155 AA.
AC Q9RIG1;
DT 01-MAY-2000 (TREMBlrel. 13, Created)
DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE RYANODINE RECEPTOR TYPE 1 (FRAGMENT).
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=SKELETAL MUSCLE;
RA Martin C., Hyvelin J.-M., Chapman K.E., Marthan R., Ashley R.H.,
RA Savineau J.P.;
RT "Pregnant rat myometrial cells show heterogeneous ryanodine- and
RT caffeine-sensitive calcium stores."
RL Am. J. Physiol. 227:0-0(1999).
DR EMBL: AF112256; AAD4889.1; -
DR INTERPRO: IPR000699; -
DR PFAM: PF01365; RYDR_1TPR; 1.
FT NON_TER 1
FT NON_TER 155
SQ SEQUENCE 155 AA; 17476 MW; A774F50D4633F5EA CRC64;

Query Match 12.8%; Score 71; DB 11; Length 155;
```

Best Local Similarity 21.1%; Pred. No. 2.8;
Matches 26; Conservative 25; Mismatches 44; Indels 28; Gaps 4;

QY 9 LKELIEELVNIQTQASLNCNGSMVSVN-----LTAGMYCAALES--LINVSDCS 56
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 1 LYELLASLRGNRTNCALEFSTNLDVLVSKLDRLASSGILEVLYCVLIESPEVLNIQEN 60

QY 57 AIQ-----RTQMLKALCSOKPAAGISSERSRDTKIE-----VIOLVKNLLTYV 100
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 61 HKSIISLLDKGRNHKVLVDVLCVCGVAVRSNODLITENLLPGRELLQTNELNYV 120

QY 101 RGV 103
Db 121 TSI 123

RESULT 13
ID O96661 PRELIMINARY; PRT; 589 AA.
AC O96661;
DT 01-MAY-1999 (TREMBlrel. 10, Created)
DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
DT 01-JUN-2000 (TREMBlrel. 14, Last annotation update)
DE PF20 HOMOLOG.
GN TWDI.
OS Trypanosoma brucei.
OC Eukaryota; Euglenozoa; Kinetoplastida; Trypanosomatidae; Trypanosoma.
OX NCBI_TaxID=5691;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=427;
RA Hsu C.B., Lin Y.T., Huang J.D.;
RT "A novel gene encoding a protein with WD40 repeat and leucine zipper motifs from Trypanosoma brucei."
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF101480; AAC83819.1;
DR INTERPRO: IPR001680;
DR PFAM: PF00400; WD40; 7.
DR PRINTS: PR00320; GPROTEINBRPT.
DR PROSITE: PS00678; WD_REPEATS; UNKNOWN.4.
SQ SEQUENCE 589 AA; 65481 MW; 2053B920666F51BF CRC64;

Query Match 12.8%; Score 71; DB 5; Length 589;
Best Local Similarity 22.9%; Pred. No. 13;
Matches 24; Conservative 23; Mismatches 40; Indels 18; Gaps 3;

QY 14 BELVNIQTQASLNCNGSMVSVNLTAGMYCAALESLINVSDCSA-----IQTQML 65
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 456 DKTVSLWDVRNCCSQTLYGHRNAVQSV--TVVGPTTNVATCDADGVVLMWDMTRMEQHL 513

QY 66 KALCSOKPAAGISSER-----SRDTKIEVIQLVKNLLTYVVG 102
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 514 TVACGPGYFANHIASDRNGHYLLVSSDDTNIKLIDVTKSVTVTLVG 558

RESULT 14
ID O10619 PRELIMINARY; PRT; 649 AA.
AC O10619; Q82480;
DT 01-JUL-1997 (TREMBlrel. 04, Created)
DT 01-JUL-1997 (TREMBlrel. 04, Last sequence update)
DT 01-NOV-1998 (TREMBlrel. 08, Last annotation update)
DE IMMEDIATE EARLY PROTEIN 1.
GN IEL.
OS Helicoverpa zea nuclear polyhedrosis virus.
OC Viruses; dsDNA viruses, no RNA stage; Baculoviridae;
OC Nucleopolyhedrovirus.
OX NCBI_TaxID=10468;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ELKAR;
RX MEDLINE=95053907; PubMed=7964631;

RA Cowan P., Bulach D., Goodge K., Robertson A., Tribe D.E.;
RT "Nucleotide sequence of the polyhedrin gene region of Helicoverpa zea single nucleocapsid nuclear polyhedrosis virus: Placement of the virus in lepidopteran nuclear polyhedrosis virus group II.";
RL J. Gen. Virol. 75:3211-3218(1994).
RN [2]
RP REVISIONS
RC STRAIN=ELKAR (ELCAR);
RA Le T.H., Wu T., Robertson A., Bulach D., Cowan P., Goodge K.,
RA Tribe D.;
RL Submitted (MAY-1997) to the EMBL/GenBank/DBJ databases.
DR EMBL: U67264; AAB54100.1;
SQ SEQUENCE 649 AA; 75522 MW; B0D133AC9FEBD0E4 CRC64;

Query Match 12.8%; Score 71; DB 14; Length 649;
Best Local Similarity 24.3%; Pred. No. 14;
Matches 26; Conservative 18; Mismatches 33; Indels 30; Gaps 3;

QY 1 SPVTPSP-----TLKELIEELVNIQTQASLNCNGSMVSVNLTAGMYCAALES 48
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 97 SPIAMSPQRIPTRSERSENVIETSLSPESLSLKQVTVSLRRGS-----GLYGNKIQN 147

QY 49 LIN-----VSDCSAIQRTQMLKALCSOKPAAGISSERSRDTK 86
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 148 LKENYKTMDPYEDSSSLPTPKPKRSNTKTIAGVGEKRSKREK 194

RESULT 15
ID Q98780 PRELIMINARY; PRT; 150 AA.
AC Q98780;
DT 01-FEB-1997 (TREMBlrel. 02, Created)
DT 01-FEB-1997 (TREMBlrel. 02, Last sequence update)
DT 01-MAY-2000 (TREMBlrel. 13, Last annotation update)
DE PHOSPHOPROTEIN (FRAGMENT).
OS Vesicular stomatitis virus.
OC Viruses; ssRNA negative-strand viruses; Mononegavirales;
OC Rhabdoviridae; Vesiculovirus.
OX NCBI_TaxID=11276;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=0986CRB2;
RX MEDLINE=97075113; PubMed=8917539;
RA Rodriguez L.L., Fitch W.M., Nichol S.T.;
RT "Ecological factors rather than temporal factors dominate the evolution of vesicular stomatitis virus."
RL Proc. Natl. Acad. Sci. U.S.A. 93:13030-13035(1996).
DR EMBL: U39212; AAB50940.1;
DR INTERPRO: IPR000224;
DR PFAM: PF00922; Phosphoprotein; 1.
FT NON_TER 1
FT NON_TER 150
SQ SEQUENCE 150 AA; 16611 MW; E3D1095B8E8A65FD CRC64;

Query Match 12.7%; Score 70.5; DB 14; Length 150;
Best Local Similarity 24.2%; Pred. No. 3;
Matches 29; Conservative 18; Mismatches 42; Indels 31; Gaps 6;

QY 2 PVTPSPTLKELIEEL-----VNITQNA-----SLCNGSMVSVN-----LTAGMY 42
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 14 PSWTQPIKENGERSLSLFPVGLTQVTEQWKKTIVTCESSKYWNLSQVITSG-N 72

QY 43 CAALESINVSDCSAIQRTQMLKALCSOKPAAGISSERSR-----DTKIEVIQIV 93
| | | | : : : : | : : : : | : : : : | : : : : | : : : :
Db 73 CLILRGVMTSDCSSAKSQN--SQSSSESPSPNSPEHASRASASPNLWDFKFTVQLI 130

Search completed: May 14, 2001, 06:01:18
Job time: 43961 sec

